



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 163902

TO: Delia Ramirez
Location: 2d74 / 2c70
Art Unit: 1652
Monday, August 29, 2005

Case Serial Number: 09371347

From: Noble Jarrell
Location: Biotech-Chem Library
Rem 1B71
Phone: 272-2556

Noble.jarrell@uspto.gov

Search Notes

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RESULT 2
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 ACCESSION AX050463
 VERSION AX050463.1 GI:12226668
 KEYWORDS
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 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 Johnson, W.G. and Stenroos, B.S.
 Methods for diagnosing, preventing, and treating developmental
 disorders due to a combination of genetic and environmental factors
 Patent: WO 0071754-A 23 NOV-2000;
 University of Medicine and Dentistry of New Jersey (US)
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ORIGIN

Query Match 100.0%; Score 2097; DB 6; Length 3259;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2097; Conservative 0;

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DEFINITION cds.
ACCESSION AF121214
VERSION AF121214.1 GI:6561338
KEYWORDS

SOURCE Homo sapiens (human)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 3291)
REFERENCE
AUTHORS Leclerc,D., Odievre,M., Wu,Q., Wilson,A., Huizenga,J.J., Rozen,R.,
Scherer,S.W. and Gravel,R.A.
TITLE Molecular cloning, expression and physical mapping of the human
methionine synthase reductase gene
JOURNAL Gene 240 (1), 75-88 (1999)
MEDLINE 20033550
PUBMED 10564814
REFERENCE
AUTHORS Leclerc,D., Odievre,M.-H., Wu,Q., Wilson,A., Huizenga,J.J.,
Johns,T., Shoubiridge,B.A., Rosenblatt,D.S., Scherer,S.W., Rozen,R.
and Gravel,R.A.
TITLE Direct Submission
JOURNAL Submitted (18-JAN-1999) Human Genetics, Montreal Children's
Hospital, 4060 Ste-Catherine West, Montreal, Quebec H3Z 2Z3, Canada
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ORIGIN

Query Match 100.0%; Score 2097; DB 9; Length 3991;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 661 ATTGAAGCTTTGAGTCTCTCACTTACCCGTTGGTACCCCACTCTCAAGCTCTCTG 720
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RESULT 5

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LOCUS CQ726091 Sequence 12025 from Patent WO02068579.
ACCESSION CQ726091
VERSION CQ726091.1 GI:42288134
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
Patent: WO 02068579-A 12025 06-SEP-2002;
JOURNAL
PE Corporation
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BC054816
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methyltransferase reductase, mRNA (cdna clone IMAGB:5205285),
partial cds.
BC054816
VERSION
KEYWORDS
SOURCE
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Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Altschul,S.F., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heib,F.,
Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Scapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Schaefer,T.E., Brownstein,M.J., Ueda,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
Mokernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.U., Hulyk,S.W.,
Villalón,D.K., Wuzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Faney,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bonifard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywicki,M.I., Skalska,U., Smailus,D.E.,
Scherer,A., Schein,J.B., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Strausberg,R.
AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
DIRECT SUBMISSION
Submitted (03-JUL-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed By: The I.M.A.G.E. Consortium (ULNL)

DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgti.nih.gov
Ahter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bonifard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlén,E., Kwong,P., Latic,P., Legaspi,R.,
Maduro,O.L., Masello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stenitrop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ULNL at: <http://image.llnl.gov>
Series: IRK Plate: 115 Row: d Column: 11
This clone was selected for full length sequencing because it
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Matches 2094; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 53 ATGAGAGAGTTCTGTTACTATATGCTACACAGAGGAGAGAGAGAGAGAGAGAGAG 112

61 GAAATGTGAGCAAGCTGTGATGATGATTTTCTGAGATCTTCACTGATATGATGA 120
113 GAAATGTGAGCAAGCTGTGATGATGATTTTCTGAGATCTTCACTGATATGATGA 172
121 TCCGATTAAGTATGATCTTAAACCGAAGACGCTCTTGTGTGTGTGTGTCTACACG 180
173 TCCGATTAAGTATGATCTTAAACCGAAGACGCTCTTGTGTGTGTGTGTCTACACG 232
181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
233 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 292
241 CTGCGGATGATTTCTTGTCTGACCTGCGGATGAGGTTCTGCGGATGATGAGAA 300
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301 TACACCTACTTTTGAAGTGGGGGAGATTAATTGATTAACGACTTCAAGAGCTTGAGCC 360
353 TACACCTACTTTTGAAGTGGGGGAGATTAATTGATTAACGACTTCAAGAGCTTGAGCC 412
361 CCGCATTTCTATGACCTGACATGCAAGATGATGATGATTTAAGCTTGTGTGTGAG 420
413 CCGCATTTCTATGACCTGACATGCAAGATGATGATGATTTAAGCTTGTGTGTGAG 472
421 CCGTGAATGCTGGAATCTGCGGACGCTCAGAAAGATTTTATGATCAAGAGAGACA 480
473 CCGTGAATGCTGGAATCTGCGGACGCTCAGAAAGATTTTATGATCAAGAGAGACA 532
481 GAGAGATTAAGTGGCGCACTCCGATGAGATCACTGATCTTGAAGAGACAGCTTGTG 540
533 GAGAGATTAAGTGGCGCACTCCGATGAGATCACTGATCTTGAAGAGACAGCTTGTG 592
541 AAGTCAGAGCTGTACATGATGATCTCAAGTCAAGCTTGTGATTCGATGATTCAGGA 600
593 AAGTCAGAGCTGTACATGATGATCTCAAGTCAAGCTTGTGATTCGATGATTCAGGA 652
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653 AGAAAGATTTCTGAGGTTTGAAGCAAAATGACAGTAAACAGCAACCAATCCATGTTGTA 712
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713 ATTGAAGACTTTGAGTCTCACTTACCCGTTCCGTTACCCCACTCTCAAGGCTCTCTG 772
721 AATATTCCTGTTTACCCCGAGAAATTTTACAGATCACTGAGAGAGTCTTTCGCCAG 780
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833 GAGGAAAGCAAGTATCTGATCTTGAAGATCCAGTTTTCATGTCCAATTTTCAAG 892
841 GCGATTCACCTTACTAGATGATGATCAATTAACCACTCTGCTGTAGAAATGAGCATTT 900
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1921 CTTCAGAGAGAGGCGCATTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
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1981 CATGATGCTCTGTGTAATTAATAGCAAGAGGTTGAGATTGAATACTTAAGAGCAATG 2040
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2041 AAAACCTGAGCACTTAAGAAAGAAAGCAAGTCAAGATTAATTTGTGATATA 2097
2093 AAAACCTGAGCACTTAAGAAAGAAAGCAAGTCAAGATTAATTTGTGATATA 2149

RESULT 7
BVI77620/c 2933 bp DNA linear STS 10-JUN-2004
LOCUS BVI77620 Human DNA (Sequenc) Homo sapiens STS genomic, sequence
DEFINITION tagged site.
ACCESSION BVI77620
VERSION BVI77620.1 GI:48013757
KEYWORDS STS.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 (bases 1 to 2933)
Nelson, R.M., Marnell, G., Kammerer, S., Hoyal, C.R., Shi, M.M.,
Cantor, C.R. and Braun, A.
TITLE Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
JOURNAL Genome Res. (2004) In press
COMMENT Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 2933.

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Query Match 63.8%; Score 1338; DB 11; Length 2933;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1778; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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375 CACTGACATGACAGATGACTGTGTAGGTTTGAACCTTGTGGTTGAGCCGTGATTCGTGG 434
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2486 GTTCCTCACTTACCGGTTGGTATACCCCACTCTCGAAGAGCTCTCGAATATTCCTGGTTT 2427
735 ACCCCAGAAATATTTACAGTATCATCTGACAGAGTCTCTTGGCCAGAGAAAGCAAGT 794
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795 ATCTGTGACTTCAGAGATTCAGATTTTCAAGTGCATTTCAAAAGGAGTTCAACTTAC 854
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855 TACGAATATGTCATTAATAACCACTGTGCTGTGAATTTGACATTTCAATTAACAGATT 914
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2006 GCGAGCCCTTGTGAGATTAATACAGTACAGTGTGTAAGAAAGCGAGCTACAGAGCTGTG 1947
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1946 CAGTAAACAAGGGGACAGCCGATTAATAGCCCTTGTATACAGATGCTGTGCTTGTGTT 1887
1275 GAATCTCTCTCTGCTGCTTTCCTTCTTGCAGCAGCACTCATGTTCTCTGCTGAACATCT 1334
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1766 GCTCCATTTTGTCTTCAACATTTGTGTAATTTCTGTCTACTGACCAACAAGAGTTCGCG 1707
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1706 GAAAGGAGTATGTATACAGCTGTGCTGCTGCTTGTGTTGCTTCAAGTCTTCAAGCAAAAT 1647
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DB 1167 TCGAATAATATAGCAAGAGCTTGAGTTGAAAACTAGAGCAATGAAAAACCTGCGCA 1108
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RESULT 8
BV178010/c 2933 bp DNA linear STS 10-JUN-2004
LOCUS eqm97996 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
DEFINITION tagged site.
ACCESSION BV178010 GI:48014252
VERSION BV178010.1
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2933)
Nelson,R.M., Marnellloe,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
Cantor,C.R. and Braun,A.
Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
Genome Res. (2004) In press

JOURNAL
COMMENT
Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 2933.

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source Location/Qualifiers
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STS
ORIGIN
Query Match 63.8%; Score 1338; DB 11; Length 2933;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1778; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

DB 2546 GGTTTTGAACAAATATGACATGAAACGAACCAATCCAAATGTTAATTGAAACCTTGA 2487
QY 675 GTTCCTACTTACCCGTTGGGTACCCCACTTCAAGAGCTCTGTAATATTCCTGGTTT 734
DB 2486 GTTCCTACTTACCCGTTGGGTACCCCACTTCAAGAGCTCTGTAATATTCCTGGTTT 2427
QY 735 ACCCCAGAAATATTTACAGATCATCTGCAAGAGTCTCTTGGCCAGAGGAAAGCCAAAT 794
DB 2426 ACCCCAGAAATATTTACAGATCATCTGCAAGAGTCTCTTGGCCAGAGGAAAGCCAAAT 2367
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DB 2366 ATCTGTACTTACAGATCATCTGCAAGAGTCTCTTGGCCAGAGTCTCTTGGCCAGAGT 2307
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DB 1946 CAGTAAACAAAGGAGAGAGCTTATACCGCTTGTGAGAGAGTGTGCTGCTGCTTGT 1887
QY 1275 GATCTCTCTCTGCTGCTTCTCTCTCTGAGCAGCAGCAGTCTGCTCTGAGACATCT 1334
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DB 1826 TCTTAAACTTCAACCCAGACATATTCGTGACAGAGCTCAAGTTATTTCAACCCAGAAA 1767
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Qy 641 GCAACCAATCCAAATGTTGAATGAAGACTTTGAGTCTCACTTACCCGTCGGTACCCC 700
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RESULT 11
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DEFINITION Homo sapiens chromosome 5 clone CITB-H1_2018B2, complete sequence.
AC010346
VERSION AC010346.6 GI:11136705
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 109626)
JOURNAL DOB Joint Genome Institute and Stanford Human Genome Center.
REFERENCE
AUTHORS Unpublished
TITLE 2 (bases 1 to 109626)
JOURNAL DOB Joint Genome Institute.
REFERENCE
AUTHORS Direct Submission
TITLE DOB Joint Genome Institute.
JOURNAL Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Nov 10, 2000 this sequence version replaced gi:9256196.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
STS Content:
WI-9255 G05749.

FEATURES

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ORIGIN

Query Match 15.7%; Score 330; DB 9; Length 109626;
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Qy 461 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGACTCCGGTGGCATCACTGCAT 520
Db 88631 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGACTCCGGTGGCATCACTGCAT 88690

Qy 521 CCTTGAGCAGACCTTGTGAAGTCAGAGCTGCTACACATTAATCTCAAGTCGACCTTC 580
Db 88691 CCTTGAGCAGACCTTGTGAAGTCAGAGCTGCTACACATTAATCTCAAGTCGACCTTC 88750
Qy 581 TGAATTCATGATTCAGAGAAAGAGATTCGAGTTTGAAGCAAAATGCAGTAACA 640
Db 88751 TGAATTCATGATTCAGAGAAAGAGATTCGAGTTTGAAGCAAAATGCAGTAACA 88810
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Db 88811 GCAACCAATCCAAATGTTGAATGAAGACTTTGAGTCTCACTTACCCGTCGGTACCCC 88870
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Db 88871 CACTCTCACAAGCTCTCTGAATATTCCTGTTTACCCCAAGATATTTACAGTAATC 88930
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Db 88931 TGCAGAGTCTCTGGCCAGG 88951

RESULT 12
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LOCUS AC025174 110756 bp DNA linear PRI 28-MAR-2002
DEFINITION Homo sapiens chromosome 5 clone CTD-2072124, complete sequence.
AC025174
VERSION AC025174.5 GI:19774456
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 110756)
JOURNAL DOB Joint Genome Institute and Stanford Human Genome Center.
REFERENCE
AUTHORS Unpublished
TITLE 2 (bases 1 to 110756)
JOURNAL DOB Joint Genome Institute.
REFERENCE
AUTHORS Direct Submission
TITLE DOB Joint Genome Institute.
JOURNAL Submitted (07-MAR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 110756)
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 110756)
REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Mar 28, 2002 this sequence version replaced gi:19224767.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.

FEATURES

source
1. 110756
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2072124"

ORIGIN

Query Match 15.7%; Score 330; DB 9; Length 110756;
Best Local Similarity 99.7%; Pred. No. 1.3e-168;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 401 GTTTAGAACTTGTGTTGAGCCGTGATTCCTGAGCTTGGCCAGCCCTCAGAAACATT 460

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Db      20100 TTAGTCAAGCAGAGGACAAGAGAGATAGTGGCGACTCCGGTGGCATCACTTCAT 20159
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Db      20160 CCTCGAGAGACAGACCTTTGTGAAGTCAAGAGCTGCTACACATTGAATCTCAAGTCAGCTTC 20219
Qy      581 TGAATTCGATGATTCAGAAAGAAAGATTCGTGAGTTTGAAGCAAAAGCAGTGAACA 640
Db      20220 TGAATTCGATGATTCAGAAAGAAAGATTCGTGAGTTTGAAGCAAAAGCAGTGAACA 20279
Qy      641 GCAACCAATCCATGTGTGTAATTGAAAGACTTGACCTCACTTACCCTGCGTACCCC 700
Db      20280 GCAACCAATCCATGTGTGTAATTGAAAGACTTGACCTCACTTACCCTGCGTACCCC 20339
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Db      20340 CACTCTCAAGAGCTCTCTGAAATTCCTGGTTTACCCTCCAGAAATATTACAGGTACATC 20399
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RESULT 13
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LOCUS AC022921
DEFINITION Homo sapiens clone RP11-138P20, WORKING DRAFT SEQUENCE, 12
unorderd pieces.
ACCESSION AC022921.2 GI:7229868
VERSION HTG: HTGS PHASE1: HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 158199)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
JOURNAL Homo sapiens, clone RP11-138P20
TITLE Unpublished
COMMENT 2 (bases 1 to 158199)

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TITLE Direct Submission
JOURNAL Submitted (07-FEB-2000) Whitehead Institute/MIT Center for Genome
COMMENT Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 12, 2000 this sequence version replaced gi:6921909.
All repeats were identified using RepeatMasker.
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

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----- Project Information
Center project name: L6314
Center clone name: 138_P.20
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 152636 bases at least Q40
Consensus quality: 155474 bases at least Q30
Consensus quality: 156388 bases at least Q20
Insert size: 178000; agarose-fp
Insert size: 157099; sum-of-contigs
Quality coverage: 4.4 in Q20 bases; agarose-fp
Quality coverage: 5.0 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1 1283: contig of 1283 bp in length
1284 1383: gap of 100 bp
1384 4203: contig of 2820 bp in length
4204 4303: gap of 100 bp
4304 6786: contig of 2483 bp in length
6787 6886: gap of 100 bp
6887 9783: contig of 2797 bp in length
9784 12902: contig of 3119 bp in length
12903 13002: gap of 100 bp
13003 16429: contig of 3427 bp in length
16430 16529: gap of 100 bp
16530 25201: contig of 8672 bp in length
25202 25301: gap of 100 bp
25302 36759: contig of 11458 bp in length
36760 36859: gap of 100 bp
36860 53921: contig of 17062 bp in length
53922 54021: gap of 100 bp
54022 72054: contig of 18033 bp in length
72055 72154: gap of 100 bp
72155 102527: contig of 30373 bp in length
102528 102627: gap of 100 bp
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Qy	461										520
Db	83584										83643
Qy	521										580
Db	83644										83703
Qy	581										640
Db	83704										83763
Qy	641										700
Db	83764										83823
Qy	701										760
Db	83824										83883
Qy	761										820
Db	83884										83943

Search completed: August 27, 2005, 09:38:49
 Job time : 6013.21 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 23:18:31 ; Search time 4546.04 Seconds
(without alignments)
17558.328 Million cell updates/sec

Title: US-09-371-347A-1

Perfect score: 2097

Sequence: 1 atgagagaggttcgttact.....ttcagatatttgcataaa 2097

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hlc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_g881:*
9: gb_g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1592	75.9	3100	3	BC062577 Homo sapi
2	956	45.6	3143	3	BC035977 Homo sapi
3	719	34.3	908	5	BM801462 AGENCOURT
4	689	32.9	874	4	BM801462 AGENCOURT
5	623	29.7	646	7	CN260357 170004241
6	586	27.9	852	5	BM431497 AGENCOURT
7	565	26.9	565	1	AUT279788 AUT279788
8	543	25.9	877	1	AUT12440 AUT12440
9	531	25.3	1061	5	BQ218755 AGENCOURT
10	517	24.7	826	4	BI772430 60305786
11	512	24.4	776	6	CB997527 AGENCOURT
12	507	24.2	834	5	BU941078 AGENCOURT
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14	455	21.7	822	1	AU132586
15	448	21.4	591	2	AM965709 EST137782
16	446	21.3	818	6	CD559384 AGENCOURT
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18	431	20.6	974	5	BX375211 BX375211
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22	367	17.5	642	2	BF346446 602020302
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37	297	14.2	416	6	CB996520	AGENCOURT
38	292	13.9	528	2	BE301292	ba89B07.x
39	291	13.9	664	7	CR768694	DKF2P459K
40	291	13.9	667	7	CR770923	DKF2P469N
41	291	13.9	767	7	CR557482	DKF2P469K
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43	272	13.0	301	1	AL704780	DKF2P686M
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45	257	12.3	366	2	BF808461	QV1-C1017

ALIGNMENTS

RESULT 1	BC062577	3100 bp	mRNA	linear	HTC 25-NOV-2003
LOCUS	Homo sapiens	CDNA	clone IMAGE:5189058,	containing frame-shift errors.	
DEFINITION	BC062577.1	GI:36511756			
ACCESSION	BC062577				
VERSION	BC062577.1	GI:36511756			
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Strausberg, R.D., Collins, P.S., Wagner, L., Scheinen, C.M., Schlier, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhut, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, D., Hsieh, F., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshitsugu, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hilyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, B., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, K., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywicki, M.I., Skalska, U., Small, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99 (26),	16899-16903	(2002)	
PMID	12477932				
REFERENCE	2 (bases 1 to 3100)				
AUTHORS	Strausberg, R.				
TITLE	Direct Submision				
JOURNAL	Submitted (24-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgabs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc.				

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgcmhgrl.nih.gov
Ahter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.M., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietsch,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stancirpop,S., Thomas,P.J., Touchman,J.W.,
Tsuneon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAK Plate: 135 Row: e Column: 21
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA g1: 4505278
This clone has the following problem: frame shifted.

FEATURES

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172 GGTCTGGTATTCAGAAATACCTACTTTGCAATGCGGGAAGATATGTAACGA 221
343 CTTCAGAGCTTGAAGCCCGCATTTCTATGACACTGACATGACATGACTGTAGT 402
232 CTTCAGAGCTTGAAGCCCGCATTTCTATGACACTGACATGACATGACTGTAGT 291
403 TTGAACTTGTGTTGACCGTGAATGCTGACACTGCGCAGCCCTCAGAAACATTT 452
292 TTGAACTTGTGTTGACCGTGAATGCTGACACTGCGCAGCCCTCAGAAACATTT 351
463 AGGTCAAGCAGAGCAGAGAGATTAAGTGGCGCACTCCCGGTGCATCACTGATCC 522
352 AGGTCAAGCAGAGCAGAGAGATTAAGTGGCGCACTCCCGGTGCATCACTGATCC 411
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412 TCAGAGCAGACCTTGTGAAGTCAAGCTGTACACATTTGAATTCAGATTCAGCTTC 471
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643 AACCAATCCAAATGTTGAATTTGAAGATTTGAGTCTCACTTACCGGTGCGATCCCA 702
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Dd		1791	CAGGTGGCGAAMTCTCCTTCACAGAGAAGGCCATATTATGTGTGGAGATGCAGAA	1850
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Dd		1851	AATATGCCAAGATGTATCATGATGCCCTTGCGAAATAATMACCAAAGATTGAAGTT	1910
Oy		2023	GAAAAACTAGAACGAATGAACCTCGGCCCTTAAGAGAAAAGCAAGCTACTTCAG	2082
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Dd		1971	GATATTTTGTCATATA	1985
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ACCESSION	BC035977.1			GI:23243305
VERSION	HTC.			
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SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 3143)			
TITLE	Strausberg,R.			
JOURNAL	Direct Submission Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov			
COMMENT	Contact: MGC help desk Email: cgapbs-rt@mail.nih.gov Tissue Procurement: CLOUTTECH CDNA Library Preparation: CLOUTTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www.shgc.stanford.edu Contact: (Dickson, Mark) mcd@pacsl.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.			
FEATURES				
Source				
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 41 Row: g Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4505278 This clone has the following problem: frame shifted.			
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Dd	52 ATGAGAGAGTTCTGTTACTATATGCTACACAGCAGGACGCAAGGCAAGCCATGCGACA	111		

6	GAATGTGTGAGCAAGCTGTGTGATACATGAAATTTCTGACAGTCTTCACTGATTAAGCA	120
112	GAATATGTGTGACAGCTGTGTGTACATGAAATTTCTGACAGTCTTCACTGATTAAGCA	171
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232	GGCACCGGAGACCCACCCGACACAGCCCGCAATTTGTAAAGAAATACGAACCAACA	291
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301	TACACCTACTTTTGGCAATGGGGGGAGATTAATGATAAGATTCAGAGCTTGGAGCC	360
352	TACACCTACTTTTGGCAATGGGGGGAGATTAATGATAAGATTCAGAGCTTGGAGCC	411
361	CGGATTTCTATGACACTGGAACATGCAATGACCTGTGTAGTTTAAACCTTGGTGTAG	420
412	CGGATTTCTATGACACTGGAACATGCAATGACCTGTGTAGTTTAAACCTTGGTGTAG	471
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481	GAGAGATTAAGTGGCGACATCCCGGTGGCATCACCTGATCTTTGAGACAGACCTTGTG	540
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541	AAGTCAGAGCTGTACATTTGAATCTCAAGTGGAGCTTCTGAGATTCAGATTCAGGA	600
592	AAGTCAGAGCTGTACATTTGAATCTCAAGTGGAGCTTCTGAGATTCAGATTCAGGA	651
601	AGAAAGATTTCTGAGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCAAATGTGTGA	660
652	AGAAAGATTTCTGAGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCAAATGTGTGA	711
661	ATTGAAGACTTGAAGTCTCACTTACCCGTTGGTACCCCACTCTCAACAAGCTCTCTG	720
712	ATTGAAGACTTGAAGTCTCACTTACCCGTTGGTACCCCACTCTCAACAAGCTCTCTG	771
721	AATATTTCTGTTTACCCCGAATATTTTACAGTTAATCTGACAGAGTCTCTTGGCCAG	780
772	AATATTTCTGTTTACCCCGAATATTTTACAGTTAATCTGACAGAGTCTCTTGGCCAG	831
781	GAGAAAGCCCAAGATCTGTGACTTCAGACAGATCAATTTTTCAAGTCCCAATTTCAAG	840
832	GAGAAAGCCCAAGATCTGTGACTTCAGACAGATCAATTTTTCAAGTCCCAATTTCAAG	891
841	GCAGTCAACTTACTACGATGATGATCCATTAACCACTCTGCTGTGTAATTTGACATT	900
892	GCAGTCAACTTACTACGATGATGATCCATTAACCACTCTGCTGTGTAATTTGACATT	951
901	TCAAAATCAGACTTTTCTATCAGCTCGAGATGATCCCTTCAAGGATTCGATTCAGGT	960
952	TCAAAATCAGACTTTTCTATCAGCTCGAGATGATCCCTTCAAGGATTCGATTCAGGT	1011
961	GATTCTGAGGTACAAAGCTTACTCAAAAGCTGAGCTTGAAGATTAAGAGACATCTGC	1020
1012	GATTCTGAGGTACAAAGCTTACTCAAAAGCTGAGCTTGAAGATTAAGAGACATCTGC	1071
1021	GTCCTTTGAATTAAGGCGACACCAAGAGAAGG	1058
1072	GTCCTTTGAATTAAGGCGACACCAAGAGAAGG	1109

DEFINITION BX348674 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
ACCESSION BX348674
VERSION BX348674.1 GI:30375301
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 908)
AUTHORS Li, W. B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Creteil, CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3392.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0BA60062B02_CS00490_1&c=3392.f

FEATURES
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Location/Qualifiers
1..908
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 34.3%; Score 719; DB 5; Length 908;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

674 AGTCTGACCTTACCCGTTGGTACCCACCTTCAGAGCCCTCTGAATATTCCTGTT 733
28 AGTCTGACCTTACCCGTTGGTACCCACCTTCAGAGCCCTCTGAATATTCCTGTT 87
734 TACCCCGAGATATTTACAGTACATCTGACAGAGCTCTTGGCCAGAGAGAGCCAG 793
88 TACCCCGAGATATTTACAGTACATCTGACAGAGCTCTTGGCCAGAGAGAGCCAG 147
794 TATCTGACCTTACAGAGATTCAGATTTTCAAGGCCAATTTCAAGAGAGAGCCAGT 853
148 TATCTGACCTTACAGAGATTCAGATTTTCAAGGCCAATTTCAAGAGAGAGCCAGT 207
854 CTAGAGATGATGCAATTAACCACTCTGCTGTGATGATGATGATGATGATGATGAT 913
208 CTAGAGATGATGCAATTAACCACTCTGCTGTGATGATGATGATGATGATGATGAT 267
914 TTTTCTTACGCGCGGAGATGCGCTTCAAGCGGATGCGCTTCAAGAGATGATGATGAT 973
268 TTTTCTTACGCGCGGAGATGCGCTTCAAGCGGATGCGCTTCAAGAGATGATGATGAT 327
974 AAAGCTACTCTCAAGAGATGCACTGATTAAGATTAAGAGAGAGAGAGAGAGAGAG 1033
328 AAAGCTACTCTCAAGAGATGCACTGATTAAGATTAAGAGAGAGAGAGAGAGAGAG 387
1034 TAAAGGAG 1093
388 TAAAGGAG 447
1094 CTCTCAGGTCATTTTACCTGCTGTCTTGAATCCAGAGCAATTCCTTAAAGAGAGATTT 1153

DB 448 CTCTCAGGTCATTTTACCTGCTGTCTTGAATCCAGAGCAATTCCTTAAAGAGAGATTT 507
OY 1154 TGGAGCCCTTGGAGCTATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1213
DB 508 TGGAGCCCTTGGAGCTATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 567
OY 1214 GCAGTAACAG 1273
DB 568 GCAGTAACAG 627
OY 1274 TGGATCTCTCTCTGCTTCCCTTCTTGGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1333
DB 628 TGGATCTCTCTCTGCTTCCCTTCTTGGCAGCAGCAGCAGCAGCAGCAGCAGCAG 687
OY 1334 TTCTTAACCTTCAACAG 1392
DB 688 TTCTTAACCTTCAACAG 746

RESULT 4
BM801462
LOCUS BM801462
DEFINITION 5', mRNA sequence.
ACCESSION BM801462
VERSION BM801462.1 GI:19118285
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 874)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM12286 row: 1 column: 14
High quality sequence stop: 710.

FEATURES
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Location/Qualifiers
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/clone="IMAGE:5560477"
/issue_type="duodenal adenocarcinoma, cell line"
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/clone_lib="NIH_MGC_88"
/note="Organ: small intestine; Vector: pCMV-Sport6;
Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 32.9%; Score 689; DB 4; Length 874;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 739; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ATAGAGAGGTTTCTGTTACTATATGCTACACAGAGAGAGAGAGAGAGAGAGAGAGAG 60
DB 50 ATAGAGAGGTTTCTGTTACTATATGCTACACAGAGAGAGAGAGAGAGAGAGAGAGAG 109
OY 61 GAATGTGTGAG 120

Db 110 GAAATATGTGACCAAGCTGTGTGATGATGATTTCTGACATCTTCACTGATTTAGTGA 169
 Qy 121 TCCGATTAAGTATGACCTAAACCCGAAGAGCTCCCTGTGTGTGTGTTCTTCAAG 180
 Db 170 TCCGATTAAGTATGACCTAAACCCGAAGAGCTCCCTGTGTGTGTGTTCTTCAAG 229
 Qy 181 GGCACCCGAGACCCACCCGACACAGCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
 Db 230 GGCACCCGAGACCCACCCGACACAGCCGCAAGTTGTTAAGAAATACAGAACCAACA 289
 Qy 241 CTGCGGATGATTTCTTGTCTCACTGCGGTATGAGTTACTGAGTCTCGGTATTCAGA 300
 Db 290 CTGCGGATGATTTCTTGTCTCACTGCGGTATGAGTTACTGAGTCTCGGTATTCAGA 349
 Qy 301 TACACCTACTTTTGCAATGGGGGAAAGATTAATGAATTAACGATTCAGAGCTTGAGCC 360
 Db 350 TACACCTACTTTTGCAATGGGGGAAAGATTAATGAATTAACGATTCAGAGCTTGAGCC 409
 Qy 361 CGGCAATTTCTATGACACTGACATGACATGATGATGATGATTTAGAGCAAGAGACAA 420
 Db 410 CGGCAATTTCTATGACACTGACATGACATGATGATGATGATTTAGAGCAAGAGACAA 469
 Qy 421 CGGTGATTTCTGATGATCTGCGCCAGCCCTCAGAAAGCATTTTAAAGTCAAGAGACAA 480
 Db 470 CGGTGATTTCTGATGATCTGCGCCAGCCCTCAGAAAGCATTTTAAAGTCAAGAGACAA 529
 Qy 481 GAGGAGATTAAGTGGGCACTCCCGGTGATGATGATGATGATGATGATGATGATGAT 540
 Db 530 GAGGAGATTAAGTGGGCACTCCCGGTGATGATGATGATGATGATGATGATGATGAT 589
 Qy 541 AAGTCAGAGCTGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
 Db 590 AAGTCAGAGCTGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 649
 Qy 601 AGAAAGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 Db 650 AGAAAGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 709
 Qy 661 ATTGAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 Db 710 ATTGAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 769
 Qy 721 AATATTCCTGATTTACCC 740
 Db 770 AATATTCCTGATTTACCC 789

RESULT 5
 CN260357 646 bp mRNA linear EST 16-MAY-2004
 DEFINITION 17000424179730 GRN_BS Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN260357
 VERSION CN260357.1 GI:47276771
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 646)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R.,
 Lebkoweki, J and Stanton, L.W.
 Transcriptome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
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FEATURES

source

Location/Qualifiers
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ORIGIN

Query Match 29.7%; Score 623; DB 7; Length 646;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 987 AAGATGACCTTGAAGATTAAGAGAGACAGCTGCTCTTTGAAATTAAGGACAGAC 1046
 Db 24 AAGATGACCTTGAAGATTAAGAGAGAGACAGCTGCTCTTTGAAATTAAGGACAGAC 83
 Qy 1047 AAG 1106
 Db 84 AAG 143
 Qy 1107 TTTTACCTGATGCTTGAAGATCCGAGCAATTCCTAAGAGAGAGAGAGAGAGAGAG 1166
 Db 144 TTTTACCTGATGCTTGAAGATCCGAGCAATTCCTAAGAGAGAGAGAGAGAGAGAG 203
 Qy 1167 GAGCTATACAGTGAAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1226
 Db 204 GAGCTATACAGTGAAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263
 Qy 1227 GAG 1286
 Db 264 GAG 323
 Qy 1287 GCTTTCCTCTTTCGAG 1346
 Db 324 GCTTTCCTCTTTCGAG 383
 Qy 1347 ACCGAG 1406
 Db 384 ACCGAG 443
 Qy 1407 CTTCAG 1466
 Db 444 CTTCAG 503
 Qy 1467 TACAG 1526
 Db 504 TACAG 563
 Qy 1527 TGAAG 1586
 Db 564 TGAAG 623
 Qy 1587 TTTTCACTTACAGATGACCCCT 1609
 Db 624 TTTTCACTTACAGATGACCCCT 646

RESULT 6

BQ431497 852 bp mRNA linear EST 24-MAY-2002
 LOCUS BQ431497
 DEFINITION AGENCOURT 7894690 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6158144
 ACCESSION BQ431497
 VERSION BQ431497.1 GI:21170583
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Db	241	AGTACCTTACCCGAGCATATACCGGGGAGTGTCTCTCAGATTCAATTTTAACTGGT	300
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Qy	1179	TGACAGTCTGAAAAAGCGCAGGCTTACAGAGCTGTGCAATAACAGAGGGAGCGATTA	1238
Db	361	TGACAGTCTGAAAAAGCGCAGGCTTACAGAGCTGTGCAATAACAGAGGGAGCGATTA	420
Qy	1239	TAGCCGCTTTGTAGAGATGCTGTGCTGTGTGGATCTCTCTCCGCTTCCCTTC	1298
Db	421	TAGCCGCTTTGTAGAGATGCTGTGCTGTGTGGATCTCTCTCCGCTTCCCTTC	480
Qy	1299	TTGCAGGCACACACTAGTCTCTGTCTGAAACATCTTCTAACTTCAACCCAGACATA	1358
Db	481	TTGCAGGCACACACTAGTCTCTGTCTGAAACATCTTCTAACTTCAACCCAGACATA	540
Qy	1359	TTGCTGTGCAGCTCAAGTTTATTT	1383
Db	541	TTGCTGTGCAGCTCAAGTTTATTT	565

RESULT	8
LOCUS	AU124440
DEFINITION	AU124440 877 bp mRNA linear EST 01-AUG-2002 AU124440 NT2RM4 Homo sapiens cDNA clone NT2RM4000010 5', mRNA sequence.
ACCESSION	AU124440
VERSION	AU124440.1
KEYWORDS	GI:10949156
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE
AUTHORS
Oka, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J.,
Euharvot, Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (pages 1 to 877)

TITLE	HHI human cDNA project (Ota,T., Makamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Iisoga,T.)
JOURNAL	Unpublished (2000)
COMMENT	Contact: Takao Iisoga!

Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel.: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES	Location/Qualifiers
source	1. .877

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precursor cells"

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ORIGIN

Query Match	25.9%	Score 543	DB 1	Length 877
Best Local Similarity	100.0%	Pred. No. 1.5e-286		
Matches 543, Conservative	0	Mismatches	0	Indels
			0	Gaps
			0	
0y	1143	AAAGGCAATTTTGGACGCCCTTTGGCATTAACAGTACAGTGTGAAAAGCCGAGGCT	1202	

Db	192	AAAGCATTTTGGGAGCCCTTGAGCATATACAGTGA	CAGTGTCTGAAAGGCCAAGCT	251
Qy	1203	ACAGAGCTGTGCACTAAACAAGGGGCA	CGCCGATTAATACCCGCTTTGTA	CGAATGCTGT 1262
Db	252	ACAGAGACTGTGCAAGTAAACAAGGGGCA	CGCCGATTAATAGCCGCTTTGTA	CGAATGCTGT 311
Qy	1263	TGCGCTGTGTGGAATCCCTCCGCTTC	CCCTTCCTTGCCAGGCA	CACTCAGTCTCT 1322
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Qy	1443	AGAGTTCTGCGGAAAGGAGTATGTACA	GGCTGGCTGGCTTGTGTGTTCA	GTCT 1502
Db	492	AGAGTTCTGCGGAAAGGAGTATGTACA	GGCTGGCTGGCTTGTGTGTTCA	GTCT 551
Qy	1503	TCAGCCAAACATACATGATCCATGAA	AGACAGGGGAAAGCCCTGGCTCTA	AGATATTC 1562
Db	552	TCAGCCAAACATACATGATCCATGAA	AGACAGGGGAAAGCCCTGGCTCTA	AGATATTC 611
Qy	1563	CATCTCTCTCGAACAAACAATTTCTTCA	CTTACAGATAGACCCCTCAATCC	CAATCAT 1622
Db	612	CATCTCTCTCGAACAAACAATTTCTTCA	CTTACAGATAGACCCCTCAATCC	CAATCAT 671
Qy	1623	AATGTGGGTTCAGAAACCGGCATAGC	CCCGTTATTGGTTCTTACA	CATAGAGAA 1682
Db	672	AATGTGGGTTCAGAAACCGGCATAGC	CCCGTTATTGGTTCTTACA	CATAGAGAA 731
Qy	1683	ACT 1685		
Db	732	ACT 734		

RESULT 9	1061 bp	mRNA	linear	EST 02-MAY-2002
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BQ218755				
DEFINITION	BQ218755			
	AGNCOCURT_7565843	NIH_MGC_92 Homo sapiens	CDNA clone IMAGE 6041670	
	5', mRNA sequence.			
ACCESSION	BQ218755			
VERSION	BQ218755.1	GI:20400155		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
	1 (bases 1 to 1061)			
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/ .			
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)			
TITLE	Unpublished (1999)			
JOURNAL	Contact: Robert Strausberg, Ph.D.			
COMMENT				

Email: cgabs-i@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
<http://image.liml.gov>
plate: LIML3279 row: n column: 07
High quality sequence stop: 518.

FEATURES

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/db_xref="taxon:9606"
/clone="IMAGE:6041670"
/tissue_type="embryonal carcinoma cell line"
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/lab host="DH10B (phage-resistant)"
/clone lib="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 25.3%; Score 531; DB 5; Length 1061;
Best Local Similarity 100.0%; Pred. No. 6,1e-280;
Matches 531; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 995 AGCTTGAAGTAAAGAGACACTGCGTCTTTGAAATTAAGGACAGACAAAGAGA 1054
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QY 1055 AAGAGCTACTTACCCAGCATATACCTGCGGATTTCTTCCAGTTCAATTTTAACT 1114
Db 61 AAGAGCTACTTACCCAGCATATACCTGCGGATTTCTTCCAGTTCAATTTTAACT 120

QY 1115 GGATCTTGAATCCGAGCAATTCCTAAAGGCAATTTTGCGAGCCCTTGTGACTATA 1174
Db 121 GGATCTTGAATCCGAGCAATTCCTAAAGGCAATTTTGCGAGCCCTTGTGACTATA 180

QY 1175 CCAAGTACAGTGTGAAAGCGAGGCTACAGAGCTGTGCAAGTAAACAAAGGCGACCG 1234
Db 181 CCAAGTACAGTGTGAAAGCGAGGCTACAGAGCTGTGCAAGTAAACAAAGGCGACCG 240

QY 1235 ATTAATACCCGCTTTGTACAGATGCTGTGCTGCTTTGATCTCTCTGCTTCC 1294
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QY 1295 CTCTCTGCGAGCCAGCACTGAGTCTGCTGCGAATCTTCTTAACTTCAACCCAGAC 1354
Db 301 CTCTCTGCGAGCCAGCACTGAGTCTGCTGCGAATCTTCTTAACTTCAACCCAGAC 360

QY 1355 CATATTCGTGTGCAAGCTCAAGTTTATTTCAACCCAGAAAGCTTCATTTGTCTTACA 1414
Db 361 CATATTCGTGTGCAAGCTCAAGTTTATTTCAACCCAGAAAGCTTCATTTGTCTTACA 420

QY 1415 TTGTGGAATTTCTGTCTACATGCGCCACACAGAGTTCTGCGAAGGAGTATGACAGCT 1474
Db 421 TTGTGGAATTTCTGTCTACATGCGCCACACAGAGTTCTGCGAAGGAGTATGACAGCT 480

QY 1475 GGCTGCGCTTGTGTGCTTCAAGTTCTTCAAGCCAAATACATGATCCC 1525
Db 481 GGCTGCGCTTGTGTGCTTCAAGTTCTTCAAGCCAAATACATGATCCC 531

RESULT 10
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LOCUS 603055786F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5205285 5',
DEFINITION mRNA sequence.
ACCESSION BI772430.1 GI:15764008
VERSION BI772430.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Place: L1M1514 row: 1 column: 22
High quality sequence stop: 824.
Location/Qualifiers

FEATURES

source

1..826
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/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 24.7%; Score 517; DB 4; Length 826;
Best Local Similarity 99.7%; Pred. No. 3e-272;
Matches 617; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAGAGGTTCTGTACTATATGCTACACAGCAGGACAGCAAGGCGATCGAGAA 60
Db 53 ATGAGAGGTTCTGTACTATATGCTACACAGCAGGACAGCAAGGCGATCGAGAA 112

QY 61 GAAATGTGAGCAAGCTGTGTACATGATGATTTCTGCAATCTTCACTGATTAAGTAA 120
Db 113 GAAATGTGAGCAAGCTGTGTACATGATGATTTCTGCAATCTTCACTGATTAAGTAA 172

QY 121 TCCGATTAATGATGACTTAAACCCGAAACAGCTCTTGTGTGTTTCTTACACG 180
Db 173 TCCGATTAATGATGACTTAAACCCGAAACAGCTCTTGTGTGTTTCTTACACG 232

QY 181 GGCACGGAGACCCACCGACACAGCCCGGAGTTGTTAAGAAATACAGAACCAACA 240
Db 233 GGCACGGAGACCCACCGACACAGCCCGGAGTTGTTAAGAAATACAGAACCAACA 292

QY 241 CTGCGGTTGATTTCTTTGTCTCACTGCGGTATGAGTTACTGCGTCTCGGTATTCAGAA 300
Db 293 CTGCGGTTGATTTCTTTGTCTCACTGCGGTATGAGTTACTGCGTCTCGGTATTCAGAA 352

QY 301 TACACTTACTTTTGCATGCGGAGGAAGATTAATGATTAACGACTTCAAGGCTTGGAGCC 360
Db 353 TACACTTACTTTTGCATGCGGAGGAAGATTAATGATTAACGACTTCAAGGCTTGGAGCC 412

QY 361 CGGCATTTCTATGACCTGACATGAGATGATGATGATGATTAAGTAACTTGTGTTGAG 420
Db 413 CGGCATTTCTATGACCTGACATGAGATGATGATGATGATTAAGTAACTTGTGTTGAG 472

QY 421 CCGTGAATTCCTGACTGTGCGCAGCCCTCAGAAACATTTTAACTTCAAGCAGAGCA 480
Db 473 CCGTGAATTCCTGACTGTGCGCAGCCCTCAGAAACATTTTAACTTCAAGCAGAGCA 532

QY 481 GAGAGATTAAGTGGCGACTCCCGGTGGCATCACTGCACTCTTGAAGAGACACTTGTG 540
Db 533 GAGAGATTAAGTGGCGACTCCCGGTGGCATCACTGCACTCTTGAAGAGACACTTGTG 592

QY 541 AAGTCAGAGTGTACACATTAATCAATCAAGTCAAGTCTTGAATTCGATTCAGGA 600
Db 593 AAGTCAGAGTGTACACATTAATCAATCAAGTCAAGTCTTGAATTCGATTCAGGA 652

QY 601 AGAAGGATTTCTGAGGTTT 619
Db 653 AGAAGGATTTCTGAGGTTT 671

RESULT	11
LOCUS	CB997527
DEFINITION	CB997527 776 bp mRNA linear EST 01-MAY-2003
ACCESSION	AGNCOURT_13620640 NIH_MGC_148 Homo sapiens cDNA clone
VERSION	IMAGE:30358684.5, mRNA sequence.
KEYWORDS	CB997527 CB997527.1 GI:30292047
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 776) NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

plate: NDAM365 row: 1 column: 21
high quality sequence stop: 564.

FEATURES	Location/Qualifiers
Source	1. .776

Query Match	24.4%	Score 512;	DB 6;	Length 776;
Best Local Similarity	99.7%;	Pred. No. 1.7e-269;		
Matches 612;	Conservative	0;	Mismatches 2;	Indels 0;
			Gaps	0

QY	1	ATGAGGAGGTTCTGTCTATATATCTACACAGCAGGGACAGGCAAGGCCCATCCGACGAA	60
Db	88	ATGAGGAGGTTCTGTCTATATCTATATCTACACAGCAGGGACAGGCAAGGCCCATCCGACGAA	147
QY	61	GAATGTGTGACGAAGCTGTGGTACATGAGATTTCTGAGAGATCTTCACTGTATTAGTGA	120
Db	148	GAATGTGTGACGAAGCTGTGGTACATGAGATTTCTGAGAGATCTTCACTGTATTAGTGA	207
QY	121	TCCGATAGTAGACCTTAAACACGAAACAGTCTCTTGTGTGTGTGTCTTCAACAG	180
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QY	181	GGCACCGGAGACCCACCCGACACAGCCCGCAGTTGTTAAGGAATACAGAACCAACA	240
Db	268	GGCACCGGAGACCCACCCGACACAGCCCGCAGTTGTTAAGGAATACAGAACCAACA	327
QY	241	CTGCCGGTTGATTTCTTGTCTCACTGGGGGTATGGGTTACTGGGCTCGGTATTCAGAA	300
Db	328	CTGCCGGTTGATTTCTTGTCTCACTGGGGGTATGGGTTACTGGGCTCGGTATTCAGAA	387

Qy	301	TAGACCTA	CTTTTG	CAATGGGGG	GAAGTA	TATGTAA	CGACTT	CAAGAC	CTTGAGCC	360
Db	388	TACACCTA	CTTTTG	CAATGGGGG	GAAGTA	TATGTAA	CGACTT	CAAGAC	CTTGAGCC	447
Qy	361	CGGCA	TTTCTA	TATGAC	ACTGCA	CATGCA	GATGACTG	TGAGTT	TGAACTTG	420
Db	448	CGGCA	TTTCTA	TATGAC	ACTGCA	CATGCA	GATGACTG	TGAGTT	TGAACTTG	507
Qy	421	CCGTGA	TTGCTG	ACTCTG	GCAGCCCT	CAGAAAGCA	TTTTAG	GTCAAGCA	GAGACAA	480
Db	508	CCGTGA	TTGCTG	ACTCTG	GCAGCCCT	CAGAAAGCA	TTTTAG	GTCAAGCA	GAGACAA	567
Qy	481	GAGAGAT	TAATGG	CGCACTCC	CGGTGC	ATCACCCT	TGATCT	CTTGAGGA	CAGACTT	540
Db	568	GAGAGAT	TAATGG	CGCACTCC	CGGTGC	ATCACCCT	TGATCT	CTTGAGGA	CAGACTT	627
Qy	541	AAGTCAGA	GCCTG	CAACAT	TGTAATCT	CAAGTGA	GGCTTC	GAGATT	CGATTC	600
Db	628	AAGTCAGA	GCCTG	CAACAT	TGTAATCT	CAAGTGA	GGCTTC	GAGATT	CGATTC	687
Qy	601	AGAAAGAT	CTTGA	614						
Db	688	AGAAAGAT	CTTGA	701						

LOCUS	BU941078	834 bp	mrna	linear	EST 18-OCT-2002
DEFINITION	AGENCECOURT_10540067	NIH_MGC_128	Homo sapiens	cdna clone	
	IMAGE:6712893	5',	mrna	sequence.	

SOURCE ORGANISM	
Homo sapiens (human)	
Homo sapiens	

REFERENCE	1 (pages 1 to 834)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

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High quality sequence stop: 586.

FEATURES
SOURCE

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/clone="IMAGB:6712893"
/tissue_type="mixed (pool of 40 RNAs)"
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/clone_lib="NH_MGC_128"
/node=Vector: pDNR-LIB; Site 1: SfiI (ggccattcggcc);
Site 2: SfiI (ggcgccctcgccg); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon
- 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AACCACTGCTATCAACGACAGTGGCATTCAGGCGCG-3' and
5'-ATCTGAGGCGCCAGCGGCGGCGCATG-dT(30)NN-3'. Full-length
enriched library was constructed using the Clontech

```

Creator SMART kit and size-selected to contain the >2 kb size fraction (other fractions present in NIH_MGC_126 and NIH_MGC_127). Library created in the laboratory of T. Uedlin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 24.2%; Score 507; DB 5; Length 834;
Best Local Similarity 99.7%; Pred. No. 9,7e-267;
Matches 607; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 379 GGACATGCAATGATGCTGTGAGTTTGAACCTGTGTGAGCCGTGAGATTCCTGACATC 438
Db 3 GGACATGCAATGATGCTGTGAGTTTGAACCTGTGTGAGCCGTGAGATTCCTGACATC 62
Qy 439 TGGCCAGCCCTCAGAAAGCAATTTAGTCAAGCAGAGACAGAGATTAAGTGGCGCA 498
Db 63 TGGCCAGCCCTCAGAAAGCAATTTAGTCAAGCAGAGACAGAGATTAAGTGGCGCA 122
Qy 499 CTCCTGGTGGCATCCTGATCCTTGAAGACAGACCTTGTGAAGTCAAGCTGTACAC 558
Db 123 CTCCTGGTGGCATCCTGATCCTTGAAGACAGACCTTGTGAAGTCAAGCTGTACAC 182
Qy 559 ATTGAATCTCAAGTCGAGCTTTTGAAGTTGATGATTCAGAGAAAGAGATTCTGAGGTT 618
Db 183 ATTGAATCTCAAGTCGAGCTTTTGAAGTTGATGATTCAGAGAAAGAGATTCTGAGGTT 242
Qy 619 TTGAAGCAAAATGAGAGAGAAAGCAATCCATGTTGTAATTGAAGCTTTGAGTCC 678
Db 243 TTGAAGCAAAATGAGAGAGAAAGCAATCCATGTTGTAATTGAAGCTTTGAGTCC 302
Qy 679 TCACTTACCCGTTGGTACCCCACTCTCAAGCCCTCTGTAATTTCTGTTTACC 738
Db 303 TCACTTACCCGTTGGTACCCCACTCTCAAGCCCTCTGTAATTTCTGTTTACC 362
Qy 739 CCAAGAAATTTTACAGTACATCTGCAAGAGTCTTTGGCCAGAGAGAAAGCCAGTATCT 758
Db 363 CCAAGAAATTTTACAGTACATCTGCAAGAGTCTTTGGCCAGAGAGAAAGCCAGTATCT 422
Qy 799 GTGACTTCAGACAGATCCAGTTTTCAGAGTGCATTTCAAGGAGTTCAACTTACTACG 858
Db 423 GTGACTTCAGACAGATCCAGTTTTCAGAGTGCATTTCAAGGAGTTCAACTTACTACG 482
Qy 859 AATGATGCCATTAATAAACCACTCTGCTGTGAATTTGACATTTCAATAACAGACTTTCC 918
Db 483 AATGATGCCATTAATAAACCACTCTGCTGTGAATTTGACATTTCAATAACAGACTTTCC 542
Qy 919 TATCAGGCTGGAATGCTTCAAGGTGATCTGCCCTTAACAGTATTTCTGAGTACAAAGC 978
Db 543 TATCAGGCTGGAATGCTTCAAGGTGATCTGCCCTTAACAGTATTTCTGAGTACAAAGC 602
Qy 979 CTACTCCAA 987
Db 603 CTACTCCAA 611

RESULT 13
LOCUS CB164340 521 bp mRNA linear EST 30-JAN-2003
DEFINITION K-ESR0225498 L17N670205n1 Homo sapiens cDNA clone
ACCESSION CB164340
VERSION CB164340.1 GI:28150466
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 521)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE ZIC Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 39 row: F column: 02
High quality sequence stop: 521.

FEATURES
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/note="Organ: Liver; Vector: pRT73-Pac; Site 1: Scott; Site 2: NotI; The library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."

ORIGIN

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Matches 520; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1600 GATGACCCCTCATATCCCATCATATATGATGGTTCAGAAACCGGATATGCCCTTTAT 1659
Db 61 GATGACCCCTCATATCCCATCATATATGATGGTTCAGAAACCGGATATGCCCTTTAT 120
Qy 1660 GGGTTCCTCAACATGAGAGAAACTCAAGAACACACCCAGATGGAATTTTGGAGCA 1719
Db 121 GGGTTCCTCAACATGAGAGAAACTCAAGAACACACCCAGATGGAATTTTGGAGCA 180
Qy 1720 ATGTGTTGTTTTTGGCTGACAGCAATTAAGATAGGATTTATTCAGAAAAAGCTC 1779
Db 181 ATGTGTTGTTTTTGGCTGACAGCAATTAAGATAGGATTTATTCAGAAAAAGCTC 240
Qy 1780 AGCATTTTCTTAAGCATGGGATCTTAATCATCTTAAAGTTTCTTCAAGATGCT 1839
Db 241 AGCATTTTCTTAAGCATGGGATCTTAATCATCTTAAAGTTTCTTCAAGATGCT 300
Qy 1840 CCTGTTGGGAGAGAGAAAGCCCGAGCAAGATATGTCAGAACATCCAGTTTCAATGGC 1899
Db 301 CCTGTTGGGAGAGAGAAAGCCCGAGCAAGATATGTCAGAACATCCAGTTTCAATGGC 360
Qy 1900 CAGCAGGTGGCGAATCTCTCTCAAGAGAACGGCCATATTTATGTGTGAGATGCA 1959
Db 361 CAGCAGGTGGCGAATCTCTCTCAAGAGAACGGCCATATTTATGTGTGAGATGCA 420
Qy 1960 AAGAAATATGGCCCAAGATGATGATGCTTGTGTGCAATATTAAGCAAAAGGTTTGA 2019
Db 421 AAGAAATATGGCCCAAGATGATGATGCTTGTGTGCAATATTAAGCAAAAGGTTTGA 480
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Db 481 GTTGAATACTAGAACATGAAGAAACCTGGCCACTTTTAA 521

RESULT 14
LOCUS AUI32586 822 bp mRNA linear EST 01-AUG-2002
DEFINITION AUI32586 NT2RPA Homo sapiens cDNA clone NT2RPA000141 5', mRNA sequence.

ACCESSION AU132586
VERSION AU132586.1 GI:10992940
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 822)
Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y., Salto, K., Yamamoto, J.,
Nishikawa, T., Nakamura, Y., Nagai, T., Sugano, S., Masuh, Y. and
Isegai, T.
TITLE HRI human cDNA project (Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y.,
Salto, K., Yamamoto, J., Nishikawa, T., Nakamura, Y., Nagai, T.,
Sugano, S., Masuh, Y., Isegai, T.)
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isegai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
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Matches 555; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 242 CTTCAAGAGCTTGAAGCCCGGCAATTTCTATGACATGACATGACATGATGATGATGAT 301
QY 403 TTGAGAACTTGTGATGAGCCGCTGATGATGCTGCGACACCTCGAAGAACATTTT 462
DB 302 TTGAGAACTTGTGATGAGCCGCTGATGATGCTGCGACACCTCGAAGAACATTTT 361
QY 463 AGTCAAGAGAGAGCAAGAGAGATTAAGTGGCGCATCCCGGTGACATCCTGATCC 522
DB 362 AGTCAAGAGAGAGCAAGAGAGATTAAGTGGCGCATCCCGGTGACATCCTGATCC 421
QY 523 TTGAGAGACAGACCTTGTGAAGTCAAGAGCTGACATGATGATGATGATGATGATGAT 582
DB 422 TGAAGAGACAGACCTTGTGAAGTCAAGAGCTGACATGATGATGATGATGATGATGAT 481
QY 583 AGATTGATGATTCAGAGAGAGAGATTTGAGAGTTTGAAGAGAGAGAGAGAGAGAGAG 642
DB 482 AGATTGATGATTCAGAGAGAGAGATTTGAGAGTTTGAAGAGAGAGAGAGAGAGAGAG 541
QY 643 AACCAATCAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 702
DB 542 AACCAATCAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 601
QY 703 CTCTCAAGAGCTCTCTGATATTTCTGTGTTTACCCCGAGATATTTTACAGGTATCTG 762

DB 602 CTCTCAAGAGCTCTCTGATATTTCTGTGTTTACCCCGAGATATTTTACAGGTATCTG 661
QY 763 CAGAGATCTCTTGGCAGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGAT 822
DB 662 CAGAGATCTCTTGGCAGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGAT 721
QY 823 CAAGTCCCAATTTTCAA 839
DB 722 CAAGTCCCAATTTTCAA 738
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ACCESSION AW965709
VERSION AW965709.1 GI:8155545
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 591)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and
Quackenbush, J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnqc@igr.org
Plate: 218
Seq primer: Reverse.
FEATURES
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Best Local Similarity 100.0%; Pred. No. 2.8e-234;
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DB 121 CTCAAGTCTCTGCTGGAACATCTTCTTAACTTCAACCCAGACATATTCGTGTGCAAC 180
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DB 181 TCAAGTTTATTTACCCAGAGAGAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCT 240
QY 1432 ACTGCACAACAGAGGTTCTGCGAAGGAGATGATGATGATGATGATGATGATGATGATGAT 1491
DB 241 ACTGCACAACAGAGGTTCTGCGAAGGAGATGATGATGATGATGATGATGATGATGATGAT 300
QY 1492 GCTTCAGTTCTTACGCCAATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1551
DB 301 GCTTCAGTTCTTACGCCAATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 360

QY 1552 CCTAAGATATCGATCTCTCTCGAACAACAATTTTTCACCTTACCAAGTGAACCCCTCA 1611
Db 361 CCTAAGATATCGATCTCTCTCGAACAACAATTTTTCACCTTACCAAGTGAACCCCTCA 420
QY 1612 ATCCCATCATATGATGGTGGTCCAGGA 1639
Db 421 ATCCCATCATATGATGGTGGTCCAGGA 448

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2097	100.0	3259	5	AA65070	AA65070 DNA encod
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4	2094	99.9	2094	11	ADM43208	ADM43208 Human wtl
5	2043	97.4	2094	11	ADM43212	ADM43212 Human met
6	2043	97.4	2094	11	ADM43212	ADM43212 Human met
7	1995	95.1	3259	3	AA58935	AA58935 DNA encod
8	1944	92.7	3270	13	ADM87538	ADM87538 Human tum
9	1851	88.3	2091	11	ADM43216	ADM43216 Human met
10	1851	88.3	2091	11	ADM43214	ADM43214 Human met
11	1752	83.5	3256	3	AA58977	AA58977 A human m
12	1691	80.6	3255	3	AA58976	AA58976 A human m
13	1062	50.6	3256	13	ADM39029	ADM39029 Human SNP
14	1062	50.6	3274	13	ADM39030	ADM39030 Human SNP
15	956	45.6	3189	13	ACN42470	ACN42470 Human dia
16	805	38.4	1986	4	AA641064	AA641064 cDNA enco
17	457	20.4	1663	4	AA641602	AA641602 cDNA enco
18	366	18.4	390	2	AA651820	AA651820 Human sec
19	330	15.7	591	12	ACH73174	ACH73174 Human gen
20	328	15.6	379	12	ACH86905	ACH86905 Human gen

21	279	13.3	591	12	ACH68540	ACH68540 Human gen
22	277	13.2	379	12	ACH82240	ACH82240 Human gen
23	225	10.7	503	5	AA65069	AA65069 DNA encod
24	188	9.0	525	12	ACH67438	ACH67438 Human gen
25	175	8.3	175	12	ACH81143	ACH81143 Human gen
26	158	7.5	2475	6	ADM32365	ADM32365 Human lun
27	158	7.5	2475	13	ADM161720	ADM161720 Human CDN
28	137	6.5	525	12	ACH73117	ACH73117 Human gen
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30	78	3.7	244	3	AA642736	AA642736 Human 5'
31	60	2.9	60	6	ABN36264	ABN36264 Human sp1
32	51	2.4	51	4	AA178548	AA178548 Human s11
33	38	1.8	1835	5	AA65071	AA65071 DNA encod
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35	26	1.2	26	3	AA58955	AA58955 PCR prime
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37	26	1.2	26	6	ABX09549	ABX09549 Arteriosc
38	26	1.2	26	6	AA143713	AA143713 Pregestat
39	26	1.2	26	11	ADM43205	ADM43205 Human met
40	26	1.2	26	11	ADM43189	ADM43189 Human met
41	25	1.2	25	3	AA58952	AA58952 PCR prime
42	25	1.2	25	3	AA58937	AA58937 PCR prime
43	25	1.2	25	3	AA58947	AA58947 PCR prime
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45	25	1.2	25	11	ADM43202	ADM43202 Human met

ALIGNMENTS

RESULT 1	AA65070	standard; cDNA; 3259 BP.
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AC	AA65070;	
XX	AA65070;	
DT	13-FEB-2002	(first entry)
XX	13-FEB-2002	(first entry)
DE	DNA encoding novel human diagnostic protein #874.	
XX	DNA encoding novel human diagnostic protein #874.	
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;	
KW	Food supplement; medical imaging; diagnostic; genetic disorder; ss.	
OS	Homo sapiens.	
XX	Homo sapiens.	
PN	WO2001/5067-A2.	
XX	WO2001/5067-A2.	
PD	11-OCT-2001.	
XX	11-OCT-2001.	
PF	30-MAR-2001; 2001WO-US008631.	
XX	30-MAR-2001; 2001WO-US008631.	
PR	31-MAR-2000; 2000US-00540217.	
XX	31-MAR-2000; 2000US-00540217.	
PR	23-AUG-2000; 2000US-00649167.	
XX	23-AUG-2000; 2000US-00649167.	
PA	(HYSE-) HYSEQ INC.	
XX	(HYSE-) HYSEQ INC.	
PI	Dmanac RT, Liu C, Tang YT;	
XX	Dmanac RT, Liu C, Tang YT;	
XX	WPI; 2001-639362/73.	
DR	P-PSDB; ABG00883.	
XX	P-PSDB; ABG00883.	
PT	New isolated polynucleotide and encoded polypeptides, useful in	
PT	diagnostics, forensics, gene mapping, identification of mutations	
PT	responsible for genetic disorders or other traits and to assess	
PT	bioreactivity.	
XX	bioreactivity.	
PS	Claim 1; SEQ ID NO 874; 103pp; English.	
XX	Claim 1; SEQ ID NO 874; 103pp; English.	
CC	The invention relates to isolated polynucleotide (I) and polypeptide (II)	
CC	sequences. (I) is useful as hybridisation probes, polymerase chain	
CC	reaction (PCR) primers, oligomers, and for chromosome and gene mapping,	
CC	and in recombinant production of (II). The polynucleotides are also used	
CC	in diagnostics as expressed sequence tags for identifying expressed	

CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantifying a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS4197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC fcp.wipo.int/pub/published_pct_sequences
CC XX
SQ Sequence 3259 BP; 944 A; 695 C; 674 G; 946 T; 0 U; 0 Other;
Query Match 100.0%; Score 2097; DB 5; Length 3259;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGAGGTTCTGTTACTATATGCTACACAGAGGACAGGCAAAAGCCATGCGAGAA 60
DB ATGAGAGGTTCTGTTACTATATGCTACACAGAGGACAGGCAAAAGCCATGCGAGAA 139
QY 61 GAAATGTGTGAGCAAGCTGTGTACATGATGATTTCTGACATCTTCACTGATTAGTAA 120
DB GAAATGTGTGAGCAAGCTGTGTACATGATGATTTCTGACATCTTCACTGATTAGTAA 199
QY 140 GAAATGTGTGAGCAAGCTGTGTACATGATGATTTCTGACATCTTCACTGATTAGTAA 199
QY 121 TCCGATTAAGTATGACCTTAAACCGAAACAGCTCTCTTGTGTGTGTTTCTACACAG 180
DB TCCGATTAAGTATGACCTTAAACCGAAACAGCTCTCTTGTGTGTGTTTCTACACAG 259
QY 181 GGCACCGGAGACCAACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
DB GGCACCGGAGACCAACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 319
QY 241 CTGCGCGGTGATTTCTTGTGCTACCTGTGGGTATGGTTACTGGGTCTCGGATTTAGAA 300
DB CTGCGCGGTGATTTCTTGTGCTACCTGTGGGTATGGTTACTGGGTCTCGGATTTAGAA 379
QY 320 CTGCGCGGTGATTTCTTGTGCTACCTGTGGGTATGGTTACTGGGTCTCGGATTTAGAA 379
QY 301 TACACCTACTTTTGCATATGGGGGAGAAATTAATTAACGACTTCAAGAGCTTGAGCC 360
DB TACACCTACTTTTGCATATGGGGGAGAAATTAATTAACGACTTCAAGAGCTTGAGCC 439
QY 380 TACACCTACTTTTGCATATGGGGGAGAAATTAATTAACGACTTCAAGAGCTTGAGCC 439
QY 361 CGGATTTCTATGACATCTGACATGACATGACATGATGATGATTTTGAAGCTTGAGAG 420
DB CGGATTTCTATGACATCTGACATGACATGACATGATGATGATTTTGAAGCTTGAGAG 499
QY 440 CGGATTTCTATGACATCTGACATGACATGACATGATGATGATTTTGAAGCTTGAGAG 499
QY 421 CCGTGAATTCCTGACCTGTGGCAGCCCTCAGAAAGATTTTAAAGTCAAGAGAGACAA 480
DB CCGTGAATTCCTGACCTGTGGCAGCCCTCAGAAAGATTTTAAAGTCAAGAGAGACAA 559
QY 500 CCGTGAATTCCTGACCTGTGGCAGCCCTCAGAAAGATTTTAAAGTCAAGAGAGACAA 559
QY 481 GAGAGATTAAGTGCAGCACTCCGGTGGCATCACCTGCATCTTGAAGACAGACCTTGTG 540
DB GAGAGATTAAGTGCAGCACTCCGGTGGCATCACCTGCATCTTGAAGACAGACCTTGTG 619
QY 541 AAGTCAGAGCTGTACATGATTTGAATTCGAATCGAGCTTGAATTCGATTCGATTCAGGA 600
DB AAGTCAGAGCTGTACATGATTTGAATTCGAATCGAGCTTGAATTCGATTCGATTCAGGA 679
QY 601 AGAAGAGATTCGAGAGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCCATGTTGTA 660
DB AGAAGAGATTCGAGAGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCCATGTTGTA 739
QY 661 ATTGAAGATTGATGCTCTCACTTAACCGTTCCGATCCGCCACTCTCAAGACCTCTCTG 720
DB ATTGAAGATTGATGCTCTCACTTAACCGTTCCGATCCGCCACTCTCTCAAGACCTCTCTG 799
QY 721 AATATCTCTGTTTACCCCGAATATTTTACAGGTACATCTGAGAGATCTCTTGGCCAG 780
DB AATATCTCTGTTTACCCCGAATATTTTACAGGTACATCTGAGAGATCTCTTGGCCAG 780

DB 800 AATATCTCTGTTTACCCCGAATATTTTACAGGTACATCTGAGAGATCTCTTGGCCAG 859
QY 781 GAGAAAGCCAAATATCTGTGACTTCAGACAGATCCAGTTTTCATAGTGCATTTCAAG 840
DB GAGAAAGCCAAATATCTGTGACTTCAGACAGATCCAGTTTTCATAGTGCATTTCAAG 919
QY 841 GCAGTTCAACTTACATGAGATGATGCAATTAACCACTCTGTGTGATGATGACATTT 900
DB GCAGTTCAACTTACATGAGATGATGCAATTAACCACTCTGTGTGATGATGACATTT 979
QY 901 TCAATACAGACTTTTCTATACAGCTGTGAGATGCTTACAGGTTATGCTCCCTAACG 960
DB TCAATACAGACTTTTCTATACAGCTGTGAGATGCTTACAGGTTATGCTCCCTAACG 1039
QY 961 GATTCGAGTACCAAGCTTCTCAAGACTGCAAGCTTGAAGATTAAGAGAGACCTGC 1020
DB GATTCGAGTACCAAGCTTCTCAAGACTGCAAGCTTGAAGATTAAGAGAGACCTGC 1099
QY 1021 GTTCCTTTGAAATTAAGGACACACAAAGAGAGAGCTTACCTTACCCGACATTA 1080
DB GTTCCTTTGAAATTAAGGACACACAAAGAGAGAGCTTACCTTACCCGACATTA 1159
QY 1100 GTTCCTTTGAAATTAAGGACACACAAAGAGAGAGCTTACCTTACCCGACATTA 1159
DB GTTCCTTTGAAATTAAGGACACACAAAGAGAGAGCTTACCTTACCCGACATTA 1159
QY 1081 CCGCGGAGATGTTCTCTCAAGTTCACTTTTACCTGAGTCTTGAATCCGAGCAATTCCT 1140
DB CCGCGGAGATGTTCTCTCAAGTTCACTTTTACCTGAGTCTTGAATCCGAGCAATTCCT 1219
QY 1160 CCGCGGAGATGTTCTCTCAAGTTCACTTTTACCTGAGTCTTGAATCCGAGCAATTCCT 1219
DB CCGCGGAGATGTTCTCTCAAGTTCACTTTTACCTGAGTCTTGAATCCGAGCAATTCCT 1279
QY 1141 AAAAGGCAATTTTGGAGAGCCCTTGTGACATATACAGTACAGTCTGAAAAAGCGCAGG 1200
DB AAAAGGCAATTTTGGAGAGCCCTTGTGACATATACAGTACAGTCTGAAAAAGCGCAGG 1279
QY 1201 CTACAGAGCTGTGACATTAACAGGGGCAAGCCGATTAATACCGCTTTGTACAGATGCC 1260
DB CTACAGAGCTGTGACATTAACAGGGGCAAGCCGATTAATACCGCTTTGTACAGATGCC 1339
QY 1280 CTACAGAGCTGTGACATTAACAGGGGCAAGCCGATTAATACCGCTTTGTACAGATGCC 1339
DB CTACAGAGCTGTGACATTAACAGGGGCAAGCCGATTAATACCGCTTTGTACAGATGCC 1320
QY 1261 TGTGCGTCTGTGTGATGATCTCTCCCTCGCTTCCCTTCCGACGACCACTCAAGTCTC 1320
DB TGTGCGTCTGTGTGATGATCTCTCCCTCGCTTCCCTTCCGACGACCACTCAAGTCTC 1399
QY 1340 TGTGCGTCTGTGTGATGATCTCTCCCTCGCTTCCCTTCCGACGACCACTCAAGTCTC 1399
DB TGTGCGTCTGTGTGATGATCTCTCCCTCGCTTCCCTTCCGACGACCACTCAAGTCTC 1459
QY 1321 CTGCTGAAATCTTCTTAACTTCAACCCAGACATATTCGTGTGCAAGCTCAAGTTTA 1380
DB CTGCTGAAATCTTCTTAACTTCAACCCAGACATATTCGTGTGCAAGCTCAAGTTTA 1459
QY 1381 TTTCACCCAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACTGCACA 1440
DB TTTCACCCAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACTGCACA 1519
QY 1460 TTTCACCCAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACTGCACA 1519
DB TTTCACCCAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACTGCACA 1500
QY 1441 ACAGAGTTCTGCGAAAGGAGATGATGACAGCTGTGCTGCTTGTGTGCTTCAAGT 1500
DB ACAGAGTTCTGCGAAAGGAGATGATGACAGCTGTGCTGCTTGTGTGCTTCAAGT 1579
QY 1501 CTTCAAGCAAACTATGATGATCCATGAAGACAGCGGGGAAAGCCCTGCTCTTAAGATA 1560
DB CTTCAAGCAAACTATGATGATCCATGAAGACAGCGGGGAAAGCCCTGCTCTTAAGATA 1639
QY 1580 CTTCAAGCAAACTATGATGATCCATGAAGACAGCGGGGAAAGCCCTGCTCTTAAGATA 1639
QY 1561 TCCATCTCTCTGGAACAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
DB TCCATCTCTCTGGAACAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1699
QY 1640 TCCATCTCTCTGGAACAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1699
DB TCCATCTCTCTGGAACAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1680
QY 1621 ATATGAGTGGGTCCAGGAACCGGATAGCCCGTTTATTTGGGTTCTTACAACTAAGAG 1680
DB ATATGAGTGGGTCCAGGAACCGGATAGCCCGTTTATTTGGGTTCTTACAACTAAGAG 1759
QY 1700 ATATGAGTGGGTCCAGGAACCGGATAGCCCGTTTATTTGGGTTCTTACAACTAAGAG 1759
DB ATATGAGTGGGTCCAGGAACCGGATAGCCCGTTTATTTGGGTTCTTACAACTAAGAG 1740
QY 1681 AAATCCAGAAACAAACCCAGATGGAATTTTGAAGCAATGTGTGTTTGTGCTGC 1740
DB AAATCCAGAAACAAACCCAGATGGAATTTTGAAGCAATGTGTGTTTGTGCTGC 1819
QY 1760 AAATCCAGAAACAAACCCAGATGGAATTTTGAAGCAATGTGTGTTTGTGCTGC 1819
DB AAATCCAGAAACAAACCCAGATGGAATTTTGAAGCAATGTGTGTTTGTGCTGC 1800
QY 1741 AGGATTAAGATGAGATTAATCTATTCAGAAAAGAGCTCAGACATTTCTTAAAGCATGG 1800
DB AGGATTAAGATGAGATTAATCTATTCAGAAAAGAGCTCAGACATTTCTTAAAGCATGG 1879
QY 1820 AGGATTAAGATGAGATTAATCTATTCAGAAAAGAGCTCAGACATTTCTTAAAGCATGG 1879
DB AGGATTAAGATGAGATTAATCTATTCAGAAAAGAGCTCAGACATTTCTTAAAGCATGG 1860
QY 1801 ATCTTAATCATCTTAAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGAGAGAGCC 1860
DB ATCTTAATCATCTTAAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGAGAGAGCC 1939

Qy	1661	CCAGCAAAAGTATGTATCAAGACAACAATCCAGCTTCATATGCGCAGCGAGTGGCGAGAAATCCTC	1920					
Db	1940	CCAGCAAAAGTATGTATCAAGACAACAATCCAGCTTCATATGCGCAGCGAGTGGCGAGAAATCCTC	1999					
Qy	1921	CTCCAGAGAAACGGCCATATTTATGTGTGTGAGAGTGCAGAAAGTAATATGGCCAAAGATGTA	1980					
Db	2000	CTCCAGAGAAACGGCCATATTTATGTGTGTGAGAGTGCAGAAAGTAATATGGCCAAAGATGTA	2059					
Qy	1981	CATGATGCCCTTGTGCAAAATATATAGCAAGAAGTTGAGATTGAAAACTTAGAACATG	2040					
Db	2060	CATGATGCCCTTGTGCAAAATATATAGCAAGAAGTTGAGATTGAAAACTTAGAACATG	2119					
Qy	2041	AAAACCCCTGGCCACTTTTAAAAAGAAAGAAAGCTACCTTCAGGATATTGTGCATPA	2097					
Db	2120	AAAACCCCTGGCCACTTTTAAAAAGAAAGAAAGCTACCTTCAGGATATTGTGCATPA	2176					
RESULT 2								
AC	AAC91226	AAC91226 standard; DNA; 3259 BP.						
AC	AAC91226;							
DT	20-MAR-2001	(first entry)						
XX	Human schizophrenia related gene SEQ ID NO: 23.							
DE	Human schizophrenia related gene SEQ ID NO: 23.							
XX	Human; schizophrenia; developmental disorder; spina bifida cystica;							
KW	Tourette's syndrome; bipolar illness; autism; conduct disorder;							
KW	attention deficit disorder; obsessive compulsive disorder;							
KW	chronic multiple tic syndrome; learning disorder; polymorphism; ds.							
XX	Homo sapiens.							
OS	Homo sapiens.							
XX	WO200071754-A1.							
PN	30-NOV-2000.							
PD	30-NOV-2000.							
XX	24-MAY-2000; 2000WO-US014354.							
PF	24-MAY-2000; 2000WO-US014354.							
XX	25-MAY-1999; 99US-00318448.							
PR	25-MAY-1999; 99US-00318448.							
XX	(UNNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.							
PA	(UNNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.							
XX	Johnson WG, Stenroos BS;							
FL	Johnson WG, Stenroos BS;							
XX	WPI; 2001-025174/03.							
DR	WPI; 2001-025174/03.							
XX	Diagnosing a developmental disorder, e.g. schizophrenia, by forming							
PT	databases (DS) of genetic (e.g. genotypes of folate metabolism alleles)							
PT	and environmental variables affecting an individual and then comparing							
PT	these DS with reference DS.							
XX	Disclosure; Page 142-143; 156pp; English.							
PS	The present invention provides a novel method of estimating the							
CC	susceptibility of an individual to a developmental disorder using genetic							
CC	and environmental variables. The method can be used in the diagnosis,							
CC	prevention and treatment of disorders such as schizophrenia, spina bifida							
CC	cystica, Tourette's syndrome, bipolar illness, autism, conduct disorders,							
CC	attention deficit disorder, obsessive compulsive disorder, chronic							
CC	multiple tic syndrome and learning disorders such as dyslexia							
XX	Sequence 3259 BP; 944 A; 695 C; 674 G; 946 T; 0 U; 0 Other;							
SQ	Sequence 3259 BP; 944 A; 695 C; 674 G; 946 T; 0 U; 0 Other;							
Query Match 100.0%; Score 2097; DB 5; Length 3259;								
Best Local Similarity 100.0%; Pred. No. 0;								
Matches 2097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;								
Qy	1 ATGAGAGAGTTTCTTACTATATGCTACACAGCAGGAGCAAGGCAATGCGAGAA 60							
Db	80 ATGAGAGAGTTTCTTACTATATGCTACACAGCAGGAGCAAGGCAATGCGAGAA 139							

QY	6	GAATGTGTGAGCAAGCTGTGTGATCATGGAATTTTCTGCAATCTTCACTGATTAATGAA	120
Db	140	GAATGTGTGAGCAAGCTGTGTGATCATGGAATTTTCTGCAATCTTCACTGATTAATGAA	199
QY	121	TCCGATTAAGTATGACCTTAAAAACCGAAACAGCTCTCTGTGTGTGTGTTTCTACACG	180
Db	200	TCCGATTAAGTATGACCTTAAAAACCGAAACAGCTCTCTGTGTGTGTGTTTCTACACG	259
QY	181	GGCACCGGAGCCACCCGACACAGCCCGGAGTTTGTAAAGAAATACAGAACCAACA	240
Db	260	GGCACCGGAGCCACCCGACACAGCCCGGAGTTTGTAAAGAAATACAGAACCAACA	319
QY	241	CTGCGGGTGTATTTCTTGTCTACCTCGGGTATGGTTACTGAGTCTCGGTATTCGAA	300
Db	320	CTGCGGGTGTATTTCTTGTCTACCTCGGGTATGGTTACTGAGTCTCGGTATTCGAA	379
QY	301	TACACCTTACTTTGCAATGGGGGGGAGATTAATTGATTAAGCATTTCAAGACTTGAAGCC	360
Db	380	TACACCTTACTTTGCAATGGGGGGGAGATTAATTGATTAAGCATTTCAAGACTTGAAGCC	439
QY	361	CGGATTTCTATGACATCGGACATGCGAGATGACCTGTGATGGTTTGAACCTGTGTGAG	420
Db	440	CGGATTTCTATGACATCGGACATGCGAGATGACCTGTGATGGTTTGAACCTGTGTGAG	499
QY	421	CCGTGATTTGTGACATCTGGCCAGCCCTCAGAAAGCATTTTAACTCAAGCAGAGACA	480
Db	500	CCGTGATTTGTGACATCTGGCCAGCCCTCAGAAAGCATTTTAACTCAAGCAGAGACA	559
QY	481	GAGGAGATTAATGGCCGACATCCCGGTGGACATCACCTGCATCTCTGAGACAGACCTTGTG	540
Db	560	GAGGAGATTAATGGCCGACATCCCGGTGGACATCACCTGCATCTCTGAGACAGACCTTGTG	619
QY	541	AAGTCAGAGCTGCATACATTTGAATCTCAAGTCAAGCTTCTGAGATTCGATGATTCAGGA	600
Db	620	AAGTCAGAGCTGCATACATTTGAATCTCAAGTCAAGCTTCTGAGATTCGATGATTCAGGA	679
QY	601	AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAATGAAACGCAACCAATCCATGTTGTA	660
Db	680	AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAATGAAACGCAACCAATCCATGTTGTA	739
QY	661	ATTGAAGCTTTGAGTCTCTCACTTAACCGGTTGGTACCCCACTCTACAAAGCCCTCTG	720
Db	740	ATTGAAGCTTTGAGTCTCTCACTTAACCGGTTGGTACCCCACTCTACAAAGCCCTCTG	799
QY	721	AATATTCCTGTGTTTACCCCGAGATATTTTACAGTACATCTGCAGAGTCTCTTGGCCAG	780
Db	800	AATATTCCTGTGTTTACCCCGAGATATTTTACAGTACATCTGCAGAGTCTCTTGGCCAG	859
QY	781	GAGGAAAGCCCAAGTATCTGTGACATTTCAAGCAGATCCAGTTTTTCAAGTCCCAATTTCAAG	840
Db	860	GAGGAAAGCCCAAGTATCTGTGACATTTCAAGCAGATCCAGTTTTTCAAGTCCCAATTTCAAG	919
QY	841	GCAGTTCAACTTACATGAGATGATGCAATAAAACAACCTGCTGATGAAATTTGGAACATT	900
Db	920	GCAGTTCAACTTACATGAGATGATGCAATAAAACAACCTGCTGATGAAATTTGGAACATT	979
QY	901	TCAATATCAGACTTTTCTTATCAGCTTGAGAGTCTTCAAGCTGATCTGCTTAAACGT	960
Db	980	TCAATATCAGACTTTTCTTATCAGCTTGAGAGTCTTCAAGCTGATCTGCTTAAACGT	1039
QY	961	GATTCCTAGAGTACAAAGCTATCTCCAAAGATGAGCTTGAAGATTAAGAGAGACATGCG	1020
Db	1040	GATTCCTAGAGTACAAAGCTATCTCCAAAGATGAGCTTGAAGATTAAGAGAGACATGCG	1099
QY	1021	GTCTCTTTGAAAATTAAGGCAGACACAAGAAAGAAAGAGCTTACCTTACCCAGCATATA	1080
Db	1100	GTCTCTTTGAAAATTAAGGCAGACACAAGAAAGAAAGAGCTTACCTTACCCAGCATATA	1159
QY	1081	CTGTGGGGATGTCTCTCCAGTCAATTTTATCTGTGTCTTGAATTCGAGCAATTCCT	1140
Db	1160	CTGTGGGGATGTCTCTCCAGTCAATTTTATCTGTGTCTTGAATTCGAGCAATTCCT	1219

QY 1141 AAAAGCATTTTGGAGCCCTTGTGACTATACAGTGAAGTGTGTAAGGCGCAG 1200
DB 1220 AAAAGGCAATTTTGGAGCCCTTGTGACTATACAGTGAAGTGTGTAAGGCGCAG 1279
QY 1201 CTACAGAGCTGTGAGTAAACAAGGGGAGCGGATTAATAGCCGCTTGTAGAGATGCG 1260
DB 1280 CTACAGAGCTGTGAGTAAACAAGGGGAGCGGATTAATAGCCGCTTGTAGAGATGCG 1339
QY 1261 TGTGCTGTGTTGTGATCTCTCTCGCTTTTCCCTTGTGCGAGCAGCACTCACTCTC 1320
DB 1340 TGTGCTGTGTTGTGATCTCTCTCGCTTTTCCCTTGTGCGAGCAGCACTCACTCTC 1399
QY 1321 CTGTCTGAACATCTTCTTAACCTTCAACCCAGACCATATTTGTGTGCAAGCTCAAGTTA 1380
DB 1400 CTGTCTGAACATCTTCTTAACCTTCAACCCAGACCATATTTGTGTGCAAGCTCAAGTTA 1459
QY 1381 TTTCACCCAGGAAGCTCCATTTTGTCTTCAACATTTGTGGAATTTCTGTCTACTGCGACA 1440
DB 1460 TTTCACCCAGGAAGCTCCATTTTGTCTTCAACATTTGTGGAATTTCTGTCTACTGCGACA 1519
QY 1441 ACAGAGTTCTGGGAGAGGAGTATGACAGCTGTGCTGTGTTGTGCTTCAAGTT 1500
DB 1520 ACAGAGTTCTGGGAGAGGAGTATGACAGCTGTGCTGTGTTGTGCTTCAAGTT 1579
QY 1501 CTTCAGCCCAACATTCATGCTATCCCATGAAGAAGCGGGAAAGCCCTGGCTCTTAAGATA 1560
DB 1580 CTTCAGCCCAACATTCATGCTATCCCATGAAGAAGCGGGAAAGCCCTGGCTCTTAAGATA 1639
QY 1561 TCCATCTCTCTGGAACAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
DB 1640 TCCATCTCTCTGGAACAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1699
QY 1621 ATATATGTGGTTCAGGAACCGGCAATAGCCCGTTTATTTGGTTCTTCAACAATAGAGAG 1680
DB 1700 ATATATGTGGTTCAGGAACCGGCAATAGCCCGTTTATTTGGTTCTTCAACAATAGAGAG 1759
QY 1681 AAATCTCCAAACAACAACCCAGATGGAATTTTGGAGCAATGTGTGTTTGTGGCTGC 1740
DB 1760 AAATCTCCAAACAACAACCCAGATGGAATTTTGGAGCAATGTGTGTTTGTGGCTGC 1819
QY 1741 AGGCTATAGGATAGGATTAATCTATTCAGAAAAAGAGTCAAGATTTCTTAAAGCATGGG 1800
DB 1820 AGGCTATAGGATAGGATTAATCTATTCAGAAAAAGAGTCAAGATTTCTTAAAGCATGGG 1879
QY 1801 ATCTTAATCATTAAGGTTTCTTCTCAAGAGATGCTCTGTGTGGGAGAGAGAGCC 1860
DB 1880 ATCTTAATCATTAAGGTTTCTTCTCAAGAGATGCTCTGTGTGGGAGAGAGAGCC 1939
QY 1861 CCAGCAAAAGTATGTAACAACAATCCAGCTTCATGGCCAGAGGTGGGAGAAATCTTC 1920
DB 1940 CCAGCAAAAGTATGTAACAACAATCCAGCTTCATGGCCAGAGGTGGGAGAAATCTTC 1999
QY 1921 CTCAGAGAGAGCGCCATATTTATGTGTGTGAGATGCAAGAATATGCGCAAGATGTA 1980
DB 2000 CTCAGAGAGAGCGCCATATTTATGTGTGTGAGATGCAAGAATATGCGCAAGATGTA 2059
QY 1981 CATGATGCCCTTGTGCAATATATPAAGCAAGAGGTTGAGTTGAAAACTAGAAGCAATG 2040
DB 2060 CATGATGCCCTTGTGCAATATATPAAGCAAGAGGTTGAGTTGAAAACTAGAAGCAATG 2119
QY 2041 AAAACCTGGCCCTTTAAAAAGAAAGAAACGCTACCTTCAAGATATTTGTCTATAA 2097
DB 2120 AAAACCTGGCCCTTTAAAAAGAAAGAAACGCTACCTTCAAGATATTTGTCTATAA 2176

RESULT 3
ID ADM43206 standard; cDNA; 3259 BP.
XX ADM43206;
XX AC
XX ADM43206;
XX DT 03-JUN-2004 (first entry)
XX

DE Human full length cDNA encoding methionine synthase reductase.
XX
XX Human; ss; gene; Methionine synthase reductase polypeptide; HsmTRR;
KW cancer; cardiovascular disease; neural tube defect;
KW hyperhomocysteinemia; chromosome 5p15.2-p15.3; SNR;
KW single nucleotide polymorphism.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 80..2176
FT /tag= a "HsmTRR"
FT /product= "HsmTRR"
FT variation replace(145,A)
FT /tag= b
FT /standard_name= "Single_nucleotide_polymorphism"
FT variation replace(189,A)
FT /tag= c
FT /standard_name= "Single_nucleotide_polymorphism"
XX
XX US2003082676-A1.
XX
XX 01-MAY-2003.
XX
XX 10-AUG-1999; 99US-00371347.
XX
XX 16-JAN-1998; 98US-0071622P.
XX 15-JAN-1999; 99US-00232028.
XX
XX (GRAY/) GRAVEL R. A.
XX (ROZE/) ROZEN R.
XX (LECL/) LECLERC D.
XX (WILS/) WILSON A.
XX (ROSE/) ROSENBLATT D.
XX
XX Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX WPI; 2003-576610/54.
XX P-PSDB; ADM43207.
XX
XX New substantially pure nucleic acid encoding a mammalian methionine
PT synthase reductase polypeptide, useful for diagnosing, preventing or
PT treating conditions associated with altered methionine synthase activity,
PT e.g. cancer.
XX
XX Example 2; SEQ ID NO 24; 26pp; English.
XX
XX The invention relates to a substantially pure nucleic acid that encodes a
XX mammalian methionine synthase reductase polypeptide, HsmTRR, or that
XX hybridises at high stringency to a nucleic acid appearing as ADM43208 or
XX ADM43209. Also included are a non-human animal where one or both genetic
XX alleles encoding the methionine synthase reductase polypeptide are
XX mutated, an antibody that specifically binds the above methionine
XX synthase reductase polypeptide, a method of detecting the presence of the
XX above polypeptide, a method for detecting sequence variants for
XX methionine synthase reductase in a mammal, methods of treating or
XX preventing cancer (or cardiovascular disease or neural tube defects) in a
XX subject, methods of screening for a compound that modulates methionine
XX synthase reductase biological activity and a method for detecting an
XX increased risk of developing a neural tube defect in a mammalian embryo
XX or fetus. The nucleic acid is useful in diagnosing, preventing or
XX treating conditions associated with altered methionine synthase activity,
XX such as cancer, cardiovascular disease or neural tube defects, or in
XX screening for a compound that modulates methionine synthase reductase
XX biological activity. Naturally occurring variants of the polypeptide are
XX also associated with hyperhomocysteinemia. The gene for HsmTRR is
XX located on chromosome 5p15.2-p15.3. The present sequence is full length
XX sequence of the wild-type human hsmTRR cDNA.
XX
XX Sequence 3259 BP; 944 A; 695 C; 674 G; 946 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 2097; DB 11; Length 3259;
XX Best Local Similarity 100.0%; Pred. No. 0;

Matches 2097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANAGAGAGTTTCTGTAATATGCTACACAGAGGACAGGCAAGCCATCGAGAA 60
DB 80 ATGAGAGGTTCTGTACTATATGCTACACAGAGGACAGGCAAGCCATCGAGAA 139
QY 61 GAAATGTGAGCACTGTGTACATGATTTTCTGAGATCTTCACTGATTAAGTAA 120
DB 140 GAAATGTGAGCACTGTGTACATGATTTTCTGAGATCTTCACTGATTAAGTAA 199
QY 121 TCCGATATGATGACCTTAAACCCGAAACAGCTCTCTTGTGTGTGTTCTACACG 180
DB 200 TCCGATATGATGACCTTAAACCCGAAACAGCTCTCTTGTGTGTGTTCTACACG 259
QY 181 GGCACCGGAGACCCACCCGACAGAGCCGCAAGTTGTTAAGAAATPACGAAACA 240
DB 260 GGCACCGGAGACCCACCCGACAGAGCCGCAAGTTGTTAAGAAATPACGAAACA 319
QY 241 CTGCGGATGATTTCTTGTCTCACCTGCGGTATGGTTACTGGGTCTCGGTATTCAGAA 300
DB 320 CTGCGGATGATTTCTTGTCTCACCTGCGGTATGGTTACTGGGTCTCGGTATTCAGAA 379
QY 301 TACACCTACTTTTGCATATGAGGAGGAAATATTAATTAACGACTTCAAGAGTTGAGCC 360
DB 380 TACACCTACTTTTGCATATGAGGAGGAAATATTAATTAACGACTTCAAGAGTTGAGCC 439
QY 361 CGGATTTCTATGACACTGACATGACATGATGATGTGTAGGTTTAAAGCTTGTGTGAG 420
DB 440 CGGATTTCTATGACACTGACATGACATGATGATGTGTAGGTTTAAAGCTTGTGTGAG 499
QY 421 CGGTGATGCTGGAATCTGCGGACGCTCAGAAAGATTTTATGATCAAGCAGAGGACAA 480
DB 500 CGGTGATGCTGGAATCTGCGGACGCTCAGAAAGATTTTATGATCAAGCAGAGGACAA 559
QY 481 GAGAGATTAAGTGGCGCATCTCCGCTGATCATCTGATCTTGAAGACAGACTTGTG 540
DB 560 GAGAGATTAAGTGGCGCATCTCCGCTGATCATCTGATCTTGAAGACAGACTTGTG 619
QY 541 AAGTCAGAGCTGCTACATTTGAATCTCAAGTGTGATTTGAGATTCATGATTCAGGA 600
DB 620 AAGTCAGAGCTGCTACATTTGAATCTCAAGTGTGATTTGAGATTCATGATTCAGGA 679
QY 601 AGAAGGATCTGAGGTTTGAAGCAAAATGACGTGAACAGCAACCAATCCAATGTTGTA 660
DB 680 AGAAGGATCTGAGGTTTGAAGCAAAATGACGTGAACAGCAACCAATCCAATGTTGTA 739
QY 661 ATTGAAGACTTGAAGTCTCACTTACCCGTTGCTGATCCCACTCTCAAGGCTCTG 720
DB 740 ATTGAAGACTTGAAGTCTCACTTACCCGTTGCTGATCCCACTCTCAAGGCTCTG 799
QY 721 AATATTCCTGTTTACCCCAAAATTTTACAGGTACATCTGACAGAGTCTTGGCCAG 780
DB 800 AATATTCCTGTTTACCCCAAAATTTTACAGGTACATCTGACAGAGTCTTGGCCAG 859
QY 781 GAGGAAAGCAAGATATGTAAGTTCAGAGATCCAGTTTTCAGAGGCAATTTCAAG 840
DB 860 GAGGAAAGCAAGATATGTAAGTTCAGAGATCCAGTTTTCAGAGGCAATTTCAAG 919
QY 841 GCAGTTCACTTACGAAATGATGCAATTAACCACTGCTGTGATGAATTTGACAT 900
DB 920 GCAGTTCACTTACGAAATGATGCAATTAACCACTGCTGTGATGAATTTGACAT 979
QY 901 TCAAAATCAGACTTTTCTATCAGCTGTGAGATGCTTCAAGCTGATCTGCTTAAGT 960
DB 980 TCAAAATCAGACTTTTCTATCAGCTGTGAGATGCTTCAAGCTGATCTGCTTAAGT 1039
QY 961 GATTTGAGGTAACAAGCTTATCTCAAGACTGAGATGCTTCAAGCTGATCTGCTTAAGT 1020
DB 1040 GATTTGAGGTAACAAGCTTATCTCAAGACTGAGATGCTTCAAGCTGATCTGCTTAAGT 1099
QY 1021 GTCTTTTGAATAAAGGACGACACAAAGAAAGAGCTTACCTTACCCAGCATATA 1080
DB 1100 GTCTTTTGAATAAAGGACGACACAAAGAAAGAGCTTACCTTACCCAGCATATA 1159

QY 1081 CTGCGGATGATTTCTCTCAGTTCAATTTTACCTGCTGTTGAAATCCGAGCAATTCCT 1140
DB 1160 CTGCGGATGATTTCTCTCAGTTCAATTTTACCTGCTGTTGAAATCCGAGCAATTCCT 1219
QY 1141 AAAAAGCATTTTGTGAGACCTTGTGACATATTAACGATGACAGTCTGAAAAGCCAG 1200
DB 1220 AAAAAGCATTTTGTGAGACCTTGTGACATATTAACGATGACAGTCTGAAAAGCCAG 1279
QY 1201 CTACAGAGCTGTGACATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
DB 1280 CTACAGAGCTGTGACATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1339
QY 1261 TGTGCTGCTGTGATCTCTCTGCTGCTTCCCTTCTTGCAGGACCACTCACTCTC 1320
DB 1340 TGTGCTGCTGTGATCTCTCTGCTGCTTCCCTTCTTGCAGGACCACTCACTCTC 1399
QY 1321 CTGCTGAAATCTTCTTAACTCAACCCAGACATATGCTGTGCAAGCTCAAGTTTA 1380
DB 1400 CTGCTGAAATCTTCTTAACTCAACCCAGACATATGCTGTGCAAGCTCAAGTTTA 1459
QY 1381 TTTCAACCGAAGAGTCCATTTTGTCTTCAATTTGTGAAATTTCTGTCTACTGCA 1440
DB 1460 TTTCAACCGAAGAGTCCATTTTGTCTTCAATTTGTGAAATTTCTGTCTACTGCA 1519
QY 1441 ACAGAGTTCTGCGAAGGAGATATGATACAGGCTGAGCTGTTGTGTTGCTTCA 1500
DB 1520 ACAGAGTTCTGCGAAGGAGATATGATACAGGCTGAGCTGTTGTGTTGCTTCA 1579
QY 1501 CTTCAGCAAAATCATCATCATCCATGAAAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
DB 1580 CTTCAGCAAAATCATCATCATCCATGAAAGACGCGGAAAGCCCTGCTCTTAAGATA 1639
QY 1561 TGCATCTCTCTGAAACAAATTTTCTCACTTACAGATACAGGATCCCTCAATCCGATC 1620
DB 1640 TGCATCTCTCTGAAACAAATTTTCTCACTTACAGATACAGGATCCCTCAATCCGATC 1699
QY 1621 ATTAATGTTGATCAGAAACCGGATAGCCGCTTATTTGGGTTCTTCAACATAGAGAG 1680
DB 1700 ATTAATGTTGATCAGAAACCGGATAGCCGCTTATTTGGGTTCTTCAACATAGAGAG 1759
QY 1681 AAATCTCAAGAACCAACCCAGATGAGAAATTTTGAAGCAATGTGTTTGTGCTGC 1740
DB 1760 AAATCTCAAGAACCAACCCAGATGAGAAATTTTGAAGCAATGTGTTTGTGCTGC 1819
QY 1741 AGGATTAAGATAGGATTTATCTTCAAGAAAGAGCTCAAGATTTCTTAAAGATGAG 1800
DB 1820 AGGATTAAGATAGGATTTATCTTCAAGAAAGAGCTCAAGATTTCTTAAAGATGAG 1879
QY 1801 ATCTTAATCATCTAAGGTTTCTCTCAAGAGATGCTCTGTGAGGAGAGAGAGCC 1860
DB 1880 ATCTTAATCATCTAAGGTTTCTCTCAAGAGATGCTCTGTGAGGAGAGAGAGCC 1939
QY 1861 CCAGCAAGATATGTAACAGACATCACTGATGAGGACAGAGGAGGAGATCTCTC 1920
DB 1940 CCAGCAAGATATGTAACAGACATCACTGATGAGGACAGAGGAGGAGATCTCTC 1999
QY 1921 CTCAGAGAGAGGCAATTTATGTGTGTGAGATGCAAGATATGCTCAAGATGTA 1980
DB 2000 CTCAGAGAGAGGCAATTTATGTGTGTGAGATGCAAGATATGCTCAAGATGTA 2059
QY 1981 CATGATGCTGTTGCAATTAATTAAGCAAGAGGTTGAGTGAAGAACTGAAAGCAATG 2040
DB 2060 CATGATGCTGTTGCAATTAATTAAGCAAGAGGTTGAGTGAAGAACTGAAAGCAATG 2119
QY 2041 AAAAACCCTGCGCATTTTAAAGAAAGAAAGCGTACCTTCAAGATATTTGTGATATA 2097
DB 2120 AAAAACCCTGCGCATTTTAAAGAAAGAAAGCGTACCTTCAAGATATTTGTGATATA 2176

RESULT 4
ADM43208
ID ADM43208 standard; cDNA; 2094 BP.

XX ADM43208;
AC 03-JUN-2004 (first entry)
DT
XX
DE Human wild-type methionine synthase reductase CDS.
KW
XX Human; 88; Methionine synthase reductase polypeptide; HsMTRR; cancer;
KW cardiovascular disease; neural tube defect; hyperhomocysteinaemia;
KW chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.
XX Homo sapiens.
OS
FH Location/Qualifiers
FH Key 1..2094
FT /tag= a
FT /product= "hsMTRR"
FT /partial
FT /note= "No stop codon shown"
FT replace(66,A)
FT /tag= b
FT /standard_name= "Single_nucleotide_polymorphism"
FT replace(110,A)
FT /tag= c
FT /standard_name= "Single_nucleotide_polymorphism"
XX US2003082676-A1.
XX 01-MAY-2003.
XX 10-AUG-1999; 99US-00371347.
XX 16-JAN-1998; 98US-0071622P.
XX 15-JAN-1999; 99US-00232028.
XX
XX (GRAV/) GRAVEL R A.
XX (ROZE/) ROZEN R.
XX (LECL/) LECLEERC D.
XX (WILS/) WILSON A.
XX (ROSE/) ROSENBLATT D.
XX
XX Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX WPI; 2003-576610/54.
XX P-PSDB; ADM43207.
XX
XX New substantially pure nucleic acid encoding a mammalian methionine
XX synthase reductase polypeptide, useful for diagnosing, preventing or
XX treating conditions associated with altered methionine synthase activity,
XX e.g. cancer.
XX
XX Claim 3; SEQ ID NO 1; 26bp; English.
XX
XX The invention relates to a substantially pure nucleic acid that encodes a
XX mammalian methionine synthase reductase polypeptide, HsMTRR, or that
XX hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
XX ADM43209. Also included are a non-human animal where one or both genetic
XX alleles encoding the methionine synthase reductase polypeptide are
XX mutated, an antibody that specifically binds the above methionine
XX synthase reductase polypeptide, a method of detecting the presence of the
XX above polypeptide, a method for detecting sequence variants for
XX methionine synthase reductase in a mammal, methods of treating or
XX preventing cancer (or cardiovascular disease or neural tube defects) in a
XX subject, methods of screening for a compound that modulates methionine
XX synthase reductase biological activity and a method for detecting an
XX increased risk of developing a neural tube defect in a mammalian embryo
XX or fetus. The nucleic acid is useful in diagnosing, preventing or
XX treating conditions associated with altered methionine synthase activity,
XX such as cancer, cardiovascular disease or neural tube defects, or in
XX screening for a compound that modulates methionine synthase reductase
XX biological activity. Naturally occurring variants of the polypeptide are
XX also associated with hyperhomocysteinaemia. The gene for HsMTRR is
XX located on chromosome 5p15.2-p15.3. The present sequence is the coding

CC sequence of the wild-type human hsMTRR cDNA.
XX
SQ Sequence 2094 BP; 591 A; 489 C; 481 G; 533 T; 0 U; 0 Other;
Query Match 99.9%; Score 2094; DB 11; Length 2094;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2094; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGAGGTTTCTGTACTATATGCTATACACAGCAGGACAGGCAAGCCATCGAGAA 60
DB 1 ATGAGAGGTTTCTGTACTATATGCTATACACAGCAGGACAGGCAAGCCATCGAGAA 60
QY 61 GAAATGTGAGCAACCTGTGTACATGATGATTTTTCGAGATCTGATATAGTGA 120
DB 61 GAAATGTGAGCAACCTGTGTACATGATGATTTTTCGAGATCTGATATAGTGA 120
QY 121 TCCGATATGATGACCTTAAACCCGAAACAGCTCTCTTGTGTGTGTCTTACACG 180
DB 121 TCCGATATGATGACCTTAAACCCGAAACAGCTCTCTTGTGTGTGTCTTACACG 180
QY 181 GGCACCGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAAACAA 240
DB 181 GGCACCGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAAACAA 240
QY 241 CTGCCGGTGTATTTCTTGTCTACCTGCGGTATAGGTTACTGGGTCCTGGTATTCAGAA 300
DB 241 CTGCCGGTGTATTTCTTGTCTACCTGCGGTATAGGTTACTGGGTCCTGGTATTCAGAA 300
QY 301 TACACCTACTTTTGCAATGGGGGAGATATATGATTAACGACTTCAGAGCTTGAAGCC 360
DB 301 TACACCTACTTTTGCAATGGGGGAGATATATGATTAACGACTTCAGAGCTTGAAGCC 360
QY 361 CGGCATTTCTATGACACTGGACATGCAATGATGACTGTGATGTTAAGACTTGTGTGAG 420
DB 361 CGGCATTTCTATGACACTGGACATGCAATGATGACTGTGATGTTAAGACTTGTGTGAG 420
QY 421 CCGTGATTTGCTGACCTGCGCCAGCCCTCAGAAACATTTTATGATCAAGAGGACAA 480
DB 421 CCGTGATTTGCTGACCTGCGCCAGCCCTCAGAAACATTTTATGATCAAGAGGACAA 480
QY 481 GAGAGATTAAGTGGCCACTCCCGGTGGCATCACTGCATCTTGAAGGACAGACTTGTG 540
DB 481 GAGAGATTAAGTGGCCACTCCCGGTGGCATCACTGCATCTTGAAGGACAGACTTGTG 540
QY 541 AAGTCAGAGCTGTACACATTTGAATCTCAAGTCAGCTTGTGATTCATGATTCAGGA 600
DB 541 AAGTCAGAGCTGTACACATTTGAATCTCAAGTCAGCTTGTGATTCATGATTCAGGA 600
QY 601 AGAAGGATTCAGAGTTTGAAGCAAAATGACGTGAACAGCAACCAATCCAAATGTTGTA 660
DB 601 AGAAGGATTCAGAGTTTGAAGCAAAATGACGTGAACAGCAACCAATCCAAATGTTGTA 660
QY 661 ATTAAGACCTTGTAGCTTCACCTTACCCGTCGTAACCCCACTTCACAGCCCTCTG 720
DB 661 ATTAAGACCTTGTAGCTTCACCTTACCCGTCGTAACCCCACTTCACAGCCCTCTG 720
QY 721 AATATTCCTGTTTACCCCAAGATATTTTACAGATCATCTGACAGAGTCTCTTGGCAG 780
DB 721 AATATTCCTGTTTACCCCAAGATATTTTACAGATCATCTGACAGAGTCTCTTGGCAG 780
QY 781 GAGAAAGCCAAATATCTGACCTGACAGAGATCCAGTTTTCAGAGCCAAATTTCAAAG 840
DB 781 GAGAAAGCCAAATATCTGACCTGACAGAGATCCAGTTTTCAGAGCCAAATTTCAAAG 840
QY 841 GCAGTTCAACTTCTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 GCAGTTCAACTTCTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 TCAAAATACAGACTTTTCTATACAGCTGAGATGCTTACAGCTGATCTGCTTACAGT 960
DB 901 TCAAAATACAGACTTTTCTATACAGCTGAGATGCTTACAGCTGATCTGCTTACAGT 960
QY 961 GATTCTGAGTACAAAGCCATCTCAAAAGCTGACCTGTAAGATTAAGAGAGCACTGC 1020

Db 961 GATTCGAGGTACAAAGCCTACTCCAAAGCTGCAGCTTGAATATAAGAGGAGCTGC 1020
 QY 1021 GTTCCTTTGAAAATAAAGGACACACAAAGAAAGAGCTACTTACCACGACATATA 1080
 Db 1021 GTTCCTTTGAAAATAAAGGACACACAAAGAAAGAGCTACTTACCACGACATATA 1080
 QY 1081 CCGGGGAGATGTTCTCCAGCTCATTTTATCGTGATCTGAATCCGAGCAATTCCT 1140
 Db 1081 CCGGGGAGATGTTCTCCAGCTCATTTTATCGTGATCTGAATCCGAGCAATTCCT 1140
 QY 1141 AAAAAGGCAATTTTGGAGCCCTTGTGACATATACAGTACAGTCTGAAAAAGCCAG 1200
 Db 1141 AAAAAGGCAATTTTGGAGCCCTTGTGACATATACAGTACAGTCTGAAAAAGCCAG 1200
 QY 1201 CTACAGAGCTGTGACGTAAACAGGGGAGCCGATTAATACCGCTTTGTACAGATGCC 1260
 Db 1201 CTACAGAGCTGTGACGTAAACAGGGGAGCCGATTAATACCGCTTTGTACAGATGCC 1260
 QY 1261 TGTGCTGCTGTGTGATCTCCCTCTCGCTTTCCTTGGACAGCCACACTCAGTCTC 1320
 Db 1261 TGTGCTGCTGTGTGATCTCCCTCTCGCTTTCCTTGGACAGCCACACTCAGTCTC 1320
 QY 1321 CTGCTGAAATCTTCTTAACTTCAACCAAGACATATTCGTGTCAAGCTCAAGTTTA 1380
 Db 1321 CTGCTGAAATCTTCTTAACTTCAACCAAGACATATTCGTGTCAAGCTCAAGTTTA 1380
 QY 1381 TTTGACCCAGAAAAGCTCCATTTTGTCTTCAATGTGAAATTTCTGTACTGCCACA 1440
 Db 1381 TTTGACCCAGAAAAGCTCCATTTTGTCTTCAATGTGAAATTTCTGTACTGCCACA 1440
 QY 1441 ACGAGGTTCTGGGAGGAGATATGACAGCTGCTGCTTGTGTGTTGCTTCAAGTT 1500
 Db 1441 ACGAGGTTCTGGGAGGAGATATGACAGCTGCTGCTTGTGTGTTGCTTCAAGTT 1500
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 Db 1501 CTTGACCCAAATATCATGTGATCCCATGAGACAGCGGAAACCTGCTCTTAAGATA 1560
 QY 1561 TCCATCTCTCTCGAACAACAAATTTCTTCACTTACCAATGACCCCTCAATCCCATC 1620
 Db 1561 TCCATCTCTCTCGAACAACAAATTTCTTCACTTACCAATGACCCCTCAATCCCATC 1620
 QY 1621 ATTAATGTTGGTTCAGAAACCGGCATAGCCCGTTTATTTGGTTCTTAACAATAGAG 1680
 Db 1621 ATTAATGTTGGTTCAGAAACCGGCATAGCCCGTTTATTTGGTTCTTAACAATAGAG 1680
 QY 1681 AAATCCAAAGAACACCCAGATGGAATTTTGAAGCAATGTTGTTTGTGCTGC 1740
 Db 1681 AAATCCAAAGAACACCCAGATGGAATTTTGAAGCAATGTTGTTTGTGCTGC 1740
 QY 1741 AGGCAATAGATAGGATTAATCTATTCAGAAAAGCTCAGACATTTCTTAAGATGG 1800
 Db 1741 AGGCAATAGATAGGATTAATCTATTCAGAAAAGCTCAGACATTTCTTAAGATGG 1800
 QY 1801 ATCTTAATCATTTAAAGTTTCTTCTCAAGAGATGCTCTGTGGGAGGAGAGGCC 1860
 Db 1801 ATCTTAATCATTTAAAGTTTCTTCTCAAGAGATGCTCTGTGGGAGGAGAGGCC 1860
 QY 1861 CCAGAAAGTATTAACAACAATCATCAGCTTCATGAGCAGAGGAGGAGGAGATCTC 1920
 Db 1861 CCAGAAAGTATTAACAACAATCATCAGCTTCATGAGCAGAGGAGGAGGAGATCTC 1920
 QY 1921 CTCAGAGAGAGCGGCATATTTATGTGTGAGATGCAAAAGATATGCGCAAGATGA 1980
 Db 1921 CTCAGAGAGAGCGGCATATTTATGTGTGAGATGCAAAAGATATGCGCAAGATGA 1980
 QY 1981 CAGGATGCTTTGTGCAAAATTAAGCAAGAGGTTGAATTAAGAACTAGAGCAATG 2040
 Db 1981 CAGGATGCTTTGTGCAAAATTAAGCAAGAGGTTGAATTAAGAACTAGAGCAATG 2040
 QY 2041 AAAACCTGGCACCCTTAAAGAAAGAAAAGCTACCTTCAAGATATTTGTGCA 2094
 Db 2041 AAAACCTGGCACCCTTAAAGAAAGAAAAGCTACCTTCAAGATATTTGTGCA 2094

Db 2041 AAAACCTGGCACCCTTAAAGAAAGAAAAGCTACCTTCAAGATATTTGTGCA 2094
 RESULT 5
 ADM43212
 ID ADM43212 standard; cDNA; 2094 BP.
 AC ADM43212;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human methionine synthase reductase CDS G110A variant.
 XX
 KW Human; ss; Methionine synthase reductase polypeptide; HsMTRR; cancer;
 KW cardiovascular disease; neural tube defect; hyperhomocysteinemia;
 KW chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2094
 FT /tag= a
 FT /product= "HsMTRR"
 FT /partial
 FT /note= "No stop codon shown"
 FT variation
 FT /tag= b
 FT /standard_name= "Single_nucleotide_polymorphism"
 FT /replace (110,G)
 FT /tag= c
 FT /standard_name= "Single_nucleotide_polymorphism"
 XX
 PN US2003082676-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 10-AUG-1999; 99US-00371347.
 XX
 PR 16-JAN-1998; 98US-0071622P.
 PR 15-JAN-1999; 99US-00233028.
 XX
 PA (GRAV/) GRAVEL R A.
 PA (ROZE/) ROZEN R.
 PA (LECL/) LECLERC D.
 PA (WILS/) WILSON A.
 PA (ROSE/) ROSENBLATT D.
 XX
 PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
 XX
 DR WPI, 2003-576610/54.
 DR P-PSDB; ADM43213.
 XX
 PT New substructially pure nucleic acid encoding a mammalian methionine
 PT synthase reductase polypeptide, useful for diagnosing, preventing or
 PT treating conditions associated with altered methionine synthase activity,
 PT e.g. cancer.
 XX
 XX
 XX Disclosure; SEQ ID NO 43; 26bp; English.
 XX
 XX The invention relates to a substructially pure nucleic acid that encodes a
 CC mammalian methionine synthase reductase polypeptide, HsMTRR, or that
 CC hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
 CC ADM43209. Also included are a non-human animal where one or both genetic
 CC alleles encoding the methionine synthase reductase polypeptide are
 CC mutated, an antibody that specifically binds the above methionine
 CC synthase reductase polypeptide, a method of detecting the presence of the
 CC above polypeptide, a method for detecting sequence variants for
 CC methionine synthase reductase in a mammal, methods of treating or
 CC preventing cancer (or cardiovascular disease or neural tube defects) in a
 CC subject, methods of screening for a compound that modulates methionine
 CC synthase reductase biological activity and a method for detecting an
 CC increased risk of developing a neural tube defect in a mammalian embryo
 CC or foetus. The nucleic acid is useful in diagnosing, preventing or

QY 1981 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGTTGGAGTTGAAACTAGAACCAATG 2040
DB 1981 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGTTGGAGTTGAAACTAGAACCAATG 2040
QY 2041 AAAACCTGCGCATTAAAGAGAAAAAGCCTACCTTCAGATATTTGTGCA 2094
DB 2041 AAAACCTGCGCATTAAAGAGAAAAAGCCTACCTTCAGATATTTGTGCA 2094
RESULT 6
ADM43209
ID ADM43209 standard; cDNA; 2094 BP.
AC ADM43209;
XX
DT 03-JUN-2004 (first entry)
DE Human methionine synthase reductase CDS G66A variant.
XX
XX Human; ss: Methionine synthase reductase polypeptide; HsMTRR; cancer;
KM cardiovascular disease; neural tube defect; hyperhomocysteinemia;
XX chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2094
FT /*tag= a
FT /product= "HsMTRR"
FT /partial
FT /note= "No stop codon shown"
FT variation /*tag= b
FT /standard_name= "Single_nucleotide_polymorphism"
FT replace(110,A)
FT /*tag= c
FT /standard_name= "Single_nucleotide_polymorphism"
XX US2003082676-A1.
XX
XX 01-MAY-2003.
PD 10-AUG-1999; 99US-00371347.
PF 16-JAN-1998; 98US-0071622P.
PR 15-JAN-1999; 99US-00232028.
XX
XX (GRAV/) GRAVEL R. A.
PA (ROZE/) ROZEN R. A.
PA (LECL/) LECLEERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
XX
PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX
XX MPI: 2003-576610/54.
XX P-PSDB: ADM43211.
XX
XX New substantially pure nucleic acid encoding a mammalian methionine
XX synthase reductase polypeptide, useful for diagnosing, preventing or
XX treating conditions associated with altered methionine synthase activity,
XX e.g. cancer.
XX
XX Claim 3; SEQ ID NO 41; 26pp; English.
XX
XX The invention relates to a substantially pure nucleic acid that encodes a
XX mammalian methionine synthase reductase polypeptide, HsMTRR, or that
XX hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
XX ADM43209. Also included are a non-human animal where one or both genetic
XX alleles encoding the methionine synthase reductase polypeptide are
XX mutated, an antibody that specifically binds the above methionine
XX synthase reductase polypeptide, a method of detecting the presence of the
XX above polypeptide, a method for detecting sequence variants for

CC methionine synthase reductase in a mammal, methods of treating or
CC preventing cancer (or cardiovascular disease or neural tube defects) in a
CC subject, methods of screening for a compound that modulates methionine
CC synthase reductase biological activity and a method for detecting an
CC increased risk of developing a neural tube defect in a mammalian embryo
CC or foetus. The nucleic acid is useful in diagnosing, preventing or
CC treating conditions associated with altered methionine synthase activity,
CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are
CC also associated with hyperhomocysteinemia. The gene for HsMTRR is
CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
CC sequence of a variant human HsMTRR cDNA.
XX
SQ Sequence 2094 BP; 592 A; 489 G; 480 G; 533 T; 0 U; 0 Other;
Query Match 97.4%; Score 2043; DB 11; Length 2094;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAGAGAGTTTCTGTTACTATATAGTCAACAGCAGGAGCAGCAAGGCCATCGCAGAA 60
DB 1 ATGAGAGAGTTTCTGTTACTATATAGTCAACAGCAGGAGCAGCAAGGCCATCGCAGAA 60
QY 61 GAAATGTGAGCAGACTGTGATCATGGAATTTCTGAGATCTTCACTGTATTAGTGA 120
DB 61 GAAATGTGAGCAGACTGTGATCATGGAATTTCTGAGATCTTCACTGTATTAGTGA 120
QY 121 TCCGATTAAGTATGACCTTAAAAACGAAACAGCTCTTGTGTTGTGTTCTACACG 180
DB 121 TCCGATTAAGTATGACCTTAAAAACGAAACAGCTCTTGTGTTGTGTTCTACACG 180
QY 181 GGCACCGAGACCCACCCGACGACCCGCAAGTTTGTAAAGAAATACAGAACCAAA 240
DB 181 GGCACCGAGACCCACCCGACGACCCGCAAGTTTGTAAAGAAATACAGAACCAAA 240
QY 241 CTGCCGTTGATTTCTTGTCTCACTGCGGTATGCGTTACTGGTCTCGGTATTCAGAA 300
DB 241 CTGCCGTTGATTTCTTGTCTCACTGCGGTATGCGTTACTGGTCTCGGTATTCAGAA 300
QY 301 TACACCTTACTTTGCAATGGGGGAAATATGATTAACGACTTCAGAGCTTGAGGCC 360
DB 301 TACACCTTACTTTGCAATGGGGGAAATATGATTAACGACTTCAGAGCTTGAGGCC 360
QY 361 CGGCATTTCTATGACATCTGACATGCAATGATGATGATTTGATTTGATTTGATG 420
DB 361 CGGCATTTCTATGACATCTGACATGCAATGATGATGATTTGATTTGATTTGATG 420
QY 421 CCGTGATTTGCTGACTGTGCGCAGCCCTCAGAAAGATTTTATAGTCAAGAGAGCAA 480
DB 421 CCGTGATTTGCTGACTGTGCGCAGCCCTCAGAAAGATTTTATAGTCAAGAGAGCAA 480
QY 481 GAGGAGATTAAGTGGGCACTCCCGGTGCGATCCTGATCTTGAAGACAGACCTTGTG 540
DB 481 GAGGAGATTAAGTGGGCACTCCCGGTGCGATCCTGATCTTGAAGACAGACCTTGTG 540
QY 541 AAGTCAGAGCTCTACATTAATCTCAATGAGCTTCTGAGATTCATGATTTACAGA 600
DB 541 AAGTCAGAGCTCTACATTAATCTCAATGAGCTTCTGAGATTCATGATTTACAGA 600
QY 601 AAGTCAGAGCTCTACATTAATCTCAATGAGCTTCTGAGATTCATGATTTACAGA 600
DB 601 AAGTCAGAGCTCTACATTAATCTCAATGAGCTTCTGAGATTCATGATTTACAGA 600
QY 601 AGAAAGATTCAGAGTTTGAAGCAAAATGAGTGAACAGAACCAATCCATGTTGTA 660
DB 601 AGAAAGATTCAGAGTTTGAAGCAAAATGAGTGAACAGAACCAATCCATGTTGTA 660
QY 661 ATTGAAGACTTGAAGTCTCACTTACCCGTTGGTATACCCCACTCAACAACTCTCTG 720
DB 661 ATTGAAGACTTGAAGTCTCACTTACCCGTTGGTATACCCCACTCAACAACTCTCTG 720
QY 721 AATATTTCTGTTTACCCCAAAATATTTACAGTACATCTGACAGAGTCTTGGCCAG 780
DB 721 AATATTTCTGTTTACCCCAAAATATTTACAGTACATCTGACAGAGTCTTGGCCAG 780
QY 781 GAGGAAGCAGATCTGTGACTTCAGACATCCAGTTTCAAGTGCCTTCAATTCNAAG 840


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Db 781 GAGAAAGCCGATCTGACTGAGCAGATCCAGTTTCAAGGCCAAATTCAMAG 840
Qy 841 GCAGTCAACTCTACGAATGATGCAATAAAACCACTGCGGTGAGAAATGGAATT 900
Db 841 GCAGTCAACTCTACGAATGATGCAATAAAACCACTGCGGTGAGAAATGGAATT 900
Qy 901 TCAATACAGACTTTTCTATCAGCCCTGAGATGCTTCAAGCGTATCTGCCCTAACAT 960
Db 901 TCAATACAGACTTTTCTATCAGCCCTGAGATGCTTCAAGCGTATCTGCCCTAACAT 960
Qy 961 GATTCTGAGGTACAAAGCTTACTCCAAAGCTGCAAGTTGAAGATTAAGAGCACTGC 1020
Db 961 GATTCTGAGGTACAAAGCTTACTCCAAAGCTGCAAGTTGAAGATTAAGAGCACTGC 1020
Qy 1021 GTGCTTTGAAAAATTAAGGAGACACAAAGAAAGAGAGCTTACCCGACATATA 1080
Db 1021 GTGCTTTGAAAAATTAAGGAGACACAAAGAAAGAGAGCTTACCCGACATATA 1080
Qy 1081 CTTGCGGAGATGTTCTCTCAAGTTCATTTTACCTGCTGATGATCCGAGCAATTCCT 1140
Db 1081 CTTGCGGAGATGTTCTCTCAAGTTCATTTTACCTGCTGATGATCCGAGCAATTCCT 1140
Qy 1141 AAAAAGGCAATTTTTCGAGCCCTTGTGACTATACAGTGAAGTCTGAAAAAGCCGAGG 1200
Db 1141 AAAAAGGCAATTTTTCGAGCCCTTGTGACTATACAGTGAAGTCTGAAAAAGCCGAGG 1200
Qy 1201 CTACAGAGGCTGTCAGTAAACAAAGGGGAGCCGATATATAGCCGCTTGTACGAGATGCC 1260
Db 1201 CTACAGAGGCTGTCAGTAAACAAAGGGGAGCCGATATATAGCCGCTTGTACGAGATGCC 1260
Qy 1261 TGTGCTGCTGTTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
Db 1261 TGTGCTGCTGTTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
Qy 1321 CTGCTGCAATCTTCTCTAACTTCAACCCAGACATATCTGTGTGCAAGTCAAGTTTA 1380
Db 1321 CTGCTGCAATCTTCTCTAACTTCAACCCAGACATATCTGTGTGCAAGTCAAGTTTA 1380
Qy 1381 TTTCAACCCAGACATATCTGTGTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1440
Db 1381 TTTCAACCCAGACATATCTGTGTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1440
Qy 1441 ACAGAGGTTCTGCGAAGGAGATATGTAAGCTGAGCTGAGCTGTTGTTGCTTCAAGTT 1500
Db 1441 ACAGAGGTTCTGCGAAGGAGATATGTAAGCTGAGCTGAGCTGTTGTTGCTTCAAGTT 1500
Qy 1501 CTTGAGCCCAACATATCTGATCCCATGAAAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
Db 1501 CTTGAGCCCAACATATCTGATCCCATGAAAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
Qy 1561 TCCATCTCTCTCTGAAACAAATTTCTTTCACCTTACAGATGACCCCTCAATCCCATC 1620
Db 1561 TCCATCTCTCTCTGAAACAAATTTCTTTCACCTTACAGATGACCCCTCAATCCCATC 1620
Qy 1621 ATATATGTTGGGTCCAGGAAACCGGATAGCCCGTTTATTTGGGTTCTTACAAATAGAG 1680
Db 1621 ATATATGTTGGGTCCAGGAAACCGGATAGCCCGTTTATTTGGGTTCTTACAAATAGAG 1680
Qy 1681 AAATCTCCAAAGAAACCCAGATGAAATTTTGAAGCAATGTGTTTGTGCTGC 1740
Db 1681 AAATCTCCAAAGAAACCCAGATGAAATTTTGAAGCAATGTGTTTGTGCTGC 1740
Qy 1741 AGGATATAGATAGGATATATCTATTCAGAAAGAGCTCAGACATTTCTTAAGCATGGG 1800
Db 1741 AGGATATAGATAGGATATATCTATTCAGAAAGAGCTCAGACATTTCTTAAGCATGGG 1800
Qy 1801 ATCTTAATCTATCTAAAGTTTCTTCTCAAGAGATGCTCTGTGTGGGAGAGAGAGCC 1860
Db 1801 ATCTTAATCTATCTAAAGTTTCTTCTCAAGAGATGCTCTGTGTGGGAGAGAGAGCC 1860
Qy 1861 CCAGCAAGATATATCAAGACATCAAGTTCATGCGCCAGCAGGTGGGAGAAATCTCTC 1920
Db 1861 CCAGCAAGATATATCAAGACATCAAGTTCATGCGCCAGCAGGTGGGAGAAATCTCTC 1920
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Db 1861 CCAGCAAGATATATCAAGACATCAAGTTCATGCGCCAGCAGGTGGGAGAAATCTCTC 1920
Qy 1921 CTCACAGAGAAAGCCCATATTTATGTGTGAGATGCAAGAAATATGGCCAGATGTA 1980
Db 1921 CTCACAGAGAAAGCCCATATTTATGTGTGAGATGCAAGAAATATGGCCAGATGTA 1980
Qy 1981 CATGATGCCCTTGTGCAATATATACCAAGAGTTGAGTTGAAAAACTAGAACATG 2040
Db 1981 CATGATGCCCTTGTGCAATATATACCAAGAGTTGAGTTGAAAAACTAGAACATG 2040
Qy 2041 AAAACCTGCGCACTTTAAAGAAAGAAACGCTACCTCAGGATATTTGTCA 2094
Db 2041 AAAACCTGCGCACTTTAAAGAAAGAAACGCTACCTCAGGATATTTGTCA 2094

RESULT 7
ID AAAS8935 standard; DNA; 3259 BP.
XX
AC AAAS8935;
XX
DT 07-NOV-2000 (first entry)
XX
DE DNA encoding a human methionine synthase reductase polypeptide.
XX
KW Human; methionine synthase reductase; MTRR; cancer;
KW cardiovascular disease; Down's Syndrome; neural tube defect;
KW premature coronary artery disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 80..2176
FT /tag= a
FT /product= "methionine synthase reductase"
XX
FN W0200042196-A2.
XX
PD 20-JUL-2000.
XX
PF 14-JAN-2000; 2000MO-IB000209.
XX
PR 15-JAN-1999; 99US-00232028.
PR 10-AUG-1999; 99US-00371347.
XX
PA (UWMC-) UNIV MCGILL.
XX
PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
DR WPI; 2000-466131/40.
DR P-PSDB; AAB07591.
XX
PT Mammalian methionine synthase reductase nucleic acid used for detecting
PT an increased risk of developing a neural tube defect. Down's Syndrome or
PT cardiovascular disease in a mammalian embryo or fetus.
XX
PS Claim 3; Fig 3; 85bp; English.
XX
CC The present sequence encodes a human methionine synthase reductase (MTRR)
CC polypeptide. Inhibitors of MTRR polypeptide and polynucleotide are used
CC for treating or preventing cancer, cardiovascular disease, Down's
CC Syndrome or neural tube defects in a subject. The cardiovascular disease
CC is premature coronary artery disease. The compounds are detected by
CC methods which screen for modulators of MTRR biological activity. MTRR
CC polypeptide or nucleic acid is examined for the presence of a
CC polymorphism in the parents or the embryo or foetus, and the information
CC used for detecting an increased risk of an embryo or foetus developing
CC cancer, cardiovascular disease, Down's Syndrome or neural tube defects
XX
SQ Sequence 3259 BP; 944 A; 706 C; 663 G; 946 T; 0 U; 0 Other;
Query Match 95.1%; Score 1995; DB 3; Length 3259;
Best Local Similarity 99.9%; Pred. No. 0;
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Matches 2095; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	1	ATGAGGAGGTTCTGTACTATATGCTACAGAGGAGGAGGCAAGGCAATCGAGAA	60	
DB	80	ATGAGGAGGTTCTGTACTATATGCTACAGAGGAGGAGGCAAGGCAATCGAGAA	139	
QY	61	GAATGTGTGACAGAGCTGTGTGACATGTATTTCTGCAGATCTTCACTGATTAATGAA	120	
DB	140	GAATGTGTGACAGAGCTGTGTGACATGTATTTCTGCAGATCTTCACTGATTAATGAA	199	
QY	121	TCCGATTAAGTATGACTTAAACCCGAAACGCTCTCTTGTGTGTGTGTCTACACG	180	
DB	200	TCCGATTAAGTATGACTTAAACCCGAAACGCTCTCTTGTGTGTGTGTCTACACG	259	
QY	181	GGACCCGGAGACCCAGCCGACAGCCGCAAGTTGTAAAGAAATTAAGAAACCAACA	240	
DB	260	GGACCCGGAGACCCAGCCGACAGCCGCAAGTTGTAAAGAAATTAAGAAACCAACA	319	
QY	241	CTGCCGTTGATTTCTTGTCTCACTGCGGTATGAGTTCTGGGTCTCGGTGATTCAGAA	300	
DB	320	CTGCCGTTGATTTCTTGTCTCACTGCGGTATGAGTTCTGGGTCTCGGTGATTCAGAA	379	
QY	301	TACACTTACTTTTGCATGAGGAGGAGATTAATTAACGACTTCAAGAGCTTGAGCC	360	
DB	380	TACACTTACTTTTGCATGAGGAGGAGATTAATTAACGACTTCAAGAGCTTGAGCC	439	
QY	361	CGGCAATTTCTATGACATGAGACATGAGATGATGTGTGATTAACCTTGTGTGAG	420	
DB	440	CGGCAATTTCTATGACATGAGACATGAGATGATGTGTGATTAACCTTGTGTGAG	499	
QY	421	CCGTGATTTGTGACATCTGCGCAGGCTCAGAAACATTTTATGATCAAGCAGAGACA	480	
DB	500	CCGTGATTTGTGACATCTGCGCAGGCTCAGAAACATTTTATGATCAAGCAGAGACA	559	
QY	481	GAGGAGATTAAGTGGCGCACTCCGCTGGGATCACTGCACTTGTGAGACAGACCTTGTG	540	
DB	560	GAGGAGATTAAGTGGCGCACTCCGCTGGGATCACTGCACTTGTGAGACAGACCTTGTG	619	
QY	541	AAGTCAGACTGCTACATGTAATTTCAAGTCGACCTTCTGATTTCAATGATTCAGAA	600	
DB	620	AAGTCAGACTGCTACATGTAATTTCAAGTCGACCTTCTGATTTCAATGATTCAGAA	679	
QY	601	AGAAAGATTTCTGAGGTTTGAAGCAAAATGACAGTAAACGACCAATCCATGTTGTA	660	
DB	680	AGAAAGATTTCTGAGGTTTGAAGCAAAATGACAGTAAACGACCAATCCATGTTGTA	739	
QY	661	ATTGAAGCTTTGAGTCTCACTTACCCGTTCCGTAACCCCACTCTCAAGCCCTCTCTG	720	
DB	740	ATTGAAGCTTTGAGTCTCACTTACCCGTTCCGTAACCCCACTCTCTCAAGCCCTCTCTG	799	
QY	721	AATATTTCTGTGTTTACCCCAAAATTTTACAGATCACTGAGAGAGTCTTGTGCGCAG	780	
DB	800	AATATTTCTGTGTTTACCCCAAAATTTTACAGATCACTGAGAGAGTCTTGTGCGCAG	859	
QY	781	GAGGAAAGCAAGTATCTGTGACCTTCAAGAGATCCAGTTTCAAGTGCATTTTCAAA	840	
DB	860	GAGGAAAGCAAGTATCTGTGACCTTCAAGAGATCCAGTTTCAAGTGCATTTTCAAA	919	
QY	841	GCAATTCATCTTACGATGATGCAATTAACCACTCTGTGTGATTAATGACATTT	900	
DB	920	GCAATTCATCTTACGATGATGCAATTAACCACTCTGTGTGATTAATGACATTT	979	
QY	901	TCAAAATCAAGACTTTTCTATGAGCTGTGAGATGCTTCAAGCTGTGCTTAAACAGT	960	
DB	980	TCAAAATCAAGACTTTTCTATGAGCTGTGAGATGCTTCAAGCTGTGCTTAAACAGT	1039	
QY	961	GATTTGAGGTACAAAGCTTCAAAAGCTCAGCTTGAAGATTAAGAGAGACACTGC	1020	
DB	1040	GATTTGAGGTACAAAGCTTCAAAAGCTCAGCTTGAAGATTAAGAGAGACACTGC	1099	
QY	1021	GTCCTTTTGAATTAAGGACACAAAGAGAAAGAGCTTACCTTACCCAGCATATA	1080	
DB	1100	GTCCTTTTGAATTAAGGACACAAAGAGAAAGAGCTTACCTTACCCAGCATATA	1159	

QY	1081	CTGCGGAGATGTTCTCTCCAGTTCAATTTTACCTGTGTCTTGAAATCCGAGCAATTCCT	1140	
DB	1160	CTGCGGAGATGTTCTCTCCAGTTCAATTTTACCTGTGTCTTGAAATCCGAGCAATTCCT	1219	
QY	1141	AAAAAGCATTTTTCGAGCCCTTGTGACATATACAGTACAGTGTCTGAAAAAGCAGG	1200	
DB	1220	AAAAAGCATTTTTCGAGCCCTTGTGACATATACAGTACAGTGTCTGAAAAAGCAGG	1279	
QY	1201	CTACAGAGCTGTGACATTAAGGAGAGCCGATTAATAGCCGCTTGTACAGATGTGC	1260	
DB	1280	CTACAGAGCTGTGACATTAAGGAGAGCCGATTAATAGCCGCTTGTACAGATGTGC	1339	
QY	1261	TGAGCTGTGTGATCTCTCCGCTTCCCTTCTTTCAGAGCAGCAGTCACTGCTC	1320	
DB	1340	TGAGCTGTGTGATCTCTCCGCTTCCCTTCTTTCAGAGCAGCAGTCACTGCTC	1399	
QY	1321	CTGCTGAAATCTTCTTAACTTCAACCCAGACATATGCTGTGACAGTCAAGTTTA	1380	
DB	1400	CTGCTGAAATCTTCTTAACTTCAACCCAGACATATGCTGTGACAGTCAAGTTTA	1459	
QY	1381	TTTCAACCCAGAAAGCTCATTTTGTCTTCAATTTGAGAAATTTCTGTCTACGCA	1440	
DB	1460	TTTCAACCCAGAAAGCTCATTTTGTCTTCAATTTGAGAAATTTCTGTCTACGCA	1519	
QY	1441	ACAGAGGTTCTGCGAAGGAGATATGATACAGGCTGAGCTGTGTGCTTGTGCTTCA	1500	
DB	1520	ACAGAGGTTCTGCGAAGGAGATATGATACAGGCTGAGCTGTGTGCTTGTGCTTCA	1579	
QY	1501	CTTCAAGCAATATCATGATCCCATGAGACAGCGGAGAAAGCCCTGTGCTCTTAAGATA	1560	
DB	1580	CTTCAAGCAATATCATGATCCCATGAGACAGCGGAGAAAGCCCTGTGCTCTTAAGATA	1639	
QY	1561	TGCATCTCTCTGAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATTC	1620	
DB	1640	TGCATCTCTCTGAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATTC	1699	
QY	1621	ATTAATGTGGTTCAGAGACCGGATAGCCCGTTTATGAGGTTCTTAACAATAGAGAG	1680	
DB	1700	ATTAATGTGGTTCAGAGACCGGATAGCCCGTTTATGAGGTTCTTAACAATAGAGAG	1759	
QY	1681	AAACTCCAAAGAACACACCCAGATGGAATTTTGAAGCAATGTGTTTTTGTGCTGC	1740	
DB	1760	AAACTCCAAAGAACACACCCAGATGGAATTTTGAAGCAATGTGTTTTTGTGCTGC	1819	
QY	1741	AGGCATTAAGATAGGATTAATCTATTCAAGAAAGAGCTCAGACATTTCTTAAGCATGG	1800	
DB	1820	AGGCATTAAGATAGGATTAATCTATTCAAGAAAGAGCTCAGACATTTCTTAAGCATGG	1879	
QY	1801	ATCTTAATCATCTAAAGGTTCTTCTCAAGAGATGCTCTGTGAGGAGAGAGAGCC	1860	
DB	1880	ATCTTAATCATCTAAAGGTTCTTCTCAAGAGATGCTCTGTGAGGAGAGAGAGCC	1939	
QY	1861	CCAGCAAGTATATGACAGACAAATCCAGCTTCAATGAGCAGAGGTGCGAATCTTC	1920	
DB	1940	CCAGCAAGTATATGACAGACAAATCCAGCTTCAATGAGCAGAGGTGCGAATCTTC	1999	
QY	1921	CTTCAGAGAAAGGCGCATATTTATGTGTGTGAGATGCAAAAGATTTGCGCAAGATGTA	1980	
DB	2000	CTTCAGAGAAAGGCGCATATTTATGTGTGTGAGATGCAAAAGATTTGCGCAAGATGTA	2059	
QY	1981	CATGATGCCCTTGTGCAATTAATTAAGCAAGGTTGAGTTGAAAACTAGAAAGCAATG	2040	
DB	2060	CATGATGCCCTTGTGCAATTAATTAAGCAAGGTTGAGTTGAAAACTAGAAAGCAATG	2119	
QY	2041	AAACCCCTGCGCACTTTAAAGAGAAAGCGCTACCTTCAAGATATTTGTCTATA	2097	
DB	2120	AAACCCCTGCGCACTTTAAAGAGAAAGCGCTACCTTCAAGATATTTGTCTATA	2176	

RESULT 8
AD087538
ID AD087538 standard; cDNA; 3270 BP.

XX ADQ87538;
XX 07-OCT-2004 (first entry)
XX
XX Human tumour-associated antigenic target (TAT) cDNA sequence #4416.
XX
XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
XX cancer; cell proliferative disorder; gene; ss.
XX
XX Homo sapiens.
XX
XX NO2004060270-A2.
XX
XX 22-JUL-2004.
XX
XX 15-OCT-2003; 2003WO-US029126.
XX
XX 18-OCT-2002; 2002US-0418988P.
XX
XX (GETH) GENENTECH INC.
XX (WUTD/) WU T D.
XX (ZHOU/) ZHOU Y.
XX
XX Wu TD, Zhou Y;
XX WPI; 2004-534300/51.
XX
XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
XX preventing or treating cell proliferative disorders such as cancer.
XX
XX Claim 1; SEQ ID NO 4416; 5504dp; English.
XX
XX The present invention describes an isolated tumour-associated antigenic
XX target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
XX sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
XX (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
XX sequence identity to (a)-(c); or (e) a sequence that hybridises to (a) -
XX (c). Also described: (1) an expression vector comprising the above
XX nucleic acid; (2) a host cell comprising the above expression vector; (3)
XX a process for producing a polypeptide; (4) an isolated polypeptide
XX comprising: (a) an amino acid sequence encoded by any of the above
XX nucleotide sequences; (b) an amino acid sequence encoded by the full-
XX length coding region of the above nucleotide sequences; or (c) a sequence
XX having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
XX comprising the above polypeptide fused to a heterologous polypeptide; (6)
XX an isolated antibody that binds to the above polypeptide; (7) a process
XX for producing the antibody; (8) an isolated oligopeptide that binds to
XX the above polypeptide; (9) a tumour-associated antigenic target (TAT)
XX binding organic molecule that binds to the above polypeptide; (10) a
XX composition of matter comprising the above (chimeric) polypeptide,
XX antibody, oligopeptide or TAT binding organic molecule, in combination
XX with a carrier; (11) an article of manufacture comprising a container and
XX the composition of matter contained within the container; (12) methods of
XX inhibiting the growth of a cell that expresses the above protein, where
XX the growth of the cell is at least in part dependent upon a growth
XX potential effect of the above protein; (13) a method of
XX therapeutically treating a mammal having a cancerous tumour comprising
XX cells that express the above protein; (14) a method of determining the
XX presence of a protein in a sample suspected of containing the protein
XX described above; (15) methods of diagnosing the presence of a tumour in a
XX mammal; (16) a method for treating or preventing a cell proliferative
XX disorder associated with increased expression or activity of the above
XX protein; and (17) a method of binding an antibody, oligopeptide or
XX organic molecule to a cell that expresses the protein described above.
XX The TAT sequences have cytostatic activities, and can be used in gene
XX therapy. The composition and methods are useful for diagnosing,
XX preventing or treating cancer. The composition is also used for preparing
XX a medicament for the therapeutic treatment or diagnostic detection of a
XX cell proliferative disorder or cancer. The present sequence represents a
XX human TAT cDNA sequence from the present invention.
XX
XX Sequence 3270 BP; 934 A; 702 C; 680 G; 954 T; 0 U; 0 Other;

Query Match 92.7%; Score 1944; DB 13; Length 3270;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2094; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGAGAGGTTTCTGTACTATATGCTTACACAGCAGGACGCAAGCCATCGACGA 60
DB 112 ATGAGAGGTTTCTGTACTATATGCTTACACAGCAGGACGCAAGCCATCGACGA 171
QY 61 GAAATGTGAGCAAGCTGTGTACATGATGATTTTCTGAGATCTTCATGATTAAGAA 120
DB 172 GAAATGTGAGCAAGCTGTGTACATGATGATTTTCTGAGATCTTCATGATTAAGAA 231
QY 121 TCCGATTAAGTAACTTAAACCGAAGAGCTCTCTGTTGTTGTTTCTTACACG 180
DB 232 TCCGATTAAGTAACTTAAACCGAAGAGCTCTCTGTTGTTGTTTCTTACACG 291
QY 181 GGCACCGGAGACCCACCCGACAGCCGCAAGTTGTTAAGAAATPACAGAACCAACA 240
DB 292 GGCACCGGAGACCCACCCGACAGCCGCAAGTTGTTAAGAAATPACAGAACCAACA 351
QY 241 CTGCGGTTGATTTCTTGTCTCACCTGCGGTATGGTTACTGGGTCTCGGTGATTCAGAA 300
DB 352 CTGCGGTTGATTTCTTGTCTCACCTGCGGTATGGTTACTGGGTCTCGGTGATTCAGAA 411
QY 301 TACACCTACTTTTGCATGAGGGGGGAAATATTAATTAACGACTTCAGAGCTTGAACC 360
DB 412 TACACCTACTTTTGCATGAGGGGGGAAATATTAATTAACGACTTCAGAGCTTGAACC 471
QY 361 CGGCAATTTTCAACACACTGACATGAGATGATGTTGTTTAAAGCTTGGTTGAG 420
DB 472 CGGCAATTTTCAACACACTGACATGAGATGATGTTGTTTAAAGCTTGGTTGAG 531
QY 421 CCGTGATGCTGAGCTGTGGCCAGCCCTCAGAAACATTTTATGCTCAAGCAGACGACAA 480
DB 532 CCGTGATGCTGAGCTGTGGCCAGCCCTCAGAAACATTTTATGCTCAAGCAGACGACAA 591
QY 481 GAGGAGATTAAGTGGGCACTCCCGTGGCATCACTGATCTTTAGAGACAGACCTTGTG 540
DB 592 GAGGAGATTAAGTGGGCACTCCCGTGGCATCACTGATCTTTAGAGACAGACCTTGTG 651
QY 541 AACTCAGCTGTACACATGAAATCTCAAGTGAAGTCTGAGTTTCAATTCAGCA 600
DB 652 AACTCAGCTGTACACATGAAATCTCAAGTGAAGTCTGAGTTTCAATTCAGCA 711
QY 601 AGAAGAGATTCAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCAATGTTGA 660
DB 712 AGAAGAGATTCAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCAATGTTGA 771
QY 661 ATTGAAGCTTTGAGTCTCTCACTTACCCTGGTACCCCACTCTCAAGCTCTCTG 720
DB 772 ATTGAAGCTTTGAGTCTCTCACTTACCCTGGTACCCCACTCTCAAGCTCTCTG 831
QY 721 AATATTCCTGTTTACCCCGAATATTTACAGGTATCTGACAGAGTCTCTGGCAG 780
DB 832 AATATTCCTGTTTACCCCGAATATTTACAGGTATCTGACAGAGTCTCTGGCAG 891
QY 781 GAGGAAAGCAATATCTGTGACTTCAGCAGATTCAGTTTCAAGTCCCAATTTCAAG 840
DB 892 GAGGAAAGCAATATCTGTGACTTCAGCAGATTCAGTTTCAAGTCCCAATTTCAAG 951
QY 841 GCAATTCACCTTACGAAATGATGCCATTAACCACTCTGCTGTGATTAATGACATT 900
DB 952 GCAATTCACCTTACGAAATGATGCCATTAACCACTCTGCTGTGATTAATGACATT 1011
QY 901 TCAAAATACAGACTTTTCTATACGCTGAGGATGCTTCAAGCTGAGTCCCTAACAGT 960
DB 1012 TCAAAATACAGACTTTTCTATACGCTGAGGATGCTTCAAGCTGAGTCCCTAACAGT 1071
QY 961 GATTTCGAGGTACAAAGCTCAATCAAGAGCTGAGTGAAGTAAAGAGACACTGC 1020
DB 1072 GATTTCGAGGTACAAAGCTCAATCAAGAGCTGAGTGAAGTAAAGAGACACTGC 1131

Qy	1021	ATCCCTTTGAAAATPAAGCGACACAAAGAAAGAAAGGATCATTACCCAGCATATA	1080
Db	1132	GTCTCTTTGAAAATPAAGCGACACAAAGAAAGAAAGGATCATTACCCAGCATATA	1191
Qy	1081	CCTGGGGATGTCTCTCAGTTCATTTTACCTGGTCTTGTAAATCCGAGCAATTCCT	1140
Db	1192	CCTGGGGATGTGTCTCTCAGTTCATTTTACCTGGTGTCTTGTAAATCCGAGCAATTCCT	1251
Qy	1141	AAAAAGGATTTTTGGCGCCCTTGTGACATATACAGTGAAGTGTCTGAAAAGCGCAGG	1200
Db	1252	AAAAAGGATTTTTGGCGCCCTTGTGACATATACAGTGAAGTGTCTGAAAAGCGCAGG	1311
Qy	1201	CTACAGAGCTGTGCAGATAAACAGAGGGCACCCGATTATACCCGCTTTGTACAGATATCC	1260
Db	1312	CTACAGAGAGCTGTGCAGATAAACAGAGGGCACCCGATTATATACCCGCTTTGTACAGATATCC	1371
Qy	1261	TGTGGCTGTGTGTGGATCTCTCTCTCGCTTTCCTTCTTGCCAGCCACCATCAGTCTC	1320
Db	1372	TGTGGCTGTGTGTGGATCTCTCTCTCGCTTTCCTTCTTGCCAGCCACCATCAGTCTC	1431
Qy	1321	CTGCTCGAAGCATCTTCTCPAAACCTTCAACCCGACGACATATGTGTGCAAGTCAAGTTTA	1380
Db	1432	CTGCTCGAAGCATCTTCTCPAAACCTTCAACCCGACGACATATGTGTGCAAGTCAAGTTTA	1491
Qy	1381	TTTCAACCCAGGAAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTCTGTCTACCTGCCACA	1440
Db	1492	TTTCAACCCAGGAAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTCTGTCTACCTGCCACA	1551
Qy	1441	ACAGAGGTTCTGCGGAAAGGAGATATATACAGCTGTGGCTGTGTGTGTCTTCAGTT	1500
Db	1552	ACAGAGGTTCTGCGGAAAGGAGATATATACAGCTGTGGCTGTGTGTGTCTTCAGTT	1611
Qy	1501	CTTGAGCCAAACATATCATGCATATCCCATGACAGCCGGAAAGCCCTGGCTCTTAAGATA	1560
Db	1612	CTTGAGCCAAACATATCATGCATATCCCATGACAGCCGGAAAGCCCTGGCTCTTAAGATA	1671
Qy	1561	TCGATCTCTCTCGAACAAACAAATTCCTTTCACATTACAGATGACCCCTCAATCCCAATC	1620
Db	1672	TCGATCTCTCTCGAACAAACAAATTCCTTTCACATTACAGATGACCCCTCAATCCCAATC	1731
Qy	1631	ATATATGATGGTCCAGGAAACCGGCGATAGCCCGCTTATTTGGGTCTCTACATATGAGAG	1680
Db	1732	ATATATGATGGTCCAGGAAACCGGCGATAGCCCGCTTATTTGGGTCTCTACATATGAGAG	1791
Qy	1681	AAACTCTCAAGAACACACCCAGATGGAATTTTGGAGCATATGTGGTGTCTTTTGGCTGC	1740
Db	1792	AAACTCTCAAGAACACACCCAGATGGAATTTTGGAGCATATGTGGTGTCTTTTGGCTGC	1851
Qy	1741	AGGCATTAAGATTAGGATTAATCTATTCAGAAAAGAGCTCAGACATTTCTTAAAGATGGG	1800
Db	1852	AGGCATTAAGATTAGGATTAATCTATTCAGAAAAGAGCTCAGACATTTCTTAAAGATGGG	1911
Qy	1801	ATCTTAACTCATTAAGAGTTTCCCTTCCAGAGATGTCCGTGTGGGAGAGAGGAAGCC	1860
Db	1912	ATCTTAACTCATTAAGAGTTTCCCTTCCAGAGATGTCCGTGTGGGAGAGAGGAAGCC	1971
Qy	1861	CCAGCAAGTATGTATCAGACACATCCAGTTCATGGCCAGCAGGTGGCGAGATCTCTC	1920
Db	1972	CCAGCAAGTATGTATCAGACACATCCAGTTCATGGCCAGCAGGTGGCGAGATCTCTC	2031
Qy	1921	CTCCAGGAGAAACGGCATATTTATGTGTGTGAGATATGCAAGATATATGGCCAGAGATATA	1980
Db	2032	CTCCAGGAGAAACGGCATATTTATGTGTGTGAGATATGCAAGATATATGGCCAGAGATATA	2091
Qy	1981	CATGATGCCCTTGTGCAATATATAAGCAAAAGGTTGAGTTGAAAACTAGAAAGCATATG	2040
Db	2092	CATGATGCCCTTGTGCAATATATAAGCAAAAGGTTGAGTTGAAAACTAGAAAGCATATG	2151
Qy	2041	AAAAACCTTGCGCATTTTAAAGAGAAAGGCTATCTTCCAGATATTTGTCTATPA	2097
Db	2152	AAAAACCTTGCGCATTTTAAAGAGAAAGGCTATCTTCCAGATATTTGTCTATPA	2208

RESULT 9	ID	ADNM43215	standard; cDNA; 2091 BP.
XX	AC	ADNM43216;	
XX	DT	03-JUN-2004	(first entry)
XX	DE	Human methionine synthase reductase CDS del 1726-1728 variant.	
XX	KM	Human; 89; Methionine synthase reductase polypeptide; HsMTRR; cancer;	
XX	KM	cardiovascular disease; neural tube defect; hyperhomocysteinemia;	
XX	KM	chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.	
OS	XX	Homo sapiens.	
XX	XX	Location/Qualifiers	
XX	XX	1..2091	
XX	XX	/*tag= a	
XX	XX	/product= "hsMTRRdelR559"	
XX	XX	/partial	
XX	XX	/note= "No stop codon shown"	
XX	XX	replace(66,A)	
XX	XX	/*tag= b	
XX	XX	/standard_name= "Single_nucleotide_polymorphism"	
XX	XX	replace(110,A)	
XX	XX	/*tag= c	
XX	XX	/standard_name= "Single_nucleotide_polymorphism"	
XX	XX	replace(1726,TTGT)	
XX	XX	/*tag= d	
XX	XX	US2003082676-A1.	
XX	XX	01-MAY-2003.	
XX	XX	10-AUG-1999;	99US-00371347.
XX	XX	16-JAN-1999;	98US-0071622P.
XX	XX	15-JAN-1999;	99US-00232028.
XX	XX	(GRAV//) GRAVEL R A.	
XX	XX	(ROZE//) ROZEN R.	
XX	XX	(LECL//) LECLERC D.	
XX	XX	(WILS//) WILSON A.	
XX	XX	(ROSE//) ROSENBLATT D.	
XX	XX	Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;	
XX	XX	WPI; 2003-576610/54.	
XX	XX	P-PSDB; ADNM43217.	
XX	XX	New substantially pure nucleic acid encoding a mammalian methionine	
XX	XX	synthase reductase polypeptide, useful for diagnosing, preventing or	
XX	XX	treating conditions associated with altered methionine synthase activity,	
XX	XX	e.g. cancer.	
XX	XX	Disclosure; SEQ ID NO 45; 26pp; English.	
XX	XX	The invention relates to a substantially pure nucleic acid that encodes a	
XX	XX	mammalian methionine synthase reductase polypeptide, HsMTRR, or that	
XX	XX	hybridizes at high stringency to a nucleic acid appearing as ADNM43208 or	
XX	XX	ADNM43209. Also included are a non-human animal where one or both genetic	
XX	XX	alleles encoding the methionine synthase reductase polypeptide are	
XX	XX	mutated, an antibody that specifically binds the above methionine	
XX	XX	synthase reductase polypeptide, a method of detecting the presence of the	
XX	XX	above polypeptide, a method for detecting sequence variants for	
XX	XX	methionine synthase reductase in a mammal, methods of treating or	
XX	XX	preventing cancer (or cardiovascular disease or neural tube defects) in a	
XX	XX	subject, methods of screening for a compound that modulates methionine	
XX	XX	synthase reductase biological activity and a method for detecting an	
XX	XX	increased risk of developing a neural tube defect in a mammalian embryo	
XX	XX	or foetus. The nucleic acid is useful in diagnosing, preventing or	
XX	XX	treating conditions associated with altered methionine synthase activity,	

CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are
CC also associated with hyperhomocysteinemia. The gene for HmTR is
CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
CC sequence of a variant human hnmTR cDNA.

XX Sequence 2091 BP; 591 A; 489 C; 480 G; 531 T; 0 U; 0 Other;

Query Match 88.3%; Score 1851; DB 11; Length 2091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2091; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 ATGAGAGGTTTCTGTTATATATGCTACACAGCAGGACGCAAGCCATCGCAGAA 60
DB 1 ATGAGAGGTTTCTGTTATATATGCTACACAGCAGGACGCAAGCCATCGCAGAA 60
QY 61 GAAATGTTGAGCAAGCTGTGTATGATGATTTCTGCAATCTTCACTGATTAAGGAA 120
DB 61 GAAATGTTGAGCAAGCTGTGTATGATGATTTCTGCAATCTTCACTGATTAAGGAA 120
QY 121 TCCGATTAAGTATGACTTAAACCGAAACAGCTCTCTGTGTGTGTGTTCTACACG 180
DB 121 TCCGATTAAGTATGACTTAAACCGAAACAGCTCTCTGTGTGTGTGTTCTACACG 180
QY 181 GGCACCCGGAACCCACCCGACACGCGCGCAAGTTTGTAAAGAAATACGAACCAACA 240
DB 181 GGCACCCGGAACCCACCCGACACGCGCGCAAGTTTGTAAAGAAATACGAACCAACA 240
QY 241 CTGCGGTTGATTTCTTGTGCTACCTGCGGTGAGTTTCTGCGGTCTCGGATTCGAA 300
DB 241 CTGCGGTTGATTTCTTGTGCTACCTGCGGTGAGTTTCTGCGGTCTCGGATTCGAA 300
QY 301 TACACCTACTTTTGGCAATGGGGGAGATTAATGATTAACGACTTCAAGACTTGAAGCC 360
DB 301 TACACCTACTTTTGGCAATGGGGGAGATTAATGATTAACGACTTCAAGACTTGAAGCC 360
QY 361 CGGCAATTTCTATGACACTGACATGACATGATCTGTGTAGTTTGAACCTTGTGTGAG 420
DB 361 CGGCAATTTCTATGACACTGACATGACATGATCTGTGTAGTTTGAACCTTGTGTGAG 420
QY 421 CCGGATTTGCTGACCTGCGCCAGCCCTCAGAAAGATTTTAAAGTAAAGAGAGACAA 480
DB 421 CCGGATTTGCTGACCTGCGCCAGCCCTCAGAAAGATTTTAAAGTAAAGAGAGACAA 480
QY 481 GAGGAGATTAAGTGGCGACCTCCCGGTGACATCACTGCACTTGAAGAGACCTTGTG 540
DB 481 GAGGAGATTAAGTGGCGACCTCCCGGTGACATCACTGCACTTGAAGAGACCTTGTG 540
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DB 541 AAGTCAAGCTGTACACATTTGAATCTCAAGTGTGAGCTTGTGAGATTCGATTCAGAA 600
QY 601 AGAAGAGATTCTGAGTTTGAAGCAAAATGCAATGCAAGCAACCAATCAATGTTGTA 660
DB 601 AGAAGAGATTCTGAGTTTGAAGCAAAATGCAATGCAAGCAACCAATCAATGTTGTA 660
QY 661 ATTGAAGACTTGAATCTTACCTTACCGGTTCGTTACCCCACTCTCAAGACCTCTCTG 720
DB 661 ATTGAAGACTTGAATCTTACCTTACCGGTTCGTTACCCCACTCTCTCAAGACCTCTCTG 720
QY 721 AATTTCTGTTTACCCCGCAATATTTTACAGGTATCATCTGCAAGAGTCTCTTGGCAG 780
DB 721 AATTTCTGTTTACCCCGCAATATTTTACAGGTATCATCTGCAAGAGTCTCTTGGCAG 780
QY 781 GAGGAAAGCCAAAGTATCTGATCTTACAGCAGATCAAGTTTGAAGTCAAG 840
DB 781 GAGGAAAGCCAAAGTATCTGATCTTACAGCAGATCAAGTTTGAAGTCAAG 840
QY 841 GCAATTCACCTTACTAGCAATGATGCAATAAACCACTCTGCTGTGTGAATTCGACATT 900
DB 841 GCAATTCACCTTACTAGCAATGATGCAATAAACCACTCTGCTGTGTGAATTCGACATT 900

QY 901 TCAAATACAGACTTTTCTATACGCTGAGATGCTTCAAGGTATCTGCCCTAACAT 960
DB 901 TCAAATACAGACTTTTCTATACGCTGAGATGCTTCAAGGTATCTGCCCTAACAT 960
QY 961 GATTGAGGTACAAAGCCCTACCAAGCTGACCTTGAAGATTAAGAGAGACTGC 1020
DB 961 GATTGAGGTACAAAGCCCTACCAAGCTGACCTTGAAGATTAAGAGAGACTGC 1020
QY 1021 GTCCCTTTGAAAATTAAGGACACACAAAGAAAGAGCTTACCTTACCAGCATATA 1080
DB 1021 GTCCCTTTGAAAATTAAGGACACACAAAGAAAGAGCTTACCTTACCAGCATATA 1080
QY 1081 CCGCGGAGATGTTCTCTCCAGTTCAATTTTCTGCTGTCTTGAATTCGAGCAATTCCT 1140
DB 1081 CCGCGGAGATGTTCTCTCCAGTTCAATTTTCTGCTGTCTTGAATTCGAGCAATTCCT 1140
QY 1141 AAAAAGCAATTTTGGAGCCCTTGTGAGCTATACAGTGAACAGTCTGAAAAGCCAGG 1200
DB 1141 AAAAAGCAATTTTGGAGCCCTTGTGAGCTATACAGTGAACAGTCTGAAAAGCCAGG 1200
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DB 1321 CTGCTGAAACATCTTCTTAACTTCAACCCAGACATATTCGTGTGAGACTCAAGTTTA 1380
QY 1381 TTTTACCCAGAAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTGTCTACTGCCACA 1440
DB 1381 TTTTACCCAGAAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTGTCTACTGCCACA 1440
QY 1441 ACAGAGTTCTGCGGAAAGGAGATATGATACAGCTGCTGCTGCTGTGTGTTTCAATT 1500
DB 1441 ACAGAGTTCTGCGGAAAGGAGATATGATACAGCTGCTGCTGCTGTGTGTTTCAATT 1500
QY 1501 CTTGAGCAAAACATACATGATGATCCCATGAAGACGCGGAAACCTTGCTCTTAAGATA 1560
DB 1501 CTTGAGCAAAACATACATGATGATCCCATGAAGACGCGGAAACCTTGCTCTTAAGATA 1560
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QY 1681 AAATCCCAAGAACAAACCCAGATGAAATTTTGGAGCAATGTGTGTTTGGCTGC 1740
DB 1681 AAATCCCAAGAACAAACCCAGATGAAATTTTGGAGCAATGTGTGTTTGGCTGC 1740
QY 1741 AGCATTAAGATAGGATTAATCTATTTCAAGAAAGCTCAGACATTTCTTAAAGCATGGG 1800
DB 1741 AGCATTAAGATAGGATTAATCTATTTCAAGAAAGCTCAGACATTTCTTAAAGCATGGG 1800
QY 1801 ATCTTAATCTATTAAGGTTTCTCTCTCAAGAGATGCTCTGTGGGAGAGAGAGGCC 1860
DB 1801 ATCTTAATCTATTAAGGTTTCTCTCTCAAGAGATGCTCTGTGGGAGAGAGAGGCC 1860
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DB 1981 CATGATGCCCTTGTGCAAAATATATAGCAAGAGGTTGAGTTGAAAACTAAGAACATG 2040

|||||
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DB 2038 AAAACCCCTGGCCACTTTAAAGAGAAACGCTACTCTCAGATTTTGTGCA 2091
RESULT 10
ADM43214
ID ADM43214 standard; cDNA, 2091 BP.
XX ADM43214;
AC
XX
XX
DT 03-JUN-2004 (first entry)
XX
XX Human methionine synthase reductase CDS del 1675-1678 variant.
XX
XX Human; ss; Methionine synthase reductase polypeptide; HsMTRR; cancer;
XX cardiovacular disease; neural tube defect; hyperhomocysteinemia;
XX chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.
XX Homo sapiens.
OS
XX
XX
FH Location/Qualifiers
FT 1. 2091
FT CDS /tag= a
FT /product= "HsMTRRdelR559"
FT /partial
FT /note= "No stop codon shown"
FT /replace(66,A)
FT variation /tag= b
FT /standard name= "Single_nucleotide polymorphism"
FT /replace(110,A)
FT /tag= c
FT /standard name= "Single_nucleotide polymorphism"
FT variation /tag= d
FT /replace(1675,AGAG)
FT /tag= d
PN US003082676-A1.
XX
XX
XX
PD 01-MAY-2003.
XX
XX 10-AUG-1999; 99US-00371347.
XX
XX PF 16-JAN-1998; 98US-0071622P.
XX PR 15-JAN-1999; 99US-00232028.
XX
XX (GRAV/) GRAVEL R. A.
XX (ROZE/) ROZEN R.
XX (LECL/) LECLERC D.
XX (WILS/) WILSON A.
XX (ROSE/) ROSENBLATT D.
XX
XX Graveil RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX MPI: 2003-576610/54.
XX P-PSDB; ADM43215.
XX
XX New substantially pure nucleic acid encoding a mammalian methionine
XX synthase reductase polypeptide, useful for diagnosing, preventing or
XX treating conditions associated with altered methionine synthase activity,
XX e.g. cancer.
XX
XX
XX Disclosure; SEQ ID NO 47; 26pp; English.
XX
XX The invention relates to a substantially pure nucleic acid that encodes a
XX mammalian methionine synthase reductase polypeptide, HsMTRR, or that
XX hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
XX ADM43209. Also included are a non-human animal where one or both genetic
XX alleles encoding the methionine synthase reductase polypeptide are
XX mutated, an antibody that specifically binds the above methionine
XX synthase reductase polypeptide, a method of detecting the presence of the

CC above polypeptide, a method for detecting sequence variants for
CC methionine synthase reductase in a mammal, methods of treating or
CC preventing cancer (or cardiovascular disease or neural tube defects) in a
CC subject, methods of screening for a compound that modulates methionine
CC synthase reductase biological activity and a method for detecting an
CC increased risk of developing a neural tube defect in a mammalian embryo
CC or foetus. The nucleic acid is useful in diagnosing, preventing or
CC treating conditions associated with altered methionine synthase activity,
CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are
CC also associated with hyperhomocysteinemia. The gene for HsMTRR is
CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
CC sequence of a variant human hsmtrr cDNA.
XX
XX
XX Sequence 2091 BP; 589 A; 489 C; 480 G; 533 T; 0 U; 0 Other;

Query Match 88.3%; Score 1851; DB 11; Length 2091;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2091; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 ATGAGAGGTTCTCTTACTATATGCTACACGACGAGGCAAGGCCATCCGAGAA 60
DB 1 ATGAGAGGTTCTCTTACTATATGCTACACGACGAGGCAAGGCCATCCGAGAA 60
QY 61 GAAATGTGTAGACAGCTGTGTACATGATTTTTCGAGATCTTCACTGTATTAGTAA 120
DB 61 GAAATGTGTAGACAGCTGTGTACATGATTTTTCGAGATCTTCACTGTATTAGTAA 120
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QY 361 CGGCATTCTATGACACTGGAATGACATGACTGTGATGAGTTTGTGTTGAG 420
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DB 421 CCGTGGATTGCTGGACTCTGGGCAAGCCCTCAGAAAGCAATTTAAGTCAGAGAGACAA 480
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QY 661 ATTGAAGCTTGAAGTCTCACTTACCCGTTGATACCCCACTCTCAAGACTCTCTG 720
DB 661 ATTGAAGCTTGAAGTCTCACTTACCCGTTGATACCCCACTCTCTCAAGACTCTCTG 720
QY 721 AATATTCCTGTTTACCCCAATATTTACAGATCATCTGACAGAGTCTTGTGCGCAG 780
DB 721 AATATTCCTGTTTACCCCAATATTTACAGATCATCTGACAGAGTCTTGTGCGCAG 780

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Qy 781 GAGAGAAAGCAAGTATCTGACTTCAGCAGATCCAGTCTTTTCAAGTCCAAATTTCAAAG 840
Db 781 GAGAGAAAGCAAGTATCTGACTTCAGCAGATCCAGTCTTTTCAAGTCCAAATTTCAAAG 840
Qy 841 GCGATTCACCTTCTAGAGTGAATGCGATTAACCACTCGCTGGTGAATTTGGAATT 900
Db 841 GCGATTCACCTTCTAGAGTGAATGCGATTAACCACTCGCTGGTGAATTTGGAATT 900
Qy 901 TCAATACAGACTTTTCTATAGCCTGAGAGATGCTTCAGCGGTATCTCCCTTAACAGT 960
Db 901 TCAATACAGACTTTTCTATAGCCTGAGAGATGCTTCAGCGGTATCTCCCTTAACAGT 960
Qy 961 GATTCTGAGGTACAAAGCCTTACTCCAAAGACTGCAAGTCTGAAGTAAAGAGCACTGC 1020
Db 961 GATTCTGAGGTACAAAGCCTTACTCCAAAGACTGCAAGTCTGAAGTAAAGAGCACTGC 1020
Qy 1021 GTCCCTTTGAAATTAAGGAGACACAAAGAAAGAGACTTACCCAGCAATATA 1080
Db 1021 GTCCCTTTGAAATTAAGGAGACACAAAGAAAGAGACTTACCCAGCAATATA 1080
Qy 1081 CTTGCGGGATGTTCTCTCAGATTCTTTTACCTGTGTCTTGAAATCCGAGCAATTCCT 1140
Db 1081 CTTGCGGGATGTTCTCTCAGATTCTTTTACCTGTGTCTTGAAATCCGAGCAATTCCT 1140
Qy 1141 AAAAAGCATTTTTCGAGCCCTTGTGACTATACAGTGAAGTCTGAAAAGCGCAGG 1200
Db 1141 AAAAAGCATTTTTCGAGCCCTTGTGACTATACAGTGAAGTCTGAAAAGCGCAGG 1200
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Db 1201 CTACAGAGAGCTGTGACAGTAAACAGAGGGGACGCGATTAATAGCGCTTTGTAGCAGATGCC 1260
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Db 1261 TGTGCTGCTTGTGATCTCTCTCTGCTTCCCTTCTTGCCAGCCACCACTCAAGTCTC 1320
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Db 1321 CTGCTCGAATCTTCTCTTAACTTCAACCCAGACATATTCGTGTGCAAGTCAAGTTTA 1380
Qy 1381 TTTTACCAGGAAAGCTCCATTTTGTCTTCAACATTTGAGAAATTTCTGTCTACTGCCACA 1440
Db 1381 TTTTACCAGGAAAGCTCCATTTTGTCTTCAACATTTGAGAAATTTCTGTCTACTGCCACA 1440
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Db 1441 ACAGAGGTTCTGCGGAAAGGAGATATGTAACAGCTGTGCGCTTGTGTGCTTCAAGT 1500
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Qy 1681 AAATCCCAAGAACACCCAGATGAGAAATTTTGGAGCAATGTGTGTTTTTGGCTGC 1740
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Qy 1741 AGGCAATAGAGTAGGAGATTAATCTATTCAGAAAAGAGCTCAGACATTTCTTAAGCATGGG 1800
Db 1741 AGGCAATAGAGTAGGAGATTAATCTATTCAGAAAAGAGCTCAGACATTTCTTAAGCATGGG 1800
Qy 1801 ATCTTAATCTAATTAAGGTTTCTTCTCAAGAGATGCTCTGTGTTGGGAGAGAGAGCC 1860
Db 1801 ATCTTAATCTAATTAAGGTTTCTTCTCAAGAGATGCTCTGTGTTGGGAGAGAGAGCC 1860
Qy 1861 CAGAGAAAGTATGTAAGAGACATCCAGCTTACGTGCGCAGCAGGTGGCGAGAAATCTCTC 1920
Db 1861 CAGAGAAAGTATGTAAGAGACATCCAGCTTACGTGCGCAGCAGGTGGCGAGAAATCTCTC 1920
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Db 1858 CCAGCAAAATATGTAACAAACAAACATCCAGCTTCAGTGCAGAGGTGGCGAGAAATCTCTC 1917
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Db 1918 CTCACAGAGAACGGCCATATTTATGTGTGAGATGCAAAAGATATGCGCAAGATGTA 1977
Qy 1981 CATGATGCCCTTGTGCAATTAATAGCAAAAGAGTTGAGCTTGAATAAATACTAGAACCAATG 2040
Db 1978 CATGATGCCCTTGTGCAATTAATAGCAAAAGAGTTGAGCTTGAATAAATACTAGAACCAATG 2037
Qy 2041 AAAACCTGCGCACTTTAAAGAGAAAGAGCTACCTCAGGATATTTGTCA 2094
Db 2038 AAAACCTGCGCACTTTAAAGAGAAAGAGCTACCTCAGGATATTTGTCA 2091
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RESULT 11

ID AA58977 standard; DNA; 3256 BP.

XX AA58977;

DT 07-NOV-2000 (first entry)

DE A human methionine synthase reductase DNA sequence with polymorphism.

XX Human; methionine synthase reductase; MTRR; cancer;

KM cardiovascular disease; Down's Syndrome; neural tube defect;

KM premature coronary artery disease; ss.

OS Homo sapiens.

XX WO200042196-A2.

XX 14-JAN-2000; 2000MO-IB000209.

XX 15-JAN-1999; 99US-00232028.

XX 10-AUG-1999; 99US-00371347.

XX (UIMC-) UNIV MCGILL.

XX Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;

XX WPI; 2000-46131/40.

PT Mammalian methionine synthase reductase nucleic acid used for detecting

PT an increased risk of developing a neural tube defect, Down's Syndrome or

PT cardiovascular disease in a mammalian embryo or fetus.

PS Claim 8; Page; 85pp; English.

XX The present sequence represents a human methionine synthase reductase (MTRR) DNA sequence, with a polymorphism comprising of a deletion of nucleotides 1726-1728. Inhibitors of MTRR polypeptide and polynucleotide are used for treating or preventing cancer, cardiovascular disease, Down's Syndrome or neural tube defects in a subject. The cardiovascular disease is premature coronary artery disease. The compounds are detected by methods which screen for modulators of MTRR biological activity. MTRR polypeptide or nucleic acid is examined for the presence of a polymorphism in the parents or the embryo or foetus, and the information used for detecting an increased risk of an embryo or foetus developing cancer, cardiovascular disease, Down's Syndrome or neural tube defects. note: the present sequence does not appear in the specification; it was created using information provided

XX Sequence 3256 BP; 943 A; 705 C; 662 G; 946 T; 0 U; 0 Other;

Query Match 83.5%; Score 1752; DB 3; Length 3256;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2092; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 1 ATGAGAGGTTCTGTACTATATGCTACACAGCAGGAGCAGGCAAAAGCCATCGAGAA 60
DB 80 ATGAGAGGTTCTGTACTATATGCTACACAGCAGGAGCAGGCAAAAGCCATCGAGAA 139
QY 61 GAAATGTGAGCAGCTGTGTACATGATTTTCTGAGATCTTCACTGTATTAGTAA 120
DB 140 GAAATGTGAGCAGCTGTGTACATGATTTTCTGAGATCTTCACTGTATTAGTAA 199
QY 121 TCCGATTAATGATGCTTAAACCGGAAACGCTCTCTGTTGTTGTTCTTACAG 180
DB 200 TCCGATTAATGATGCTTAAACCGGAAACGCTCTCTGTTGTTGTTCTTACAG 259
QY 181 GGCACCGGAGACCCACCCGACAGAGCCGCAAGTTGTTAAGGAATAACGAACCAACA 240
DB 260 GGCACCGGAGACCCACCCGACAGAGCCGCAAGTTGTTAAGGAATAACGAACCAACA 319
QY 241 CTGCGGTTGATTTCTTTGTCTCACTGCGGTATGGGTTACTGGGTCCTGGTATTCAGAA 300
DB 320 CTGCGGTTGATTTCTTTGTCTCACTGCGGTATGGGTTACTGGGTCCTGGTATTCAGAA 379
QY 301 TACACTACTTTTGTGCAATGGGGGGAAGATTAATGATTAACGACTTCAAGAGCTTGAAGCC 360
DB 380 TACACTACTTTTGTGCAATGGGGGGAAGATTAATGATTAACGACTTCAAGAGCTTGAAGCC 439
QY 361 CGCATTTTCTATGACATGACATGACATGACATGACATGACATGACATGACATGACATGAC 420
DB 440 CGCATTTTCTATGACATGACATGACATGACATGACATGACATGACATGACATGACATGAC 499
QY 421 CCGTGTATTTCTGTGACATGACATGACATGACATGACATGACATGACATGACATGACATGAC 480
DB 500 CCGTGTATTTCTGTGACATGACATGACATGACATGACATGACATGACATGACATGACATGAC 559
QY 481 GAGGAAATAGTGGCCGACATCCCGGTGGACATCACTGACATCTTGTGAGACAGACCTTGTG 540
DB 560 GAGGAAATAGTGGCCGACATCCCGGTGGACATCACTGACATCTTGTGAGACAGACCTTGTG 619
QY 541 AAGTCAGAGCTGTACACATGATGATCTCAAGTCAGAGCTTGTGATTCGATTCAGTACAGA 600
DB 620 AAGTCAGAGCTGTACACATGATGATCTCAAGTCAGAGCTTGTGATTCGATTCAGTACAGA 679
QY 601 AGAAGAGATTTCTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCCATGTTGTA 660
DB 680 AGAAGAGATTTCTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCCATGTTGTA 729
QY 661 ATTGAAGATTTGAGTCTTCACTTACCCGTTGGTACCCCACTCTCAACAGCTCTCTG 720
DB 740 ATTGAAGATTTGAGTCTTCACTTACCCGTTGGTACCCCACTCTCTCAACAGCTCTCTG 799
QY 721 AATATTCGTGGTTTACCCCGAATATTTACAGGTACATGACAGAGTCTCTTGGCCAG 780
DB 800 AATATTCGTGGTTTACCCCGAATATTTACAGGTACATGACAGAGTCTCTTGGCCAG 859
QY 781 GAGGAAAGCCAGATCTGTGACTTCAAGCATGAGTCTTCAAGTCCCAATTTCAAG 840
DB 860 GAGGAAAGCCAGATCTGTGACTTCAAGCATGAGTCTTCAAGTCCCAATTTCAAG 919
QY 841 GCACTTCACTTACAGAAATGATGCAATTAACCACTGCTGTGTAATGACATTT 900
DB 920 GCACTTCACTTACAGAAATGATGCAATTAACCACTGCTGTGTAATGACATTT 979
QY 901 TCAATATACAGACTTTTCTATGAGCTGAGATGAGCTTCAAGGATCTGAGCTTCAAGT 960
DB 980 TCAATATACAGACTTTTCTATGAGCTGAGATGAGCTTCAAGGATCTGAGCTTCAAGT 1039
QY 961 GATTTGAGGTACAAAGCTTACTCAAGATGACAGTCTTGAAGATTAAGAGACACTGC 1020
DB 1040 GATTTGAGGTACAAAGCTTACTCAAGATGACAGTCTTGAAGATTAAGAGACACTGC 1099
QY 1021 GTCTTTTGAATAAAGGAGACCAAAAGAAAGAAAGAGACTTACCTTACCCGACATATA 1080
DB 1100 GTCTTTTGAATAAAGGAGACCAAAAGAAAGAAAGAGACTTACCTTACCCGACATATA 1159
QY 1081 CTGCGGAGATGTTCTCTCAGATTCATTTTACCTGAGTGTGAAATCCGAGCAATTCCT 1140

DB 1160 CTGCGGAGATGTTCTCTCAGATTCATTTTACCTGAGTGTGAAATCCGAGCAATTCCT 1219
QY 1141 AAAAAGGCAATTTTGTGAGACCTTGTGACATTAACAGAGACAGCTTAAAGCCAG 1200
DB 1220 AAAAAGGCAATTTTGTGAGACCTTGTGACATTAACAGAGACAGCTTAAAGCCAG 1279
QY 1201 CTACAGAGCTGTGACATTAACAGAGAGGAGCCGATTAATAGCCGCTTGTACAGATGCC 1260
DB 1280 CTACAGAGCTGTGACATTAACAGAGAGGAGCCGATTAATAGCCGCTTGTACAGATGCC 1339
QY 1261 TGTGCTGTGTGTGATCT 1320
DB 1340 TGTGCTGTGTGTGATCT 1399
QY 1321 CTGCTGAAACATTTCTTAACTTCAACCCAGACCATATTCGTGTGACAGCTCAAGTTTA 1380
DB 1400 CTGCTGAAACATTTCTTAACTTCAACCCAGACCATATTCGTGTGACAGCTCAAGTTTA 1459
QY 1381 TTTCAACCGAGAAAGCTCAATTTTGTCTCAACATTTGAGAAATTTCTGTACTGACACA 1440
DB 1460 TTTCAACCGAGAAAGCTCAATTTTGTCTCTCAACATTTGAGAAATTTCTGTACTGACACA 1519
QY 1441 ACAGAGGTTCTGCGAAGGAGATGATACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1500
DB 1520 ACAGAGGTTCTGCGAAGGAGATGATACAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 1579
QY 1501 CTTCAGCCAAACATACATGATCCATGAAAGACAGGAGGAAAGCCCTGCTCTAAGATA 1560
DB 1580 CTTCAGCCAAACATACATGATCCATGAAAGACAGGAGGAAAGCCCTGCTCTAAGATA 1639
QY 1561 TCCATCTCTCTGAAACAAATTTCTTCACTTACAGATGAGACCCCTCAATCCCATC 1620
DB 1640 TCCATCTCTCTGAAACAAATTTCTTCACTTACAGATGAGACCCCTCAATCCCATC 1699
QY 1621 ATATAGTGGGTTCAGAGAACCGGCAATGCCCCGTTATTTGAGTTCTTCAACATAGAGAG 1680
DB 1700 ATATAGTGGGTTCAGAGAACCGGCAATGCCCCGTTATTTGAGTTCTTCAACATAGAGAG 1756
QY 1681 AAACTCAGAAACACACCCAGATGGAATTTTGGAGCAATGTTGTTTGGCTGC 1740
DB 1757 AAACTCAGAAACACACCCAGATGGAATTTTGGAGCAATGTTGTTTGGCTGC 1816
QY 1741 AGGCAATAGATGAGATTAATCTAATGAGAAAGCTCAGACATTTCTTAAAGCATGG 1800
DB 1817 AGGCAATAGATGAGATTAATCTAATGAGAAAGCTCAGACATTTCTTAAAGCATGG 1876
QY 1801 ATCTTAATCATCTAAGGTTTCTCTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1860
DB 1877 ATCTTAATCATCTAAGGTTTCTCTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1936
QY 1861 CCAGCAAGATGATACAGACACATCAGCTTCAATGCGAGAGAGTGGCAGAAATCTC 1920
DB 1937 CCAGCAAGATGATACAGACACATCAGCTTCAATGCGAGAGAGTGGCAGAAATCTC 1996
QY 1921 CTCACAGAAAGGCGCATTTATATGTTGAGAGATGCAAGAAATATGGCAAGATGTA 1980
DB 1997 CTCACAGAAAGGCGCATTTATATGTTGAGAGATGCAAGAAATATGGCAAGATGTA 2056
QY 1981 CATGATGCCCTTGTGCAATTAATAGCAAGAGTGTGAGTTGAAAAAATAGAAAGCAATG 2040
DB 2057 CATGATGCCCTTGTGCAATTAATAGCAAGAGTGTGAGTTGAAAAAATAGAAAGCAATG 2116
QY 2041 AAAACCTTGGCCACTTTAAAGAGAAACGCTTACAGATATTTGGTCAATA 2097
DB 2117 AAAACCTTGGCCACTTTAAAGAGAAACGCTTACAGATATTTGGTCAATA 2173

RESULT 12
AAAS8976
ID AAAS8976 standard; DNA; 3255 BP.
XX
AC AAAS8976;

Db 1460 TTTCAACCCAGAAAGCTCCATTTTGTCTTCAACATTTGGAATTTCTGTCTACTGCCACA 1519
Qy 1441 ACAGAGTTCTGCGGAGGAGATGTAGAGGCTGGCTGCTGTTGGTGTCTCAGTT 1500
Db 1520 ACAGAGTTCTGCGGAGGAGATGTAGAGGCTGGCTGCTGTTGGTGTCTCAGTT 1579
Qy 1501 CTTGAGCCAAATACATCATCTCCATGAGACAGCGGAAAGCCCTGGCTCTAAGATA 1560
Db 1580 CTTGAGCCAAATACATCATCTCCATGAGACAGCGGAAAGCCCTGGCTCTAAGATA 1639
Qy 1561 TCCATCTCTCTGCAACAAATTTCTTCACTTACCAAGATGACCTTCAATCCCATC 1620
Db 1640 TCCATCTCTCTGCAACAAATTTCTTCACTTACCAAGATGACCTTCAATCCCATC 1695
Qy 1621 ATAAATGTTGGTCCAGAACCCGCAATGCGCTTATTTGGTCTTACCAATGAGAG 1680
Db 1696 ATAAATGTTGGTCCAGAACCCGCAATGCGCTTATTTGGTCTTACCAATGAGAG 1755
Qy 1681 AAATCTCAGAACAAACCCAGATGGAATTTTGGAGCAATGTGTTGTTTGGCTGC 1740
Db 1756 AAATCTCAGAACAAACCCAGATGGAATTTTGGAGCAATGTGTTGTTTGGCTGC 1815
Qy 1741 AGGCATTAAGATGAGATTTATCTTATTCAGAAAAGCTCAGACATTTCTTAAGCATGCG 1800
Db 1816 AGGCATTAAGATGAGATTTATCTTATTCAGAAAAGCTCAGACATTTCTTAAGCATGCG 1875
Qy 1801 ATCTTAACCTCATTAAGGTTCTCTTCAAGAGATGCTCTGTTGGGAGAGAGAGGC 1860
Db 1876 ATCTTAACCTCATTAAGGTTCTCTTCAAGAGATGCTCTGTTGGGAGAGAGAGGC 1935
Qy 1861 CCAGCAAGATATGACAAACAAATCCAGCTTCAATGCGCAGCAGGTGCGAATCTCTC 1920
Db 1936 CCAGCAAGATATGACAAACAAATCCAGCTTCAATGCGCAGCAGGTGCGAATCTCTC 1995
Qy 1921 CTCGAGAGAGACGGCCATTTATGTGTGTGATGCAAGAAATATGCGCAAGATGTA 1980
Db 1996 CTCGAGAGAGACGGCCATTTATGTGTGTGATGCAAGAAATATGCGCAAGATGTA 2055
Qy 1981 CATGATGCTCTGTGCAATTAATTAAGCAAGAGGTTGGAATTAAGCAAGCAATG 2040
Db 2056 CATGATGCTCTGTGCAATTAATTAAGCAAGAGGTTGGAATTAAGCAAGCAATG 2115
Qy 2041 AAAACCTGCGCACTTTAAAGAAAGAAACGCTACCTCAGGATTTTGGTCATA 2097
Db 2116 AAAACCTGCGCACTTTAAAGAAAGAAACGCTACCTCAGGATTTTGGTCATA 2172

RESULT 13
ADQ39029
ID ADQ39029 standard; DNA; 3256 BP.
XX
AC ADQ39029;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 692.
XX
KM Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX
KW cardiant; gene therapy; human; gene; ds.
OS
XX Homo sapiens.
PN WO2004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003WO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX

PA (Appl.) APPLERA CORP.
XX
PI Cargill M, Devlin JF, Iakoubova O;
XX
DR WPI: 2004-533949/51.
XX
P-PSDB; ADQ39857.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
PS Claim 7; SEQ ID NO 692; 145bp; English.
XX
CC The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SQ Sequence 3256 BP; 927 A; 691 C; 669 G; 940 T; 0 U; 29 Other;
Query Match 50.6%; Score 1062; DB 13; Length 3256;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2012; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 67 TGTGAGCAAGCTGTGTATCATGATTTTCTGCAAGATCTTCACTGTATTAGTAATCCGAT 126
Db 160 TGTGAGCAAGCTGTGTATCATGATTTTCTGCAAGATCTTCACTGTATTAGTAATCCGAT 219
Qy 127 AAGTATGACTTAAACCGAAACAGCTCTCTTGTGTGTGTGTTCTACACGGGACCC 186
Db 220 AAGTATGACTTAAACCGAAACAGCTCTCTTGTGTGTGTGTTCTACACGGGACCC 279
Qy 187 GGAGACCCACCGGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACACTGCGG 246
Db 280 GGAGACCCACCGGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACACTGCGG 339
Qy 247 GTTGATTTCTTGTCTACCTGGGTATGAGGTTACTGGGCTTGGGTATTCAGAAATACCC 306
Db 340 GTTGATTTCTTGTCTACCTGGGTATGAGGTTACTGGGCTTGGGTATTCAGAAATACCC 399
Qy 307 TACTTTTGAATGGGGGGAAGATTAATGATTAACAGATTCAGAGCTTGGACCCGGCAT 366
Db 400 TACTTTTGAATGGGGGGAAGATTAATGATTAACAGATTCAGAGCTTGGACCCGGCAT 459
Qy 367 TTTATGACACTGACATGACAGATGACTGTGAGGTTAGACTGTGTGTTGAGCGGTGG 426
Db 460 TTTATGACACTGACATGACAGATGACTGTGAGGTTAGACTGTGTGTTGAGCGGTGG 519
Qy 427 ATTGCTGACTCTGGCCAGCCCTCAGAAAGATTTTAAAGTCAAGACAGACAGAGAGAG 486

Db 520 ATTGCTGACCTGCGCAGCCCTCAGAAAGCATTTTAAAGTCAAGAGGACAAGAGG 579
Qy 487 ATAAAGGAGGACCTCCGGGTGATCATCTGATCTCTTGAGAGACAGACTTGAAGTCA 546
Db 580 ATTAAGTGGGCACTCCCGGTGGATCATCTGATCTCTTGAGAGACAGACTTGAAGTCA 639
Qy 547 GAGCTGCTACACATTTGAATCTCAAGTGCCTTCTGAGATTCGATATTCAGGAAGAA 606
Db 640 GAGCTGCTACACATTTGAATCTCAAGTGCAGCTTCTGAGATTCGATATTCAGGAAGAA 699
Qy 607 GATTGAGGTTTGAAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 666
Db 700 GATTGAGGTTTGAAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 759
Qy 667 GACTTGAAGTCTCATCTTACCCGTGGTACCCCACTCTCAGAGCTCTTGAATAT 726
Db 760 GACTTGAAGTCTCATCTTACCCGTGGTACCCCACTCTCAGAGCTCTTGAATAT 819
Qy 727 CTTGTTTACCCCGAGAAATTTTACAGGTACATCTGAGAGAGTCTTGGCCAGAGAGAA 786
Db 820 CTTGTTTACCCCGAGAAATTTTACAGGTACATCTGAGAGAGTCTTGGCCAGAGAGAA 879
Qy 787 AGCAGATATCTGAGATTCAGAGAGATCCAGTTTTCAGTGGCAATTTCAAGAGGAGTT 846
Db 880 AGCAGATATCTGAGATTCAGAGAGATCCAGTTTTCAGTGGCAATTTCAAGAGGAGTT 939
Qy 847 CAATTTACTAGATGATGCAATTAATAAACAATCTGCTGTAGATTTGACATTTCAAT 906
Db 940 CAATTTACTAGATGATGCAATTAATAAACAATCTGCTGTAGATTTGACATTTCAAT 999
Qy 907 ACAAGCTTTTCTATCAGCTGAGATGCTTACGCTGATCTGCTTAAAGATGATCT 966
Db 1000 ACAAGCTTTTCTATCAGCTGAGATGCTTACGCTGATCTGCTTAAAGATGATCT 1059
Qy 967 GAGGTAAAGGCTTACCTCAAGAGCTGAGATGAGATTAAGAGAGAGAGAGAGAGAGAG 1026
Db 1060 GAGGTAAAGGCTTACCTCAAGAGCTGAGATGAGATTAAGAGAGAGAGAGAGAGAGAG 1119
Qy 1027 TTGAAATTAAGGAGAGACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1086
Db 1120 TTGAAATTAAGGAGAGACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1179
Qy 1087 GATGTTCTCTCAGATCATTTTAACTGCTGCTTGAATTCGAGCAATTTCTAAAG 1146
Db 1180 GATGTTCTCTCAGATCATTTTAACTGCTGCTTGAATTCGAGCAATTTCTAAAG 1239
Qy 1147 GCATTTTGGAGGCTTGGAGATATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1206
Db 1240 GCATTTTGGAGGCTTGGAGATATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1299
Qy 1207 GAGCTGTGAGATTAACAAGGGGAGCCGATTAATAGCCGCTTGTATGAGATGCTGTGCC 1266
Db 1300 GAGCTGTGAGATTAACAAGGGGAGCCGATTAATAGCCGCTTGTATGAGATGCTGTGCC 1359
Qy 1267 TGCCTTGTGAGATCTCTCTCTGCTTTCCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1326
Db 1360 TGCCTTGTGAGATCTCTCTCTGCTTTCCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1419
Qy 1327 GAACATCTCTTAACTTCAACCCAGAGACATATCGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 1386
Db 1420 GAACATCTCTTAACTTCAACCCAGAGACATATCGTGTGAGAGAGAGAGAGAGAGAGAGAGAG 1479
Qy 1387 CAGAGAAAGCTCAATTTGTCTTCAACATTTGTGAGATTTCTGTACTGTCCACAAGAGAG 1446
Db 1480 CAGAGAAAGCTCAATTTGTCTTCAACATTTGTGAGATTTCTGTACTGTCCACAAGAGAG 1539
Qy 1447 GTTCTGAGAGAGAGAGATGATCAGAGCTGCTGCTTGTGTTGCTTCACTTCTTCAAG 1506
Db 1540 GTTCTGAGAGAGAGAGATGATCAGAGCTGCTGCTTGTGTTGCTTCACTTCTTCAAG 1599
Qy 1507 CCAAAACATACATGATCCATGAG 1566
Db 1600 CCAAAACATACATGATCCATGAG 1659

Qy 1567 TCTCTCGAACAACAATTTCTTCCATTACAGATGACCCCTCAATCCCATCATATAG 1626
Db 1660 TCTCTCGAACAACAATTTCTTCCATTACAGATGACCCCTCAATCCCATCATATAG 1719
Qy 1627 GTGGGTCCAGAAACCGGCAATACCCCGTTATTTGGGTTCTTCAACATGAGAGAACTC 1686
Db 1720 GTGGGTCCAGAAACCGGCAATACCCCGTTATTTGGGTTCTTCAACATGAGAGAACTC 1779
Qy 1687 CAAGAAACAACCCAGATGAAATTTTGGAGCAATGTGGTTGTTTTTGGCTGAGAGAT 1746
Db 1780 CAAGAAACAACCCAGATGAAATTTTGGAGCAATGTGGTTGTTTTTGGCTGAGAGAT 1839
Qy 1747 AAGATGAGGATTTATCTATTCAGAAAAGCTCAGACATTTCTTAAAGATGGATCTTA 1806
Db 1840 AAGATGAGGATTTATCTATTCAGAAAAGCTCAGACATTTCTTAAAGATGGATCTTA 1899
Qy 1807 ACTCATCTAAAGTTTCTTCTCAAGAGATGCTGTTGGGAGAGAGAGAGAGAGAGAGAG 1866
Db 1900 ACTCATCTAAAGTTTCTTCTCAAGAGATGCTGTTGGGAGAGAGAGAGAGAGAGAGAG 1959
Qy 1867 AAGTATGTACAAGACAATCCAGCTTCAATGGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 1926
Db 1960 AAGTATGTACAAGACAATCCAGCTTCAATGGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 2019
Qy 1927 GAGAACGCGCATATTTATGTGTGTGAGATGCAAGAAATATGGCCAAAGATGTACATGAT 1986
Db 2020 GAGAACGCGCATATTTATGTGTGTGAGATGCAAGAAATATGGCCAAAGATGTACATGAT 2079
Qy 1987 GCCCTGTGCAATATTAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2046
Db 2080 GCCCTGTGCAATATTAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2139
Qy 2047 CTGGCCACTTTTAAAG 2097
Db 2140 CTGGCCACTTTTAAAG 2190

RESULT 14
ID ADQ39030
ADQ39030 standard; DNA; 3274 BP.
XX
AC ADQ39030;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 693.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiant; gene therapy; human; gene; de.
XX
OS Homo sapiens.
XX
PN NC0204058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003MO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-046412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) ABPLERA CORP.
XX
PI Cargill M, Devlin J, Iakubova O;
XX
XX WPI; 2004-533949/51.
XX P-PSDB; ADQ39858.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in

PT the individual's nucleic acids.

XX Claim 7, SEQ ID NO 693; 145bp; English.

XX The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This polynucleotide sequence represents a human myocardial infarction-associated gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the MIPD website.

SQ Sequence 3274 BP; 932 A; 694 C; 672 G; 946 T; 0 U; 30 Other;

Query Match 50.6%; Score 1062; DB 13; Length 3274;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2012; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 67 TGTGAGCAAGCTGTGTATCATGATTTTCTGCAGATCTCTGTTAGTGAATCCAT 126
DB 178 TGTGAGCAAGCTGTGTATCATGATTTTCTGCAGATCTCTGTTAGTGAATCCAT 237
QY 127 AAGTAGACCTAAACCGAAACAGCTCTGTTGTTGTTCTGACACGGGAC 186
DB 238 AAGTAGACCTAAACCGAAACAGCTCTGTTGTTGTTCTGACACGGGAC 297
QY 187 GGAGACCCACCGACACAGCCCGCAAGTTGTTAAGGAATACAGAACCAACCTGCC 246
DB 298 GGAGACCCACCGACACAGCCCGCAAGTTGTTAAGGAATACAGAACCAACCTGCC 357
QY 247 GTTGATTTCTTTGCTCACTGGGTTAGGTTACTGGGTTCTGGTATTCAGATAC 306
DB 358 GTTGATTTCTTTGCTCACTGGGTTAGGTTACTGGGTTCTGGTATTCAGATAC 417
QY 307 TACTTTGCAATGGGGGGAATTAATGATTAACGACTTCAAGAGCTTGAAGCCGGCAT 366
DB 418 TACTTTGCAATGGGGGGAATTAATGATTAACGACTTCAAGAGCTTGAAGCCGGCAT 477
QY 367 TTCTATGACACTGACATGACATGCTGTAGTTAGAACTTGTGTTGACCGTGG 426
DB 478 TTCTATGACACTGACATGACATGCTGTAGTTAGAACTTGTGTTGACCGTGG 537
QY 427 ATTGCTGACTCTGGCAGCCCTCAGAAACATTTTAGTCAAGAGAGACAGAGAG 486
DB 538 ATTGCTGACTCTGGCAGCCCTCAGAAACATTTTAGTCAAGAGAGACAGAGAG 597
QY 487 ATTAAGGGGCACTCCGGTGGCATCACTGATCTTGAAGACAGACCTTGAAGTCA 546
DB 598 ATTAAGGGGCACTCCGGTGGCATCACTGATCTTGAAGACAGACCTTGAAGTCA 657
QY 547 GAGCTGCTACATTTGATCTCAAGTCAAGTCTTGAATTCAGATGATTCAGAGAGAG 606
DB 658 GAGCTGCTACATTTGATCTCAAGTCAAGTCTTGAATTCAGATGATTCAGAGAGAG 717

QY 607 GATTCGAGGTTTGAAGCAAAATGACAGTAACAGCAACCAATCCATTTGTAATTGA 666
DB 718 GATTCGAGGTTTGAAGCAAAATGACAGTAACAGCAACCAATCCATTTGTAATTGA 777
QY 667 GACTTGAAGTCTCACTTACCCGTTGCGTACCCCACTTCAAGACCTCTGTGAATAT 726
DB 778 GACTTGAAGTCTCACTTACCCGTTGCGTACCCCACTTCAAGACCTCTGTGAATAT 837
QY 727 CTTGTTTACCCCGAATTTTACAGGTACATCTGCAGAGTCTTTGGCCAGAGGAA 786
DB 838 CTTGTTTACCCCGAATTTTACAGGTACATCTGCAGAGTCTTTGGCCAGAGGAA 897
QY 787 AGCCAGATCTGTGACTTACAGCAGATCCAGTCTTCAAGTSCCAATTTCAAGGAGTT 846
DB 898 AGCCAGATCTGTGACTTACAGCAGATCCAGTCTTCAAGTSCCAATTTCAAGGAGTT 957
QY 847 CAATTTACTACGATGATGCCATAAAACCACTGCTGTGTGAATTTGACATTTCAAT 906
DB 958 CAATTTACTACGATGATGCCATAAAACCACTGCTGTGTGAATTTGACATTTCAAT 1017
QY 907 ACGACTTTTCTATACGCTGGAATGCTTCAAGCTGATCTGCTTAAAGTATTT 966
DB 1018 ACGACTTTTCTATACGCTGGAATGCTTCAAGCTGATCTGCTTAAAGTATTT 1077
QY 967 GAGGTAAAGGCTTCCAAAGACGCTTGAAGATTAAGAGAGCACTGCGCTT 1026
DB 1078 GAGGTAAAGGCTTCCAAAGACGCTTGAAGATTAAGAGAGCACTGCGCTT 1137
QY 1027 TTGAATAATTAAGGACAGACCAAGAGAAAGAGCTACTTACCCAGCATATACCTGCG 1086
DB 1138 TTGAATAATTAAGGACAGACCAAGAGAAAGAGCTACTTACCCAGCATATACCTGCG 1197
QY 1087 GATGTTCTCTCACTTATTTTACCTGTGTCTTGAATTCGAGCAATTCCTTAAAG 1146
DB 1198 GATGTTCTCTCACTTATTTTACCTGTGTCTTGAATTCGAGCAATTCCTTAAAG 1257
QY 1147 GCAATTTTGGAGCCCTTGTGACTATACCACTGACAGTCTGAAGAGCGAGCTACAG 1206
DB 1258 GCAATTTTGGAGCCCTTGTGACTATACCACTGACAGTCTGAAGAGCGAGCTACAG 1317
QY 1207 GAGCTGTGACATTAACAAGGGGACCGGATTAATGACCGCTTGTACAGATCTGTGCG 1266
DB 1318 GAGCTGTGACATTAACAAGGGGACCGGATTAATGACCGCTTGTGTAGAGATGCTGTGCG 1377
QY 1267 TGTGTTGATCTCTCTCTGCTTCTCTTCTGACGACCACTCACTGCTCTGCTC 1326
DB 1378 TGTGTTGATCTCTCTCTGCTTCTCTTCTGACGACCACTCACTGCTCTGCTC 1437
QY 1327 GAAATCTTCCCTAACTTCAACCGACACCATATGTTGTGAGAGCTCAAGTTATTTCAC 1386
DB 1438 GAAATCTTCCCTAACTTCAACCGACACCATATGTTGTGAGAGCTCAAGTTATTTCAC 1497
QY 1387 CCAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACCTGCAACAGAG 1446
DB 1498 CCAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACCTGCAACAGAG 1557
QY 1447 GTTCTGCGAAGAGATGTAACAGGCTGCTGCTGCTTGTGTTGTTGCTTCACTTCA 1506
DB 1558 GTTCTGCGAAGAGATGTAACAGGCTGCTGCTGCTTGTGTTGTTGCTTCACTTCA 1617
QY 1507 CCAACATATCAGTATCCCATGAAGACAGCGGGAAGCCCTGCTCTTAAGATTCATC 1566
DB 1618 CCAACATATCAGTATCCCATGAAGACAGCGGGAAGCCCTGCTCTTAAGATTCATC 1677
QY 1567 TCTCTCGAACAACAATTTCTTCACTTACAGATGACCCCTCAATCCCATCATATG 1626
DB 1678 TCTCTCGAACAACAATTTCTTCACTTACAGATGACCCCTCAATCCCATCATATG 1737
QY 1627 GTGGGTCCAGAAACGGGATACCCCGTTTATTTGGTTCTTCAACATTAAGAGAACTC 1686
DB 1738 GTGGGTCCAGAAACGGGATACCCCGTTTATTTGGTTCTTCAACATTAAGAGAACTC 1797

QY 1687 CAGAACCAACCCAGATGGAATTTTGGAGCAATGTGTTGTTTTTGGCTGACGGCAT 1746
CC
DB 1798 CAGAACCAACCCAGATGGAATTTTGGAGCAATGTGTTGTTTTTGGCTGACGGCAT 1857
CC
QY 1747 AAGGATGGGATTTATCTATTCAGAAAAAGACTCAGACATTTCTTAAAGCATGGGATCTTA 1806
CC
DB 1858 AAGGATGGGATTTATCTATTCAGAAAAAGACTCAGACATTTCTTAAAGCATGGGATCTTA 1917
CC
QY 1807 ACTCATCTAAAGGTTTCTTCTCTCAGAGATGCTCTGTGTTGGGAGAGAGAACCCAGCA 1866
CC
DB 1918 ACTCATCTAAAGGTTTCTTCTCTCAGAGATGCTCTGTGTTGGGAGAGAGAACCCAGCA 1977
CC
QY 1867 AAGTATGTACAGACACATCCAGCTTCATGSCCAGCAGGTTGCGAGATCTCTTCAG 1926
CC
DB 1978 AAGTATGTACAGACACATCCAGCTTCATGSCCAGCAGGTTGCGAGATCTCTTCAG 2037
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QY 1927 GAGAACGGCCATTTTATGTGTGTGTGAGATGCAAAAGATTTGGCCAAAGATGTACATGAT 1986
CC
DB 2038 GAGAACGGCCATTTTATGTGTGTGTGAGATGCAAAAGATTTGGCCAAAGATGTACATGAT 2097
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QY 1987 GCCCTGTGCAATTAATTAAGCAAAAGAGTTGAGTTGAAAACTAGAACATGAAAAAC 2046
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DB 2098 GCCCTGTGCAATTAATTAAGCAAAAGAGTTGAGTTGAAAACTAGAACATGAAAAAC 2157
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QY 2047 CTGGCCACTTTAAAGAGAAAAACGCTACCTTCAGATATTTGTCTATA 2097
CC
DB 2158 CTGGCCACTTTAAAGAGAAAAACGCTACCTTCAGATATTTGTCTATA 2208
CC
RESULT 15
ACN42470
ID ACN42470 standard; cDNA; 3189 BP.
XX
AC ACN42470:
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1345.
XX
KM ss: gene; gene therapy; human diagnostic and therapeutic polynucleotide;
KM dltbp.
XX
OS Homo sapiens.
XX
PN MO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WC-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCYTE) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Hartshorne TA, Suchorolski MT, Altus CM, Pites SJ, Elder LV,
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP,
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LI,
PI Lagace RE, Spito PA, Stewart EA, Wingrove J, Vilt UA, Kirtson ES,
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI: 2004-329368/30.
XX P-PSDB: ABM83818.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
PS Claim 1; Page; 190pp; English.

XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dltbp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorder,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dltbp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germ-line
CC gene therapy. The present sequence represents a dltbp polynucleotide of
CC the invention. Note: The sequence data for this patent is not represented
CC in the printed specification, but was obtained in electronic format
CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 3189 BP; 916 A; 679 C; 665 G; 929 T; 0 U; 0 Other;
Query Match 45.6%; Score 956; DB 13; Length 3189;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1056; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAGAGGTTTCTGTTACTATATGCTATACAGACAGGACAGCAAGCCATCGCAGAA 60
DB 112 ATGAGAGGTTTCTGTTACTATATGCTATACAGACAGGACAGCAAGCCATCGCAGAA 171
QY 61 GAAATGTGAGCAAGCTGTGTGATCATGATTTCTTGCAGATCTCATATTAAGGAA 120
DB 172 GAAATGTGAGCAAGCTGTGTGATCATGATTTCTTGCAGATCTCATATTAAGGAA 231
QY 121 TCCGATATGATGACCTTAAACCAAGCAAGCTCTTGTGTTGTGTTCTACACG 180
DB 232 TCCGATATGATGACCTTAAACCAAGCAAGCTCTTGTGTTGTGTTCTACACG 291
QY 181 GGCACCGAGAGCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACGAACCAACA 240
DB 292 GGCACCGAGAGCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACGAACCAACA 351
QY 241 CTGCGGTTGATTTCTTGTGCTACCTGCGGTATGAGTTACTGGGTCCTCGGTGATTGAA 300
DB 352 CTGCGGTTGATTTCTTGTGCTACCTGCGGTATGAGTTACTGGGTCCTCGGTGATTGAA 411
QY 301 TACACCTACTTTTGCATGAGGAGGAGATATGATTAACGACTTCAGAGCTTGAAGCC 360
DB 412 TACACCTACTTTTGCATGAGGAGGAGATATGATTAACGACTTCAGAGCTTGAAGCC 471
QY 361 CGGATTTCTATGACACTGACATGACATGATGATCTGTAGTTTAAAGCTTGTGTTGAG 420
DB 472 CGGATTTCTATGACACTGACATGACATGATGATCTGTAGTTTAAAGCTTGTGTTGAG 531
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QY 481 GAGAGATTAAGTGGCGCACTCCGTTGACATCTGACATCTTGAAGACAGACTTGTG 540
DB 592 GAGAGATTAAGTGGCGCACTCCGTTGACATCTGACATCTTGAAGACAGACTTGTG 651
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QY 601 AGAAGGATTTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCAATGTTGTA 660
DB 712 AGAAGGATTTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCAATGTTGTA 771
QY 661 ATTGAAGACTTTGAGTCTCTACCTTACCCGTTGAGTACCCCACTCTCAGAGCTCTCTG 720
DB 772 ATTGAAGACTTTGAGTCTCTACCTTACCCGTTGAGTACCCCACTCTCAGAGCTCTCTG 831
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Qy      961 GATTCTGAGGTACAAAGCCTACTCCAAAGACTGCACTTGAAGATTAAGAGCACTGC 1020
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Qy      1021 GTCTTTTGAATAAAGGACAGACAAAGAGAAAGG 1058
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OM nucleic - nucleic search, using sw model

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Title: US-09-371-347A-1

Perfect score: 2097

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Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2097	100.0	3259	3	US-09-318-448-23	Sequence 23, Appl
2	1944	92.7	3242	4	US-09-949-016-4215	Sequence 4215, Ap
3	386	18.4	390	3	US-08-905-223-71	Sequence 71, Appl
4	330	15.7	601	4	US-09-849-016-150019	Sequence 150019, A
5	279	13.3	35916	4	US-09-849-016-150020	Sequence 150020, A
6	279	13.3	601	4	US-09-849-016-150037	Sequence 150037, A
7	189	9.0	601	4	US-09-849-016-150030	Sequence 150030, A
8	189	9.0	601	4	US-09-849-016-150030	Sequence 150030, A
9	155	7.4	601	4	US-09-849-016-150030	Sequence 150030, A
10	145	6.9	601	4	US-09-849-016-150030	Sequence 150030, A
11	137	6.5	601	4	US-09-849-016-150046	Sequence 150046, A
12	137	6.5	601	4	US-09-849-016-150047	Sequence 150047, A
13	125	6.0	601	4	US-09-849-016-150029	Sequence 150029, A
14	121	5.8	601	4	US-09-849-016-150041	Sequence 150041, A
15	121	5.8	601	4	US-09-849-016-150042	Sequence 150042, A
16	119	5.7	601	4	US-09-849-016-150008	Sequence 150008, A
17	119	5.7	601	4	US-09-849-016-150008	Sequence 150008, A
18	110	5.2	601	4	US-09-849-016-150055	Sequence 150055, A
19	94	4.5	601	4	US-09-849-016-150048	Sequence 150048, A
20	78	3.7	244	4	US-09-471-276-495	Sequence 495, App
21	78	3.7	601	4	US-09-849-016-150007	Sequence 150007, A
22	76	3.6	601	4	US-09-849-016-150018	Sequence 150018, A
23	30	1.4	1681	4	US-09-823-685-453	Sequence 453, Appl
24	20	1.0	273	4	US-09-513-999C-14761	Sequence 14761, A
25	20	1.0	440	3	US-09-397-787-305	Sequence 305, Appl
26	20	1.0	444	4	US-09-621-976-14139	Sequence 14139, A
27	20	1.0	445	3	US-09-397-787-274	Sequence 274, App

C 28	20	1.0	174259	4	US-09-949-016-11968	Sequence 11968, A
C 29	20	1.0	174262	4	US-09-949-016-14259	Sequence 14259, A
C 30	19	0.9	169	1	US-08-166-346A-8	Sequence 8, Appl1
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C 32	19	0.9	3969	3	US-09-518-386B-4	Sequence 4, Appl1
C 33	19	0.9	4396	3	US-09-821-736-1	Sequence 1, Appl1
C 34	19	0.9	14721	4	US-09-949-016-13507	Sequence 13507, A
C 35	19	0.9	25199	4	US-09-949-016-13361	Sequence 13361, A
C 36	19	0.9	129658	4	US-09-949-016-17195	Sequence 17195, A
C 37	19	0.9	186734	4	US-09-949-016-14870	Sequence 14870, A
C 38	19	0.9	193689	4	US-09-949-016-12350	Sequence 12350, A
C 39	19	0.9	193689	4	US-09-949-016-13088	Sequence 13088, A
C 40	19	0.9	200663	4	US-09-949-016-12569	Sequence 12569, A
C 41	19	0.9	203093	4	US-09-949-016-14445	Sequence 14445, A
C 42	18	0.9	78	2	US-08-749-852-56	Sequence 56, Appl
C 43	18	0.9	78	2	US-08-749-852-58	Sequence 58, Appl
C 44	18	0.9	511	4	US-09-902-540-1374	Sequence 1374, Ap
C 45	18	0.9	531	4	US-09-252-991A-2223	Sequence 2223, Ap

ALIGNMENTS

RESULT 1						
US-09-318-448-23						
; Sequence 23, Application US/09318448						
; Patent No. 6210950						
; GENERAL INFORMATION:						
; APPLICANT: Johnson, William G.						
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING						
; FILE REFERENCE: 601-1-057						
; CURRENT APPLICATION NUMBER: US/09/318,448						
; NUMBER OF SEQ ID NOS: 46						
; SOFTWARE: PatentIn Ver. 2.0						
; SEQ ID NO 23						
; LENGTH: 3259						
; TYPE: DNA						
; ORGANISM: Homo sapiens						
; US-09-318-448-23						
Query Match						
Best Local Similarity 100.0%; Score 2097; DB 3; Length 3259;						
Matches 2097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
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DB	80	ATGAGGAGGTTCTGTACTATATCTACACAGCAGGAGGAGCAAGGCCATCGCAGAA	139			
QY	61	GAAATGTGTGACCAAGCTGTGTACATGATTTTCGACATCTTCACTGTATAGTAA	120			
DB	140	GAAATGTGTGACCAAGCTGTGTACATGATTTTCGACATCTTCACTGTATAGTAA	199			
QY	121	TCCGTAATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA	180			
DB	200	TCCGTAATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA	259			
QY	181	GCGACCGAGAGCCACCCGACAGCCGACAGTTGTTAAAGAAATACAGAACCAACA	240			
DB	260	GCGACCGAGAGCCACCCGACAGCCGACAGTTGTTAAAGAAATACAGAACCAACA	319			
QY	241	CTGCGGTTGATTTCTTCTGCTACCTGCGGTAGGTTAAGTAAAGTAAAGTAAAGTAA	300			
DB	320	CTGCGGTTGATTTCTTCTGCTACCTGCGGTAGGTTAAGTAAAGTAAAGTAAAGTAA	379			
QY	301	TACACTTATTTTGAATGGGGGAGAAATTTGAATTTGAATTTGAATTTGAATTTGA	360			
DB	380	TACACTTATTTTGAATGGGGGAGAAATTTGAATTTGAATTTGAATTTGAATTTGA	439			
QY	361	CGGATTTTATGACATGACATGACATGACATGACATGACATGACATGACATGACATG	420			

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Db 440 CGGCAATTTCTATGACACTGACATGACATGACTGTGTAGGTTTGAACCTTGGTTGAG 499
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Db 500 CCGTGATGCTGGAAGCTGCGCCAGCCCTCAGAAAGCAATTTAGTCAACAGAGCAAA 559
Qy 481 GAGGAGATTAAGTGGCGCACTCCGGTGGCATCACCTGCATCTTGAAGACAGACTTGTG 540
Db 560 GAGGAGATTAAGTGGCGCACTCCGGTGGCATCACCTGCATCTTGAAGACAGACTTGTG 619
Qy 541 AAGTCAGAGCTGCTCAACATTTGAATCTCAAGTGGAGCTTGGAGTTGAGATTCAGGA 600
Db 620 AAGTCAGAGCTGCTCAACATTTGAATCTCAAGTGGAGCTTGGAGATTCAGGA 679
Qy 601 AGAAGAGATTTCTGAGTTTGAAGCAAAATGCAAGTGAAGCAACCAATCCAAATGTGTA 660
Db 680 AGAAGAGATTTCTGAGTTTGAAGCAAAATGCAAGTGAAGCAACCAATCCAAATGTGTA 739
Qy 661 ATTGAAGATTTGAGTCTCTCACTTACCCTGGTGGTACCCCACTCTCAACAGCTCTCTG 720
Db 740 ATTGAAGATTTGAGTCTCTCACTTACCCTGGTGGTACCCCACTCTCAACAGCTCTCTG 799
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Qy 1081 CCTGCGGAGATTTCTCTCAAGTCAATTTTACCTGATGCTTGAAGTCCGAGCAATTCCT 1140
Db 1160 CCTGCGGAGATTTCTCTCAAGTCAATTTTACCTGATGCTTGAAGTCCGAGCAATTCCT 1219
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Qy 1201 CTAAGAGAGCTGTGCAATTAAGGCGGCGCATTAATAGCCCTTTTGAAGAGATGCC 1260
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Qy 1261 TGTGCTGCTGTTGAGATCTCTCTGCTTCCCTTTTTCGAGCAGCACTGAGTCTC 1320
Db 1340 TGTGCTGCTGTTGAGATCTCTCTGCTTCCCTTTTTCGAGCAGCACTGAGTCTC 1399
Qy 1321 CTGCTCGAATCTTCTCTAAACCTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTA 1380
Db 1400 CTGCTCGAATCTTCTCTAAACCTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTA 1459
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Db 1460 TTTTCAACCGAAGAGCTTCATTTTGTCTTCAACATTTGTGAAATTTGTCTACTGCCACA 1519
Qy 1441 ACAGAGGTTCTGCGAAGGAGATATGTAACAGGCTGCGCTTGTGTTGTTGCTTCAAGTT 1500
Db 1520 ACAGAGGTTCTGCGAAGGAGATATGTAACAGGCTGCGCTTGTGTTGTTGCTTCAAGTT 1579
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Qy 1501 CTTACAGCAAAATACATGATGATCCATGAAGACAGCGGAAAGCCCTGCTCTTAAGATA 1560
Db 1580 CTTACAGCAAAATACATGATGATCCATGAAGACAGCGGAAAGCCCTGCTCTTAAGATA 1639
Qy 1561 TCCATCTCTCTGGAACCAAAATTTCTTCACTTAACAGATACACCCCTCAATCCCATC 1620
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Qy 1621 ATAAATGAGGATCCAGAAACCGGATAGCCCGTTATTGGTTCCTACAACTAGAGAG 1680
Db 1700 ATAAATGAGGATCCAGAAACCGGATAGCCCGTTATTGGTTCCTACAACTAGAGAG 1759
Qy 1681 AAATCTCAAGAAACCAACCCAGATGAAATTTTGAAGCAATGTGTTTGTGCTGC 1740
Db 1760 AAATCTCAAGAAACCAACCCAGATGAAATTTTGAAGCAATGTGTTTGTGCTGC 1819
Qy 1741 AGGCATTAAGATGGAATTAATCTAATTCAGAAAGACTCAGATTTCTTAAGCATGGG 1800
Db 1820 AGGCATTAAGATGGAATTAATCTAATTCAGAAAGACTCAGATTTCTTAAGCATGGG 1879
Qy 1801 ATCTTAATCATTAAGGTTTCTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1860
Db 1880 ATCTTAATCATTAAGGTTTCTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1939
Qy 1861 CCAAGCAAGTATGTAACAACAATCCAGCTTCATGCGCAGAGGTGGCGAATCTTC 1920
Db 1940 CCAAGCAAGTATGTAACAACAATCCAGCTTCATGCGCAGAGGTGGCGAATCTTC 1999
Qy 1921 CTCAGAGAAAGCGCCATATTTATGTGTGAGATGCAAGAAATATGCGCAAGATGTA 1980
Db 2000 CTCAGAGAAAGCGCCATATTTATGTGTGAGATGCAAGAAATATGCGCAAGATGTA 2059
Qy 1981 CATGATGCCCTTGTGCAAAATTAATAGCAAAAGAGTTGAGTTGAAAACTAGAAAGCATG 2040
Db 2060 CATGATGCCCTTGTGCAAAATTAATAGCAAAAGAGTTGAGTTGAAAACTAGAAAGCATG 2119
Qy 2041 AAAACCTGCGCACTTTAAAGAAAGAAAGCGTACCTTCAGAGATTTGCTCATTA 2097
Db 2120 AAAACCTGCGCACTTTAAAGAAAGAAAGCGTACCTTCAGAGATTTGCTCATTA 2176

RESULT 2
US-09-949-016-4215
; Sequence 4215, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4215
; LENGTH: 3242
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4215

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 2094; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
1 ATGAGAGGTTTCTGTTACTATATGCTACACAGAGGAAAGGCGCATGCGAGAA 60
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APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: win95
SOFTWARE: word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
TISSUE TYPE: Brain
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 289..357
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 6.9
OTHER INFORMATION: seq SLSLASHSVSC/SN
US-08-905-223-71

Query Match 18.4%; Score 386; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 3.5e-188;
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3 GTACAAAGCTCTCTCAAGAGCTGACGCTTGAAGATAAAGAGCACTGCGCTCTTTG 62
QY 1030 AAAATAAGGAGCAGCAAAAGAGAGAGCTACCTTACCCGAGCATATACCTGGGGA 1089
DB 63 AAAATAAGGAGCAGCAAAAGAGAGAGCTACCTTACCCGAGCATATACCTGGGGA 122
QY 1090 TGTCTCTCCAGTTCATTTTACCTGCTGCTTGAATCCGAGCAATTCCTAAAAAGCA 1149
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QY 1210 CTGTCAGTAAACAAGGGGAGCCGATATAGCCGCTTGAAGAGATGCTGAGCTGC 1269
DB 243 CTGTCAGTAAACAAGGGGAGCCGATATAGCCGCTTGAAGAGATGCTGAGCTGC 302
QY 1270 TTGTGATCTGAA 1329
DB 303 TTGTGATCTGAA 362
QY 1330 CATCTTCTAAACTTCAACCCAGACC 1355

DB 363 CATCTTCTAAACTTCAACCCAGACC 388

RESULT 4
US-09-949-016-150019
Sequence 150019, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 150019
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-150019

Query Match 15.7%; Score 330; DB 4; Length 601;
Best Local Similarity 99.7%; Pred. No. 2.5e-159;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGTGAGCCCTGTGATGCTGGACTTGGCCAGCCCTCAGAAACATT 460
DB 178 GTTTAGAACTTGTGTGAGCCCTGTGATGCTGGACTTGGCCAGCCCTCAGAAACATT 237
QY 461 TTAGTCAAGCAGAGCAAGAGAGATTAAGTGGGCACTCCGGTGGCATCCTGCAT 520
DB 238 TTAGTCAAGCAGAGCAAGAGAGATTAAGTGGGCACTCCGGTGGCATCCTGCAT 297
QY 521 CTTGAGGAGCAGCCTTGAAGTCAAGCTGACATGTAATCAAGTGAAGCTTC 580
DB 298 CTTGAGGAGCAGCCTTGAAGTCAAGCTGACATGTAATCAAGTGAAGCTTC 357
QY 581 TGAGATTCGATGATGAGGAAGAGATTTGAGGTTTGAAGCAAAATGACGTGACA 640
DB 358 TGAGATTCGATGATGAGGAAGAGATTTGAGGTTTGAAGCAAAATGACGTGACA 417
QY 641 GCAACCAATCAATGTTGTAATGAAGACTTGAAGTCTTACCTTACCCGAGATTTTACAGTACATC 700
DB 418 GCAACCAATCAATGTTGTAATGAAGACTTGAAGTCTTACCTTACCCGAGATTTTACAGTACATC 477
QY 701 CACTTCACAAGCTCTGTAATTTCTGTTTACCCGAGATTTTACAGTACATC 760
DB 478 CACTTCACAAGCTCTGTAATTTCTGTTTACCCGAGATTTTACAGTACATC 537
QY 761 TGCAGAGTCTCTGGCCAGG 781
DB 538 TGCAGAGTCTCTGGCCAGG 558

RESULT 5
US-09-949-016-159957
Sequence 159957, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 15957
LENGTH: 35916
TYPE: DNA
ORGANISM: Human
US-09-949-016-15957

Query Match 15.7%; Score 330; DB 4; Length 35916;
Best Local Similarity 99.7%; Pred. No. 3.1e-159;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGTTGAGCCGTGATTCCTGAGCTGCGCCAGCCCTCAGAAAGCATT 460
DB 10781 GTTTAGAACTTGTGTTGAGCCGTGATTCCTGAGCTGCGCCAGCCCTCAGAAAGCATT 10840
QY 461 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCGGTGGCATCCTGCAT 520
DB 10841 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCGGTGGCATCCTGCAT 10900
QY 521 CCTTGAAGCAGACCTTGTGAATCTGAGCTGCTACACATTTCAATCTCAAGTGCAGCTTC 580
DB 10901 CCTTGAAGCAGACCTTGTGAATCTGAGCTGCTACACATTTCAATCTCAAGTGCAGCTTC 10960
QY 581 TGAGATTCATGATTCAGAGAAAGAAAGATTCTGAGTTTGAAGCAAAATGACGTAAACA 640
DB 10961 TGAGATTCATGATTCAGAGAAAGAAAGATTCTGAGTTTGAAGCAAAATGACGTAAACA 11020
QY 641 GCAACCAATCCAAATGTTGTAATTAAGTGAAGTCTTCACTTACCCGTTGGTACCCC 700
DB 11021 GCAACCAATCCAAATGTTGTAATTAAGTGAAGTCTTCACTTACCCGTTGGTACCCC 11080
QY 701 CACTTCACAAGCCTCTGGAATATTCCTGTTTACCCCAAGATTTTACAGGTACATC 760
DB 11081 CACTTCACAAGCCTCTGGAATATTCCTGTTTACCCCAAGATTTTACAGGTACATC 11140
QY 761 TGCAGAGTCTCTTGGCCAGG 781
DB 11141 TGCAGAGTCTCTTGGCCAGG 11161

RESULT 6

US-09-949-016-150020
Sequence 150020, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 150020
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-150020

Query Match 13.3%; Score 279; DB 4; Length 601;

Best Local Similarity 99.5%; Pred. No. 4.6e-133;
Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGTTGAGCCGTGATTCCTGAGCTGCGCCAGCCCTCAGAAAGCATT 460
DB 165 GTTTAGAACTTGTGTTGAGCCGTGATTCCTGAGCTGCGCCAGCCCTCAGAAAGCATT 224
QY 461 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCGGTGGCATCCTGCAT 520
DB 225 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCGGTGGCATCCTGCAT 284
QY 521 CCTTGAAGCAGACCTTGTGAATCTGAGCTGCTACACATTTCAATCTCAAGTGCAGCTTC 580
DB 285 CCTTGAAGCAGACCTTGTGAATCTGAGCTGCTACACATTTCAATCTCAAGTGCAGCTTC 344
QY 581 TGAGATTCATGATTCAGAGAAAGAAAGATTCTGAGTTTGAAGCAAAATGACGTAAACA 640
DB 345 TGAGATTCATGATTCAGAGAAAGAAAGATTCTGAGTTTGAAGCAAAATGACGTAAACA 404
QY 641 GCAACCAATCCAAATGTTGTAATTAAGTGAAGTCTTCACTTACCCGTTGGTACCCC 700
DB 405 GCAACCAATCCAAATGTTGTAATTAAGTGAAGTCTTCACTTACCCGTTGGTACCCC 464
QY 701 CACTTCACAAGCCTCTGGAATATTCCTGTTTACCCCAAGATTTTACAGGTACATC 760
DB 465 CACTTCACAAGCCTCTGGAATATTCCTGTTTACCCCAAGATTTTACAGGTACATC 524
QY 761 TGCAGAGTCTCTTGGCCAGG 781
DB 525 TGCAGAGTCTCTTGGCCAGG 545

RESULT 7

US-09-949-016-150037
Sequence 150037, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 150037
TYPE: DNA
ORGANISM: Human
US-09-949-016-150037

Query Match 9.0%; Score 189; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1e-86;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1369 AGCTCAAGTTATTTTACCCAGAGAAAGCTCAATTTTGTCTTCAACATTTGGAATTTCTG 1428
DB 18 AGCTCAAGTTATTTTACCCAGAGAAAGCTCAATTTTGTCTTCAACATTTGGAATTTCTG 77
QY 1429 TCTACTGCCACAAGAGGTTCTGCGAAGGAGATATGTACAGGCTGCTGCGCTTGTG 1488
DB 78 TCTACTGCCACAAGAGGTTCTGCGAAGGAGATATGTACAGGCTGCTGCGCTTGTG 137
QY 1489 GTTGTCTCAGTTCTTCAAGCAAAATATCATGATCCATGAAAGACAGCGGAAAGCCCTG 1548
DB 138 GTTGTCTCAGTTCTTCAAGCAAAATATCATGATCCATGAAAGACAGCGGAAAGCCCTG 197

QY	1549	GCTCCTAAG	1557
Db	198	GCTCCTAAG	206

RESULT 8
US-09-566-921-88
; Sequence 88, Application US/09566921

QY 525 GAGGACAGACCTTGTGAGTCAGAGCTGCTACACATTGAATCTCAAGTCGAGCTTCTGAG 584

Qy 585 ATTGCATGATT CAGGAAGAAAGCATTCGAGCTTTTGAAGCAAAATGCAGTGAACAGCA 644

Db 76 ATTCGATGATT CAGGAAGAAAGCATTCGAGCTTTTGAAGCAAAATGCAGTGAACAGCA 135

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QY      645 CCAATCCAATGTTGTAATTGAAGACTTTGAGTCCCTCAC 682
          |||||
Db      136 CCAATCCAATGTTGTAATTGAAGACTTTGAGTCCCTCAC 173

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RESULT 9
US-09-949-016-150030
; Sequence 150030, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 150030
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150030

```

Query Match	7.4%	Score 155;	DB 4;	Length 601;
Best Local Similarity	100.0%;	Pred. No. 3.4e-69;		
Matches 155;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	DB	QY	DB
904	320	964	380
AAATACAGACTTTCTCTATCAGCGCTGGAGAGATGCTTTCAGCGGTGATCTGGCTTACAGTGAT	AAATACAGACTTTTCTCTATCAGCGCTGGAGAGATGCTTTCAGCGGTGATCTGGCTTACAGTGAT	TCTGAGGTACAAAGCCTTACTTCCAAAGACTGACGCTTTGAGATTAAGAAGACACTGCGTC	TCTGAGGTACAAAGCCTTACTTCCAAAGACTGACGCTTTGAGATTAAGAAGACACTGCGTC
963	379	1024	440
CTTTTGAATAATAAAGGCAGACACAAAGAGAAAGG	CTTTTGAATAATAAAGGCAGACACAAAGAGAAAGG	CTTTTGAATAATAAAGGCAGACACAAAGAGAAAGG	CTTTTGAATAATAAAGGCAGACACAAAGAGAAAGG
1058	474		

```

RESULT 10
US-09-949-016-150031
: Sequence 150031, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C1001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 150031
: LENGTH: 601
: TYPE: DNA
: ORGANISM: Human
: US-09-949-016-150031

```

Query Match	6.9%;	Score 145;	DB 4;	Length 601;
Best Local Similarity	100.0%;	Pred. No. 4.8e-64;		
Matches 145;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Oy	904	AATACAGACTTTTCTCTATCAGCCGAGATGCCTTCAGCGTGATCTGCCCTTAACAGTGAT	963
Db	156	AATAACAATTCTTCTATCAGCCGTGGAGATCCCTTACCGTGATGTGCCCTMACAGTGAT	215
Oy	964	TCTGAGGTAAAGAACCCTACTCCAAAGACTGCCTTGAAGATTAAGAAGAGCACTGCCTC	1022
Db	216	TCTGAGGTAAAGAACCCTACTCCAAAGACTGCAGCTTGAAGATTAAGAAGAGCACTGCCTC	275
Oy	1024	CTTTGAAAATAAAGCAGACACA	1048
Db	276	CTTTGAAAATAAAGCAGACACA	300

```

RESULT 11
US-09-949-016-150046
: Sequence 150046, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CLO01307
: CURRENT APPLICATION NUMBER: US/09/949, 016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768

```

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:
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FASTSEQ for Windows Version 4.0.
: SEQ ID NO 150046
: LENGTH: 601
: TYPE: DNA
: ORGANISM: Human
:
US-03-949-016-150046

```

Query Match	6.5%	Score 137;	DB 40;	Length 601;
Best Local Similarity	99.5%	Pred. NO. 6.3e-60;		
Matches 187;	Conservative	0;	Mismatches 1;	Indels 0;
			Gaps	0

QY	165	TTGAAAAGAGCTCAGCATTTCTTTAGAGTGGATCTTAATCATCTAAAGTTCC	182
Db	413	TTGAAAAGAGCTCAGCATTTCTTTAGCATGGATCTTACTCATCTAAGGTTCC	472
QY	1825	TTCTCAAGAGATGCTCTTGTGGGAGAGGAGGCCCGACAAATATGTATCAAGACAAC	1884
Db	473	TTCTCAAGAGATGCTCTTGTGGGAGAGGAGAGGCCCGACAAATATGTGCAAGACAAC	532
QY	1885	ATCCAGCTTCAATGGCCAGCAGGTGGCGAAGATCTCTCTCCAGGAGAAAGGCATATTTAT	1944
Db	533	ATCCAGCTTCAATGGCCAGCAGGTGGCGAAGATCTCTCTCCAGGAGAAAGGCATATTTAT	592
QY	1945	GTGTGTGG 1952	
Db	593	GTGTGTGG 600	

```

12 RESULT 12
13 US-09-949-016-150047
14 ; Sequence 150047, Application US/09949016
15 ; Patent No. 6812339
16 ; GENERAL INFORMATION:
17 ; APPLICANT: VENTER, J. Craig et al.
18 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
19 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
20 ; FILE REFERENCE: CLO01307
21 ; CURRENT APPLICATION NUMBER: US/09/949, 016
22 ; CURRENT FILING DATE: 2000-04-14
23 ; PRIOR APPLICATION NUMBER: 60/241,755
24 ; PRIOR FILING DATE: 2000-10-20
25 ; PRIOR APPLICATION NUMBER: 60/237,768
26 ; PRIOR FILING DATE: 2000-10-03
27 ; PRIOR APPLICATION NUMBER: 60/231,498
28 ; PRIOR FILING DATE: 2000-09-08
29 ; NUMBER OF SEQ ID NOS: 207012
30 ; SOFTWARE: FastSeq for Windows Version 4.0
31 ; SEQ ID NO 150047
32 ; LENGTH: 601
33 ; TYPE: DNA
34 ; ORGANISM: Human
35 ; US-09-949-016-150047

```

	Query Match	Similarity	6-5%	Score 137	DB 4	Length 601	
	Best Local	Similarity	99.5%	Pred. No. 6.3e-60			
	Matches 187	Conservative	0	Mismatches 1	Indels 0	Gaps 0	
Qy	1765	TTTCAGAAAGAGCTCAGACATTTCTTAAAGCATGTGAGATCTTAACATCTAAAGGTTTCC					182
Db	191	TTTCAGAAAGAGCTCAGACATTTCTTAAAGCATGTGAGATCTTAACATCTAAAGGTTTCC					250
Qy	1825	TTTCAGAGAGTCTCTCTGTTGGGAGGAGAGGCCCCAGCAAAGTATGTACAGCAAC					188
Db	251	TTTCAGAGAGTCTCTCTGTTGGGAGGAGAGGCCCCAGCAAAGTATGTACAGCAAC					310
Qy	1885	ATTCAGCTTCATGGCAGAGGTGCGAGAAATCTCTCCACAGAGAAAGCGCATATTAT					194
Db	311	ATTCAGCTTCATGGCAGAGGTGCGAGAAATCTCTCCACAGAGAAAGCGCATATTAT					370

Qy	1945	GTGTGTGG	1952
Db	371	GTGTGTGG	378

RESULT 13
 US-09-949-016-150029
 : Sequence 150029, Application US/09949016
 : Patent No. 681239
 : GENERAL INFORMATION:
 : APPLICANT: VENTER, J. Craig et al.
 : TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 : TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 : FILE REFERENCE: C1001307
 : CURRENT APPLICATION NUMBER: US/09/949,016
 : CURRENT FILING DATE: 2000-04-14
 : PRIOR APPLICATION NUMBER: 60/241,755
 : PRIOR FILING DATE: 2000-10-20
 : PRIOR APPLICATION NUMBER: 60/237,768
 : PRIOR FILING DATE: 2000-10-03
 : PRIOR APPLICATION NUMBER: 60/231,458
 : PRIOR FILING DATE: 2000-09-08
 : NUMBER OF SEQ ID NOS: 207012
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 150029
 : LENGTH: 601
 : TYPE: DNA
 : ORGANISM: Human
 : US-09-949-016-150029

	Query Match	Similarity	100.0%	Score 125	DB 4	Length 601	
	Best Local	Similarity	100.0%	Pred. No. 9.5e-54			
	Matches	125	Conservative	0	Mismatches	0	Indels
							Gaps 0
Qy	779	AGAGAAAGCCAGTATCTGTGACTTCAGCAGATCCAGTTTTCAGTGGCAATTTCAA					838
Db	379	AGAGAAAGCCAGTATCTGTGACTTCAGCAGATCCAGTTTTCAGTGGCAATTTCAA					438
Qy	839	AGGCAATTCAACTTACTACGATATGTCATTAACCACTCTGCTGTAGATTGGACA					898
Db	439	AGGCAATTCAACTTACTACGATATGTCATTAACCACTCTGCTGTAGATTGGACA					498
Qy	899	TTTCA 903					
Db	499	TTTCA 503					

```

RESULT 14
US-09-949-016-150041
; Sequence 150041, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150041
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150041

```

Query Match 5.8%; Score 121; DB 4; Length 601;

Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1556 AGATATCCATCTCTCTCGAACAACAATTTCTTCCACTTACGATGACCCCTCAATCC 1615

DB 124 AGATATCCATCTCTCTCGAACAACAATTTCTTCCACTTACGATGACCCCTCAATCC 183

QY 1616 CCATCATTAATGTTGGGTCCAGAAACCGGCAATAGCCCGTTTATTGGGTTCCTACACATA 1675

DB 184 CCATCATTAATGTTGGGTCCAGAAACCGGCAATAGCCCGTTTATTGGGTTCCTACACATA 243

QY 1676 G 1676

DB 244 G 244

RESULT 15

US-09-949-016-150042

/ Sequence 150042; Application US/09949016

/ Patent No. 6812339

/ GENERAL INFORMATION:

/ APPLICANT: VENTER, J. Craig et al.

/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

/ FILE REFERENCE: CU001307

/ CURRENT APPLICATION NUMBER: US/09/949,016

/ CURRENT FILING DATE: 2000-04-14

/ PRIOR APPLICATION NUMBER: 60/241,755

/ PRIOR FILING DATE: 2000-10-20

/ PRIOR APPLICATION NUMBER: 60/237,768

/ PRIOR FILING DATE: 2000-10-03

/ PRIOR APPLICATION NUMBER: 60/231,498

/ NUMBER OF SEQ ID NOS: 207012

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 150042

/ LENGTH: 601

/ TYPE: DNA

/ ORGANISM: Human

US-09-949-016-150042

Query Match 5.8%; Score 121; DB 4; Length 601;

Best Local Similarity 100.0%; Pred. No. 1.1e-51;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1556 AGATATCCATCTCTCTCGAACAACAATTTCTTCCACTTACGATGACCCCTCAATCC 1615

DB 95 AGATATCCATCTCTCTCGAACAACAATTTCTTCCACTTACGATGACCCCTCAATCC 154

QY 1616 CCATCATTAATGTTGGGTCCAGAAACCGGCAATAGCCCGTTTATTGGGTTCCTACACATA 1675

DB 155 CCATCATTAATGTTGGGTCCAGAAACCGGCAATAGCCCGTTTATTGGGTTCCTACACATA 214

QY 1676 G 1676

DB 215 G 215

Search completed: August 27, 2005, 16:18:14
Job time : 238.757 secs

Dh 1 ATGAGAGGTTTCTGTTACTATATGCTACACAGAGGGACAGGCAAAAGCCATCGCAGAA 60
Qy 61 GAAATGTGAGCAAGCTGTGTGATCATGATATTTCTGCAGATCTTCACTGATTAATGAA 120
Dh 61 GAAATGTGAGCAAGCTGTGTGATCATGATATTTCTGCAGATCTTCACTGATTAATGAA 120
Qy 121 TCGGATTAAGTATGACTTAAACCCGAAACAGCTCTCTTGTGTGTGTTCTACACAG 180
Dh 121 TCGGATTAAGTATGACTTAAACCCGAAACAGCTCTCTTGTGTGTGTTCTACACAG 180
Qy 181 GGGACGGGAGACCAACCGGACAGAGCCGGAAGTTGTTAAGAAATAGCAACCAACA 240
Dh 181 GGGACGGGAGACCAACCGGACAGAGCCGGAAGTTGTTAAGAAATAGCAACCAACA 240
Qy 241 CTGCGGTTGATTTCTTGTCTCACTGCGGATAGGTTTACTGGGCTCGGTTGATTCAGAA 300
Dh 241 CTGCGGTTGATTTCTTGTCTCACTGCGGATAGGTTTACTGGGCTCGGTTGATTCAGAA 300
Qy 301 TACACCTACTTTTGCATTTGGGGGAGATTAATGATTAACGACTTCAAGACTTTGAGCC 360
Dh 301 TACACCTACTTTTGCATTTGGGGGAGATTAATGATTAACGACTTCAAGACTTTGAGCC 360
Qy 361 CGGATTTCTATGACATGACATGAGATGACTGTGTAGGTTTAAAGACTTCAAGAGCTTGAG 420
Dh 361 CGGATTTCTATGACATGAGATGACTGTGTAGGTTTAAAGACTTCAAGAGCTTGAG 420
Qy 421 CCGTGATGCTGGAATCTGCGCAGCCCTCAGAAAGATTTTAAAGTCAAGCAGAGCA 480
Dh 421 CCGTGATGCTGGAATCTGCGCAGCCCTCAGAAAGATTTTAAAGTCAAGCAGAGCA 480
Qy 481 GAGGAGTAAGTGGCGCATCTCCGCTGGCATCACCTGATCTTGAAGACAGACTTTG 540
Dh 481 GAGGAGTAAGTGGCGCATCTCCGCTGGCATCACCTGATCTTGAAGACAGACTTTG 540
Qy 541 AAGTCAGAGCTGACACATTTGATCTCAAGTGAAGCTTTCAGATTCAGATTCAGAA 600
Dh 541 AAGTCAGAGCTGACACATTTGATCTCAAGTGAAGCTTTCAGATTCAGATTCAGAA 600
Qy 601 AGAAAGATTTCTGAGTTTGAAGCAAAATGCACTGAGCAAGCAACCAATCAATGTTGA 660
Dh 601 AGAAAGATTTCTGAGTTTGAAGCAAAATGCACTGAGCAAGCAACCAATCAATGTTGA 660
Qy 661 ATTGAAGATTTGATGCTCACTTACCCGTTCCGTTACCCCACTCTCAAGCTCTCTG 720
Dh 661 ATTGAAGATTTGATGCTCACTTACCCGTTCCGTTACCCCACTCTCAAGCTCTCTG 720
Qy 721 AATATTCCTGTTTACCCCGAGATTTTACAGGTATCATGAGAGAGTCTCTTGCCAG 780
Dh 721 AATATTCCTGTTTACCCCGAGATTTTACAGGTATCATGAGAGAGTCTCTTGCCAG 780
Qy 781 GAGGAAAGCCAAAGTATCTGTGACTTTCAGCAGATCAGATTTTCAAGTCCAAATTCAA 840
Dh 781 GAGGAAAGCCAAAGTATCTGTGACTTTCAGCAGATCAGATTTTCAAGTCCAAATTCAA 840
Qy 841 GCAATTCATTTACTAGATGATGCAATTAACCACTGCTGTGATTAATGAGCAAT 900
Dh 841 GCAATTCATTTACTAGATGATGCAATTAACCACTGCTGTGATTAATGAGCAAT 900
Qy 901 TCAAAATCAGACTTTCTATCAGCTGAGAGATGCTTCAAGCTGAGCTGAGCTGAGCT 960
Dh 901 TCAAAATCAGACTTTCTATCAGCTGAGAGATGCTTCAAGCTGAGCTGAGCTGAGCT 960
Qy 961 GATTTCTGAGGTACAAAGCTTCTCAAGAGCTGAGCTGAGTGAATTAAGAGAGCACTGC 1020
Dh 961 GATTTCTGAGGTACAAAGCTTCTCAAGAGCTGAGCTGAGTGAATTAAGAGAGCACTGC 1020
Qy 1021 GTCTTTTGAATAAAGGAGAGCAACAAAGAAAGAGCTTACCTTACCCAGCATATA 1080
Dh 1021 GTCTTTTGAATAAAGGAGAGCAACAAAGAAAGAGCTTACCTTACCCAGCATATA 1080
Qy 1081 CTTGCGGAGATGTTCTCTCAGATTTTCTGATTTTCTGATTTTCTGATTTTCTGATTT 1140
Dh 1081 CTTGCGGAGATGTTCTCTCAGATTTTCTGATTTTCTGATTTTCTGATTTTCTGATTT 1140

Qy 1141 AAAAAGCATTTTGTGAGCCCTTGTGACTATACCAATGACAGTGTGAAAAAGCCAG 1200
Dh 1141 AAAAAGCATTTTGTGAGCCCTTGTGACTATACCAATGACAGTGTGAAAAAGCCAG 1200
Qy 1201 CTACAGAGCTGTGCAATTAACAGGGGAGCCGATTAATAGCCGCTTTTGAAGATG 1260
Dh 1201 CTACAGAGCTGTGCAATTAACAGGGGAGCCGATTAATAGCCGCTTTTGAAGATG 1260
Qy 1261 TGTGCTGCTGTGTGATCTCTCTGCTTCCCTTCTTGCAGAGCACAACACTGCTC 1320
Dh 1261 TGTGCTGCTGTGTGATCTCTCTGCTTCCCTTCTTGCAGAGCACAACACTGCTC 1320
Qy 1321 CTGCTGAAATCTTCTTAACTTCAACCCAGACCAATATTCGTGCAAGCTCAAGTTTA 1380
Dh 1321 CTGCTGAAATCTTCTTAACTTCAACCCAGACCAATATTCGTGCAAGCTCAAGTTTA 1380
Qy 1381 TTTTCAACCCAGAAAGCTCAATTTGTCTTCAACATTTGAGAAATTTCTGCTACGCA 1440
Dh 1381 TTTTCAACCCAGAAAGCTCAATTTGTCTTCAACATTTGAGAAATTTCTGCTACGCA 1440
Qy 1441 ACAGAGTTCTGCGAAGGAGATATGATACAGGCTGAGCTGCTTGTGTGCTTCAATT 1500
Dh 1441 ACAGAGTTCTGCGAAGGAGATATGATACAGGCTGAGCTGCTTGTGTGCTTCAATT 1500
Qy 1501 CTTGAGCCAAACATACATGATCCCATGAAAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
Dh 1501 CTTGAGCCAAACATACATGATCCCATGAAAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
Qy 1561 TCCATCTCTCTGCAACAAATTTCTTCCATTAACAGATGACCCCTCAATCCCATC 1620
Dh 1561 TCCATCTCTCTGCAACAAATTTCTTCCATTAACAGATGACCCCTCAATCCCATC 1620
Qy 1621 ATATAGTGGTTCAGAAACCGGACATAGCCGCTTATTTAGGTTCTTCAACATAGAG 1680
Dh 1621 ATATAGTGGTTCAGAAACCGGACATAGCCGCTTATTTAGGTTCTTCAACATAGAG 1680
Qy 1681 AAATCTCAAGAACCAACCCAGATGAAATTTTGAAGCAATGTGTTTGTGCTGC 1740
Dh 1681 AAATCTCAAGAACCAACCCAGATGAAATTTTGAAGCAATGTGTTTGTGCTGC 1740
Qy 1741 AGGCAATTAAGATTAATCTATTCAGAAAGACTCAGACATTTCTTAAGATGG 1800
Dh 1741 AGGCAATTAAGATTAATCTATTCAGAAAGACTCAGACATTTCTTAAGATGG 1800
Qy 1801 ATCTTAATCATTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1860
Dh 1801 ATCTTAATCATTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1860
Qy 1861 CCAGAAAGTATGATCAAGCAATCCAGCTTCAATGCGAGGAGGAGAAATCTC 1920
Dh 1861 CCAGAAAGTATGATCAAGCAATCCAGCTTCAATGCGAGGAGGAGAAATCTC 1920
Qy 1921 CTTCAGAGAAACGGCAATTTATGTGTGAGAGATGCAAGAAATTTGCGCAAGATGA 1980
Dh 1921 CTTCAGAGAAACGGCAATTTATGTGTGAGAGATGCAAGAAATTTGCGCAAGATGA 1980
Qy 1981 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGTGTGAGTTGAAAAACTAGAGCAATG 2040
Dh 1981 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGTGTGAGTTGAAAAACTAGAGCAATG 2040
Qy 2041 AAAACCTGCGCATTTTAAAGAAAGAAACGCTACCTTCAAGATATTTGTCTATA 2097
Dh 2041 AAAACCTGCGCATTTTAAAGAAAGAAACGCTACCTTCAAGATATTTGTCTATA 2097

RESULT 2
US-09-371-347-24
; Sequence 24, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE;


```

; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 24
; LENGTH: 3259
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-371-347-24

Query Match      100.0%; Score 2097; DB 10; Length 3259;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGAGGTTCTGTACTATATGCTACACAGCAGGAGCAGGCAAAAGCCATCGAGAA 60
DB ATGAGAGAGGTTCTGTACTATATGCTACACAGCAGGAGCAGGCAAAAGCCATCGAGAA 139
QY 61 GAAATGTGAGAGACCTGTGTACATGATTTTCTGAGATCTTCACTATTAAGTAA 120
DB GAAATGTGAGAGACCTGTGTACATGATTTTCTGAGATCTTCACTATTAAGTAA 199
QY 121 TCCGATATGATGACCTTAAACCGGAAACAGCTCTCTGTGTGTGTGTTCTACACAG 180
DB TCCGATATGATGACCTTAAACCGGAAACAGCTCTCTGTGTGTGTGTTCTACACAG 259
QY 200 TCCGATATGATGACCTTAAACCGGAAACAGCTCTCTGTGTGTGTGTTCTACACAG 259
DB 181 GGGACCGGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACAAACA 240
DB 260 GGGACCGGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACAAACA 319
QY 241 CTGCGGTTGATTTCTTGTCTACCTGCGGTATGAGTTAAGTGTCTCGGTATTCAGAA 300
DB 320 CTGCGGTTGATTTCTTGTCTACCTGCGGTATGAGTTAAGTGTCTCGGTATTCAGAA 379
QY 301 TACACCTACTTTTGAATGGGGGAGATTAATTGATTAAGCACTTCAAGAGTTGAGACC 360
DB 380 TACACCTACTTTTGAATGGGGGAGATTAATTGATTAAGCACTTCAAGAGTTGAGACC 439
QY 361 CGGCACTTCTATGACACTGACATGACATGATGATGTGTAGTTAAGAACTTGTGTGAG 420
DB 440 CGGCACTTCTATGACACTGACATGACATGATGATGTGTAGTTAAGAACTTGTGTGAG 499
QY 421 CCGTGTATGCTGACACTGCGCAGCCCTCAAGAAAGCACTTTAGTCAAGAGAGACAA 480
DB 500 CCGTGTATGCTGACACTGCGCAGCCCTCAAGAAAGCACTTTAGTCAAGAGAGACAA 559
QY 481 GAGAGATAGTGGCGCACTCCGGTGGCATCACTGCACTCTTGAAGGACAGACTTGTG 540
DB 560 GAGAGATAGTGGCGCACTCCGGTGGCATCACTGCACTCTTGAAGGACAGACTTGTG 619
QY 541 AAGTCAGAGCTGCTACATTTGAATCTCAAGTCAAGCTTCTGAGATTCAGATTTCAGAA 600
DB 620 AAGTCAGAGCTGCTACATTTGAATCTCAAGTCAAGCTTCTGAGATTCAGATTTCAGAA 679
QY 601 AGAAAGATTTCTGAGCTTTGAAGCAAAATGACAGTGAACAGCAACCAATTCATTTGTA 660
DB 680 AGAAAGATTTCTGAGCTTTGAAGCAAAATGACAGTGAACAGCAACCAATTCATTTGTA 739
QY 661 ATGAGAGACTTTGAGTCTCACTTACCCGTTCCGTTACCCCACTCTCAAGCCTCTCTG 720
DB 740 ATGAGAGACTTTGAGTCTCACTTACCCGTTCCGTTACCCCACTCTCAAGCCTCTCTG 799
QY 721 AATATTCCTGTGTTACCCCAAGATATTTAAGGTATCATCTGACAGAGTCTCTTGCCAG 780
DB 800 AATATTCCTGTGTTACCCCAAGATATTTAAGGTATCATCTGACAGAGTCTCTTGCCAG 859

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QY 781 GAGAAAGCCAGATATCTGTGACTTCAGAGATCCAGTTTTCAGATGCCAATTTCAAG 840
DB GAGAAAGCCAGATATCTGTGACTTCAGAGATCCAGTTTTCAGATGCCAATTTCAAG 919
QY 841 GCAATTCAACTTACTACGAATATGCAATTAATAACCACTCTGCTGTAGATTTGAGACT 900
DB 920 GCAATTCAACTTACTACGAATATGCAATTAATAACCACTCTGCTGTAGATTTGAGACT 979
QY 901 TGAATATCAAGACTTTTCCATCAGCGTGGAGATGCTTCAAGGTATCTGCCCTAACGT 960
DB 980 TGAATATCAAGACTTTTCCATCAGCGTGGAGATGCTTCAAGGTATCTGCCCTAACGT 1039
QY 961 GATTCTGAGTACAAAGCCTTACCAAGACTGACACTTGAAGATTAAGAGAGCAGCTGC 1020
DB 1040 GATTCTGAGTACAAAGCCTTACCAAGACTGACACTTGAAGATTAAGAGAGCAGCTGC 1099
QY 1021 GTCTTTTGAATAAAGGACAGACAAAGAAAGAAAGAGCTTACCTTACCCAGCATATA 1080
DB 1100 GTCTTTTGAATAAAGGACAGACAAAGAAAGAAAGAGCTTACCTTACCCAGCATATA 1159
QY 1081 CCGCGGGGATGTTCTCTCAGTTCAATTTTACCTGTGCTTGAATCCGAGCAATTCCT 1140
DB 1160 CCGCGGGGATGTTCTCTCAGTTCAATTTTACCTGTGCTTGAATCCGAGCAATTCCT 1219
QY 1141 AAAAAGCATTTTGTGAGACCCCTTGTGACTATACAGTGAAGTGTGAAAAGGCGCAG 1200
DB 1220 AAAAAGCATTTTGTGAGACCCCTTGTGACTATACAGTGAAGTGTGAAAAGGCGCAG 1279
QY 1201 CTACAGAGCTGTGACGTAAACAGAGGAGCCGATTAATAGCCGTTTGTACAGATGCC 1260
DB 1280 CTACAGAGCTGTGACGTAAACAGAGGAGCCGATTAATAGCCGTTTGTACAGATGCC 1339
QY 1261 TGTGCTGCTGTGTGATCTCTCTGCTTCCCTTCTTGGCAAGCAGCACTCACTCTC 1320
DB 1340 TGTGCTGCTGTGTGATCTCTCTGCTTCCCTTCTTGGCAAGCAGCACTCACTCTC 1399
QY 1321 CTGCTGAAACATCTTCTTAACTTCAACCCAGACATATTCGTGTCAAGCTCAAGTTTA 1380
DB 1400 CTGCTGAAACATCTTCTTAACTTCAACCCAGACATATTCGTGTCAAGCTCAAGTTTA 1459
QY 1381 TTTCAACCAAGAAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTCTGTACTGTCACA 1440
DB 1460 TTTCAACCAAGAAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTCTGTACTGTCACA 1519
QY 1441 ACAAGGTTCTGCGGAGGAGATATGATACAGCTGCTGCTTGTGTGTGTTCAAGTT 1500
DB 1520 ACAAGGTTCTGCGGAGGAGATATGATACAGCTGCTGCTTGTGTGTGTTCAAGTT 1579
QY 1501 CTTCAGCCAAACATACATGATCCCATGGAAGACAGCGGAAAGCCCTGGCTCTTAAGATA 1560
DB 1580 CTTCAGCCAAACATACATGATCCCATGGAAGACAGCGGAAAGCCCTGGCTCTTAAGATA 1639
QY 1561 TCCATCTCTCTGCAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCCTATC 1620
DB 1640 TCCATCTCTCTGCAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCCTATC 1699
QY 1621 ATATATGTGGTCTCAGAAACCGGATATGCCGTTTATGTGGTTCTTACAACTAAGAG 1680
DB 1700 ATATATGTGGTCTCAGAAACCGGATATGCCGTTTATGTGGTTCTTACAACTAAGAG 1759
QY 1681 AAATCTCAAGAAACAACCCAGATGGAATTTTGAAGCAATGTGTTTGTGTGCTGC 1740
DB 1760 AAATCTCAAGAAACAACCCAGATGGAATTTTGAAGCAATGTGTTTGTGTGCTGC 1819
QY 1741 AGGCAATAGGATAGGATTAATCTATTCAAGAAAGACTCAGACATTTCTTAAAGATGG 1800
DB 1820 AGGCAATAGGATAGGATTAATCTATTCAAGAAAGACTCAGACATTTCTTAAAGATGG 1879
QY 1801 ATCTTAATCATCTTAAAGGTTTCTTCTCAAGAGATGCTCTGTGTGGAGAGGAGAGCC 1860
DB 1880 ATCTTAATCATCTTAAAGGTTTCTTCTCAAGAGATGCTCTGTGTGGAGAGGAGAGCC 1939
QY 1861 CAGCAAAAGTATGTACAGAAACAATCAGCTTCATGCGCAGCAGGTGGCGAATCTCTC 1920

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Db 1940 CCGAGCAAGATGATGACAAAGCAACATCAGCTTCATGCGCAGATGGGAGAAATCTTC 1999
Qy 1921 CTCACAGAGAACGGCCATATTTATGTGTGAGATGCAAGAAATATGCGCAAGATGTA 1980
Db 2000 CTCACAGAGAACGGCCATATTTATGTGTGAGATGCAAGAAATATGCGCAAGATGTA 2059
Qy 1981 CATGATCCCTTGTGCAATTAATTAAGCAAGAGGTTGAGTTGAAAACTAGAAGCATG 2040
Db 2060 CATGATCCCTTGTGCAATTAATTAAGCAAGAGGTTGAGTTGAAAACTAGAAGCATG 2119
Qy 2041 AAAACCTGGCCACTTAAAAAGAAAGCAAGCTTACCTTACGATATTTGTCATTA 2097
Db 2120 AAAACCTGGCCACTTAAAAAGAAAGCAAGCTTACCTTACGATATTTGTCATTA 2176
RESULT 3
US-09-371-347-41
; Sequence 41, Application US/09371347
; Publication No. US2003082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371.347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071.622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232.028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-371-347-41
Query March 97.6%; Score 2046; DB 10; Length 2097;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGAGAGGTTCTGTACTATATATGCTACACAGCAGGAGCAAGCAAGGCCATGCGAGAA 60
Db 1 ATGAGAGGTTCTGTACTATATATGCTACACAGCAGGAGCAAGCAAGGCCATGCGAGAA 60
Qy 61 GAAATGTGTAGCAAGCTGTGTGATCATGAGATTTCTGCAATCTTCACTGTATTAAGTAA 120
Db 61 GAAATGTGTAGCAAGCTGTGTGATCATGAGATTTCTGCAATCTTCACTGTATTAAGTAA 120
Qy 121 TCCGATTAAGTATGACTTAAAAACCGAAACAGCTCTCTGTGTGTGTGGTTTCTACCAAG 180
Db 121 TCCGATTAAGTATGACTTAAAAACCGAAACAGCTCTCTGTGTGTGTGGTTTCTACCAAG 180
Qy 181 GGCACCGGAGACCCACCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
Db 181 GGCACCGGAGACCCACCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
Qy 241 CTGCGCGGTGATTTCTTTGCTCACCTGCGGTATAGGTTTCTGGGTCTCGGTGATTCAAA 300
Db 241 CTGCGCGGTGATTTCTTTGCTCACCTGCGGTATAGGTTTCTGGGTCTCGGTGATTCAAA 300
Qy 301 TACACCTACTTTTGCATAGGGGGAGATTAATGTATAAGCACTTCAAGAGCTTGAAGCC 360
Db 301 TACACCTACTTTTGCATAGGGGGAGATTAATGTATAAGCACTTCAAGAGCTTGAAGCC 360
Qy 361 CCGGATTTCTATGACACTGACATGACATGACATGCTGTAGGTTTGAAGCTTGTGGTTGAG 420
Db 361 CCGGATTTCTATGACACTGACATGACATGACATGCTGTAGGTTTGAAGCTTGTGGTTGAG 420
Qy 421 CCGTGATTTGCTGAGACTCTGCGCAGCCCTCAGAAAGCATTTTGTAGGTCAAGCAGAGCAA 480

Db 421 CCGTGATTTGCTGAGACTCTGCGCAGCCCTCAGAAAGCATTTTGTAGGTCAAGCAGAGCAA 480
Qy 481 GAGAGATTAAGTGGCGCACTCCCGGTGGATCATCTGCATCTTGTAGGACAGACTTGTG 540
Db 481 GAGAGATTAAGTGGCGCACTCCCGGTGGATCATCTGCATCTTGTAGGACAGACTTGTG 540
Qy 541 AAGTCAGAGCTGTCACATTTGATATCTCAAGTCGAGCTTCTGAGATTCGATGATTCAAGA 600
Db 541 AAGTCAGAGCTGTCACATTTGATATCTCAAGTCGAGCTTCTGAGATTCGATGATTCAAGA 600
Qy 601 AGAAGAGATTCGAGGTTTGAAGCAAAATGCAAGTGAAGCAAGCAACCAATCCATGTTGTA 660
Db 601 AGAAGAGATTCGAGGTTTGAAGCAAAATGCAAGTGAAGCAAGCAACCAATCCATGTTGTA 660
Qy 661 ATTGAAGACTTGAAGTCTCATCTTACCCGTTGGATACCCCACTCTCAAGAGCTCTCTG 720
Db 661 ATTGAAGACTTGAAGTCTCATCTTACCCGTTGGATACCCCACTCTCAAGAGCTCTCTG 720
Qy 721 AATATTCCTGTTTACCCCGAGATATTTTACAGTATCATCTGACAGAGTCTCTGGCCAG 780
Db 721 AATATTCCTGTTTACCCCGAGATATTTTACAGTATCATCTGACAGAGTCTCTGGCCAG 780
Qy 781 GAGGAAGCCAGATATCTGTGACTTACAGAGATCCAGTTTCAAGTGCATTTGAAG 840
Db 781 GAGGAAGCCAGATATCTGTGACTTACAGAGATCCAGTTTCAAGTGCATTTGAAG 840
Qy 841 GCAGTTCACCTTACTACGATGATGCAATTAACCACTCTGCTGTAGATTTGACATT 900
Db 841 GCAGTTCACCTTACTACGATGATGCAATTAACCACTCTGCTGTAGATTTGACATT 900
Qy 901 TCAATATCAGACTTTTCTATACAGCTTGAAGATGCTTCAAGCGTATCTGCCATACGT 960
Db 901 TCAATATCAGACTTTTCTATACAGCTTGAAGATGCTTCAAGCGTATCTGCCATACGT 960
Qy 961 GATTCGAGGTCAAAAGCCCTACCCAAAGCTGACCTTGAAGATTAAGAGAGCACTGC 1020
Db 961 GATTCGAGGTCAAAAGCCCTACCCAAAGCTGACCTTGAAGATTAAGAGAGCACTGC 1020
Qy 1021 GTCCCTTTGAAATTAAGGACAGACAAAGAAAGAGAGCTTACCTTACCCGACATATA 1080
Db 1021 GTCCCTTTGAAATTAAGGACAGACAAAGAAAGAGAGCTTACCTTACCCGACATATA 1080
Qy 1081 CCGCGGAGATGTTCTCTCAAGTTCATTTTCTGCTGTCTGTAATTCGAGCAATTCCT 1140
Db 1081 CCGCGGAGATGTTCTCTCAAGTTCATTTTCTGCTGTCTGTAATTCGAGCAATTCCT 1140
Qy 1141 AAAAAGGCAATTTTGGAGGCCCTGTGGAATATACAGAGACAGTCTGAAAAAGCGCAG 1200
Db 1141 AAAAAGGCAATTTTGGAGGCCCTGTGGAATATATACAGAGACAGTCTGAAAAAGCGCAG 1200
Qy 1201 CTACAGAGCTGTGACAGTAAACAAGGGGAGCCGATTAAGCCCTTGTATCAGATGCGC 1260
Db 1201 CTACAGAGCTGTGACAGTAAACAAGGGGAGCCGATTAAGCCGCTTGTATCAGATGCGC 1260
Qy 1261 TGTGCTGCTGTGTGATCTCTCTGCTTCTCTTCTTTCAGGACCACTCAAGTCTC 1320
Db 1261 TGTGCTGCTGTGTGATCTCTCTGCTTCTCTTCTTTCAGGACCACTCAAGTCTC 1320
Qy 1321 CTGCTGGAACATTTCTTAACTTCAACCCAGACCAATTCGTGTGACAGCTCAAGTTTA 1380
Db 1321 CTGCTGGAACATTTCTTAACTTCAACCCAGACCAATTCGTGTGACAGCTCAAGTTTA 1380
Qy 1381 TTTCAACCCAGGAAGCTCATTTTGTCTTCAACATTTGTGAATTTGTCTACTGCGACA 1440
Db 1381 TTTCAACCCAGGAAGCTCATTTTGTCTTCAACATTTGTGAATTTGTCTACTGCGACA 1440
Qy 1441 ACAGAGGTTCTGCGAAGGAGATATGATACAGGCTGCGCTGCTGTTGTTGCTTCAGTT 1500
Db 1441 ACAGAGGTTCTGCGAAGGAGATATGATATACAGGCTGCGCTGCTGTTGTTGCTTCAGTT 1500
Qy 1501 CTTCAAGCCAAACATATATGATATCCCATGAAAGACAGGGGAAACCTGCTGCTTAAGATA 1560

Db 1501 CTTGAGCCAAACATACATCATCCATGAAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
Qy 1561 TCCATCTCCCTCGAACAAATTTCTTCCATTAACAGATGACCCCTCAATCCCACATC 1620
Db 1561 TCCATCTCCCTCGAACAAATTTCTTCCATTAACAGATGACCCCTCAATCCCACATC 1620
Qy 1621 ATAAATGTTGGTTCAGGAACCGGATAGCCCGCTTAATGGGTTCTTAACAATAGAG 1680
Db 1621 ATAAATGTTGGTTCAGGAACCGGATAGCCCGCTTAATGGGTTCTTAACAATAGAG 1680
Qy 1681 AAATCTCAAGAACACACCCAGATGGAATTTTGAAGCAATGTGTTTTTGGCTGC 1740
Db 1681 AAATCTCAAGAACACACCCAGATGGAATTTTGAAGCAATGTGTTTTTGGCTGC 1740
Qy 1741 AAGCATTAAGATAGGATTAATCTAATCAAAAAAGACTGACATTTCTTAAAGATGG 1800
Db 1741 AAGCATTAAGATAGGATTAATCTAATCAAAAAAGACTGACATTTCTTAAAGATGG 1800
Qy 1801 ATCTTAATCATCTTAAGAGTTTCTTCTGAGAGATGCTCTGTGGGAGAGAGAGCC 1860
Db 1801 ATCTTAATCATCTTAAGAGTTTCTTCTGAGAGATGCTCTGTGGGAGAGAGAGCC 1860
Qy 1861 CCAGCAAAAGTATGTACAGACAAATCATGAGCTTCATGCGCAGAGGTGGCAGAAATCTC 1920
Db 1861 CCAGCAAAAGTATGTACAGACAAATCATGAGCTTCATGCGCAGAGGTGGCAGAAATCTC 1920
Qy 1921 CTCACAGAAACGGCCATTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
Db 1921 CTCACAGAAACGGCCATTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
Qy 1981 CATGATGCTTGTGTGCAATTAATTAAGCAAGAGTTGAGTTGAAAACTAGAGCAATG 2040
Db 1981 CATGATGCTTGTGTGCAATTAATTAAGCAAGAGTTGAGTTGAAAACTAGAGCAATG 2040
Qy 2041 AAAACCTGCGCCACTTTAAAGAAAGAAAAAGCTTACCTTCAAGATATTTGTCTATA 2097
Db 2041 AAAACCTGCGCCACTTTAAAGAAAGAAAAAGCTTACCTTCAAGATATTTGTCTATA 2097

RESULT 4
; Sequence 43, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-43

Query Match 97.6%; Score 2046; DB 10; Length 2097;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATAGAGAGGTTTCTGTAATATATGCTACACAGAGGACAGCAAGGCATGCGAGAA 60
Db 1 ATAGAGAGGTTTCTGTAATATATGCTACACAGAGGACAGCAAGGCATGCGAGAA 60
Qy 61 GAATGTGTGAGCAAGCTGTGTATGATGATTTTCTGAGATCTTCACTGATTAAGTAA 120
Db 61 GAATGTGTGAGCAAGCTGTGTATGATGATTTTCTGAGATCTTCACTGATTAAGTAA 120

Db 61 GAATGTGTGAGCAAGCTGTGTATGATGATTTTCTGAGATCTTCACTGATTAAGTAA 120
Qy 121 TCCGATTAAGTATGACCTAAAAACGAAACAGCTCTGTTGTGTGTGTGTGTGTGTGTGT 180
Db 121 TCCGATTAAGTATGACCTAAAAACGAAACAGCTCTGTTGTGTGTGTGTGTGTGTGTGT 180
Qy 181 GGCACCGGAGACCCACCGGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
Db 181 GGCACCGGAGACCCACCGGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
Qy 241 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGGGTTATCTGGGTCTCGGTATTCAGA 300
Db 241 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGGGTTATCTGGGTCTCGGTATTCAGA 300
Qy 301 TACACCTACTTTTGAATGGGGGGAAGATTAATGAATTAACGACTTCAAGAGCTGGAGCC 360
Db 301 TACACCTACTTTTGAATGGGGGGAAGATTAATGAATTAACGACTTCAAGAGCTGGAGCC 360
Qy 361 CGGCAATTTCTATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 420
Db 361 CGGCAATTTCTATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 420
Qy 421 CCGTGATTTGCTGACTGTGCGCAGCCCTCAGAAAGCATTTTAAGTCAAGAGAGACA 480
Db 421 CCGTGATTTGCTGACTGTGCGCAGCCCTCAGAAAGCATTTTAAGTCAAGAGAGACA 480
Qy 481 GAGGATTAAGTGGGCACTCCCGGTGGATACCTGATCCTTGAAGACACACCTGTG 540
Db 481 GAGGATTAAGTGGGCACTCCCGGTGGATACCTGATCCTTGAAGACACACCTGTG 540
Qy 541 AAGTCAGAGCTCTACATTAATCTCAATGAGCTTCTGAGATTCAGATTCAGAGA 600
Db 541 AAGTCAGAGCTCTACATTAATCTCAATGAGCTTCTGAGATTCAGATTCAGAGA 600
Qy 601 AAAAAAGATTCGAGGTTTGAAGCAAAATGACGTAACAGCAACCAATTCATGTTGA 660
Db 601 AAAAAAGATTCGAGGTTTGAAGCAAAATGACGTAACAGCAACCAATTCATGTTGA 660
Qy 661 ATTGAAGACTTGAAGTCTTCACTTACCCGTTGGATACCCCACTCTCAAGCCTCTCG 720
Db 661 ATTGAAGACTTGAAGTCTTCACTTACCCGTTGGATACCCCACTCTCAAGCCTCTCG 720
Qy 721 AATATTCCTGTTTACCCCAATTTTACAGATTCAGAGATTCAGAGATTCAGAGATTC 780
Db 721 AATATTCCTGTTTACCCCAATTTTACAGATTCAGAGATTCAGAGATTCAGAGATTC 780
Qy 781 GAGGAAAGCAAGTATCTGTGACTTCAGAGATTCAGAGATTCAGAGATTCAGAGATTC 840
Db 781 GAGGAAAGCAAGTATCTGTGACTTCAGAGATTCAGAGATTCAGAGATTCAGAGATTC 840
Qy 841 GCAATTCATTAATGCAATGATGCAATTAACCACTCTGTGTATTAATTTGACATTT 900
Db 841 GCAATTCATTAATGCAATGATGCAATTAACCACTCTGTGTATTAATTTGACATTT 900
Qy 901 TCAAAATACAGACTTTTCTATCAGCTGTGAGATGCTTCAAGGATTCAGGATTCAG 960
Db 901 TCAAAATACAGACTTTTCTATCAGCTGTGAGATGCTTCAAGGATTCAGGATTCAG 960
Qy 961 GATTTGAGGTAACAAAGCTTCTCAAGACTGCAAGCTTGAAGATTAAGAGAGACCTGC 1020
Db 961 GATTTGAGGTAACAAAGCTTCTCAAGACTGCAAGCTTGAAGATTAAGAGAGACCTGC 1020
Qy 1021 GTTCCTTTTAAATTAAGGACACACAAAGAAAGAGAGTACCTTACCCAGCATTA 1080
Db 1021 GTTCCTTTTAAATTAAGGACACACAAAGAAAGAGAGTACCTTACCCAGCATTA 1080
Qy 1081 CCGCGGAGATTTCTCTCAAGTTCAATTTTACCTGTGCTTGAATCCGAGCAATTCCT 1140
Db 1081 CCGCGGAGATTTCTCTCAAGTTCAATTTTACCTGTGCTTGAATCCGAGCAATTCCT 1140
Qy 1141 AAAAAGCAATTTTGGAGCCCTTGTGACATATACAGTACAGTGTGAAAAAGCGCAGG 1200
Db 1141 AAAAAGCAATTTTGGAGCCCTTGTGACATATACAGTGTGAAAAAGCGCAGG 1200

QY 1201 CTACAGAGCTGTGCTAGTAAACAAGGGGAGCCGATTAATAGCCGCTTGTAGCAGATGCC 1260
DB 1201 CTACAGAGAGCTGTGCTAGTAAACAAGGGGAGCCGATTAATAGCCGCTTGTAGCAGATGCC 1260
QY 1261 TGTGCTGTGCTTGTGATCT 1320
DB 1261 TGTGCTGTGCTTGTGATCT 1320
QY 1321 CTGCTGACATCTTCTTAACTTCAACCCAGACCATATTCGTGTGACAGCTCAAGTTTA 1380
DB 1321 CTGCTGACATCTTCTTAACTTCAACCCAGACCATATTCGTGTGACAGCTCAAGTTTA 1380
QY 1381 TTTCACCCAGAGAAAGCTCCATTTTGTCTTCAACATTTGTGATTTCTGTACTGCCACA 1440
DB 1381 TTTCACCCAGAGAAAGCTCCATTTTGTCTTCAACATTTGTGATTTCTGTACTGCCACA 1440
QY 1441 ACAGAGGTTCTGCGAGAGGAGTATGTACAGGCTGTGCTGTGTGTGTGTGTGTGTGTGT 1500
DB 1441 ACAGAGGTTCTGCGAGAGGAGTATGTACAGGCTGTGCTGTGTGTGTGTGTGTGTGTGT 1500
QY 1501 CTTCAGCCAAACATACATGATCCCATGAGAGACGCGGAAAGCCCTGCTCCCTAAGATA 1560
DB 1501 CTTCAGCCAAACATACATGATCCCATGAGAGACGCGGAAAGCCCTGCTCCCTAAGATA 1560
QY 1561 TCCATCTCTCTCGAACACAAATCTTTCATCTTACAGATGACCCCTCAATCCCATC 1620
DB 1561 TCCATCTCTCTCGAACACAAATCTTTCATCTTACAGATGACCCCTCAATCCCATC 1620
QY 1621 ATATATGTTGGTCCAGAGACCGGATAGCCCGTTTATTTGGGTTCTTACAACTAAGAG 1680
DB 1621 ATATATGTTGGTCCAGAGACCGGATAGCCCGTTTATTTGGGTTCTTACAACTAAGAG 1680
QY 1681 AAATCTCAAGAAACAACCCAGATGAGAAATTTTGAAGCAATGTGTGTGTGTGTGTGTGTGT 1740
DB 1681 AAATCTCAAGAAACAACCCAGATGAGAAATTTTGAAGCAATGTGTGTGTGTGTGTGTGTGT 1740
QY 1741 AGGATTAAGATAGGATTAATCTATTCAGAAAGAGCTCAGACATTTCTTTAAGCATGG 1800
DB 1741 AGGATTAAGATAGGATTAATCTATTCAGAAAGAGCTCAGACATTTCTTTAAGCATGG 1800
QY 1801 ATCTTAATCTATCTTAAGGTTTCTTCTCAGAGATCTCTCTGTGGGAGAGAGAGAGCC 1860
DB 1801 ATCTTAATCTATCTTAAGGTTTCTTCTCAGAGATCTCTCTGTGGGAGAGAGAGAGAGCC 1860
QY 1861 CCAGCAAGATATGACAAAGACATCATCGCTTATGAGCAGAGAGAGAGAGAGATCTCTC 1920
DB 1861 CCAGCAAGATATGACAAAGACATCATCGCTTATGAGCAGAGAGAGAGAGAGATCTCTC 1920
QY 1921 CTCCAGAGAAAGGCAATATTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
DB 1921 CTCCAGAGAAAGGCAATATTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1980
QY 1981 CATATATCTCTTGT 2040
DB 1981 CATATATCTCTTGT 2040
QY 2041 AAAACCTGGGCACTTTTAAAGAGAGAAAGCTTACCTTCAGATTTTGTGTGTGTGTGT 2097
DB 2041 AAAACCTGGGCACTTTTAAAGAGAGAAAGCTTACCTTCAGATTTTGTGTGTGTGTGT 2097

RESULT 5

US-09-371-347-45
; Sequence 45, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347

; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 45
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-45

Query Match 88.4%; Score 1854; DB 10; Length 2094;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2094; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 ATGAGAGGTTTCTGTACTTATATGCTTACACAGAGGAGCAGGCAAGCCATCGAGAA 60
DB 1 ATGAGAGGTTTCTGTACTTATATGCTTACACAGAGGAGCAGGCAAGCCATCGAGAA 60
QY 61 GAAATGTGAGCAAGCTGTGTACATGATTTTCTGAGATCTTCACTGATTAAGTGA 120
DB 61 GAAATGTGAGCAAGCTGTGTACATGATTTTCTGAGATCTTCACTGATTAAGTGA 120
QY 121 TCCGATTAATGATGACCTTAAACCCGAAACAGCTCTTGTGTGTGTGTGTGTGTGTGTGT 180
DB 121 TCCGATTAATGATGACCTTAAACCCGAAACAGCTCTTGTGTGTGTGTGTGTGTGTGTGT 180
QY 181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
DB 181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
QY 241 CTGCGGATGATTTCTTGTCTCACTGCGGATAGGTTACTGGGCTCTGGTATTCAGAA 300
DB 241 CTGCGGATGATTTCTTGTCTCACTGCGGATAGGTTACTGGGCTCTGGTATTCAGAA 300
QY 301 TACACCTACTTTTGAATGGGGGAAATTAATGATTAACGACTTCAAGAGCTTGAAGCC 360
DB 301 TACACCTACTTTTGAATGGGGGAAATTAATGATTAACGACTTCAAGAGCTTGAAGCC 360
QY 361 CGGATTTCTATGACACTGACATGAGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 361 CGGATTTCTATGACACTGACATGAGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 421 CGGTGATTTGCTGACTGTGCGCAGCCCTCAGAAACATTTTGAAGTCAAGCAGAGCAA 480
DB 421 CGGTGATTTGCTGACTGTGCGCAGCCCTCAGAAACATTTTGAAGTCAAGCAGAGCAA 480
QY 481 GAGAGATTAAGTGGGCACTCCGGTGGCATCCTGATCTTGTGAGACAGACCTTGTG 540
DB 481 GAGAGATTAAGTGGGCACTCCGGTGGCATCCTGATCTTGTGAGACAGACCTTGTG 540
QY 541 AATCTGAGCTGTACACATTAATCTCAAGTGTGAGCTTGTGAGTGTGTGTGTGTGTGTGTGT 600
DB 541 AATCTGAGCTGTGTACACATTAATCTCAAGTGTGAGCTTGTGAGTGTGTGTGTGTGTGTGT 600
QY 601 AGAAGGATTTCTAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCAATGTTGTA 660
DB 601 AGAAGGATTTCTAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCAATGTTGTA 660
QY 661 ATTGAAGCTTTGAGTCTTCACTTACCCGTTGGTATCCCCACTCTTCAAGGCTTCTG 720
DB 661 ATTGAAGCTTTGAGTCTTCACTTACCCGTTGGTATCCCCACTCTTCAAGGCTTCTG 720
QY 721 AATATTCCTGTTTACCCCGCAATTTTACAGATATCTGTGAGAGAGTCTTGTGGCAG 780
DB 721 AATATTCCTGTTTACCCCGCAATTTTACAGATATCTGTGAGAGAGTCTTGTGGCAG 780
QY 781 GAGGAAAGCAATATCTGTGACTTCAAGCAGATCCAGTTTCAAGTGTGTGTGTGTGTGTGTGT 840
DB 781 GAGGAAAGCAATATCTGTGACTTCAAGCAGATCCAGTTTCAAGTGTGTGTGTGTGTGTGTGT 840

QY 841 GGAGTTCACCTTAACGATGATGCGCATTAACCACTCTGTGTAGATTTGACATT 900
DB 841 GGAGTTCACCTTAACGATGATGCGCATTAACCACTCTGTGTAGATTTGACATT 900
QY 901 TCAATATACGACTTTTCTATCAGCTGAGATGCTTCAAGGTGATCTGCTTAACAGT 960
DB 901 TCAATATACGACTTTTCTATCAGCTGAGATGCTTCAAGGTGATCTGCTTAACAGT 960
QY 961 GATTCGAGGTACAAAGCTTACCAAGATGCGAGCTTGAAGATTAAGAGAGACATGC 1020
DB 961 GATTCGAGGTACAAAGCTTACCAAGATGCGAGCTTGAAGATTAAGAGAGACATGC 1020
QY 1021 GTCTCTTTGAAATTAAGGACAGACAAAGAAAGAGACTTACCTTACCCAGCATATA 1080
DB 1021 GTCTCTTTGAAATTAAGGACAGACAAAGAAAGAGACTTACCTTACCCAGCATATA 1080
QY 1081 CCTGCGGAGATGTTCTCTCAAGTTCATTTTACCTGCTGCTTGAATTCGAGCAATTCCT 1140
DB 1081 CCTGCGGAGATGTTCTCTCAAGTTCATTTTACCTGCTGCTTGAATTCGAGCAATTCCT 1140
QY 1141 AAAAGGCAATTTTGGAGAGCCCTTGGAGCTATACAGAGACAGTGTGAAAAGGCAAG 1200
DB 1141 AAAAGGCAATTTTGGAGAGCCCTTGGAGCTATACAGAGACAGTGTGAAAAGGCAAG 1200
QY 1201 CTACAGAGCTGTCAGTAAACAAAGGGGAGCCGATTTATAGCCGTTTGTACAGATGTC 1260
DB 1201 CTACAGAGCTGTCAGTAAACAAAGGGGAGCCGATTTATAGCCGTTTGTACAGATGTC 1260
QY 1261 TGTGCTGCTTGTGATCTCTCTCGCTTCTCTGCTTCTGTCAGGCAACACTCACTCTC 1320
DB 1261 TGTGCTGCTTGTGATCTCTCTCGCTTCTCTGCTTCTGTCAGGCAACACTCACTCTC 1320
QY 1321 CTGCTGGAACATTTCTTAACCTTCAACCCAGACATATTCGTCAGGCTCAAGCTTAA 1380
DB 1321 CTGCTGGAACATTTCTTAACCTTCAACCCAGACATATTCGTCAGGCTCAAGCTTAA 1380
QY 1381 TTTCACCCGAGAAAGCTTCTTCAACATTTGTGGAATTTCTGCTACCTGACACA 1440
DB 1381 TTTCACCCGAGAAAGCTTCTTCAACATTTGTGGAATTTCTGCTACCTGACACA 1440
QY 1441 ACAGAGGTTCTGCGAAGGAGATGATGATACAGCTGCTGCTTGTGCTTCACTTCACT 1500
DB 1441 ACAGAGGTTCTGCGAAGGAGATGATGATACAGCTGCTGCTTGTGCTTCACTTCACT 1500
QY 1501 CTTCAGCCAAACATATGATGATCCCATGAAGACAGCGGGAAGCCCTGCTCTTAAGATA 1560
DB 1501 CTTCAGCCAAACATATGATGATCCCATGAAGACAGCGGGAAGCCCTGCTCTTAAGATA 1560
QY 1561 TCCATCTCTCTGGAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
DB 1561 TCCATCTCTCTGGAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
QY 1621 ATTAATGTGGGTCCAGAAACCGGATAGCCCGTTTATTTGGGTTCTTCAACATAGAGAG 1680
DB 1621 ATTAATGTGGGTCCAGAAACCGGATAGCCCGTTTATTTGGGTTCTTCAACATAGAGAG 1680
QY 1681 AAACTCCAAAGAACCAACCCAGATGGAATTTTGAAGCAATGTG--GTTTTTGGCTGC 1740
DB 1681 AAACTCCAAAGAACCAACCCAGATGGAATTTTGAAGCAATGTG--GTTTTTGGCTGC 1740
QY 1741 AGGCAATTAAGATAGGATTTATCTATCAAGAAAGAGCTGAGATTTCTTAAAGCATGGG 1800
DB 1741 AGGCAATTAAGATAGGATTTATCTATCAAGAAAGAGCTGAGATTTCTTAAAGCATGGG 1800
QY 1801 ATCTTAATCATCTTAAGGTTTCTTCAAGAGATGCTCTGTGAGGAGAGAGAGCC 1860
DB 1801 ATCTTAATCATCTTAAGGTTTCTTCAAGAGATGCTCTGTGAGGAGAGAGAGCC 1860
QY 1861 CCAGCAAAAGTATGACAAAGCAATTCAGACTTATGCGCAGAGAGGTGGGCAAGATCTTC 1920
DB 1861 CCAGCAAAAGTATGACAAAGCAATTCAGACTTATGCGCAGAGAGGTGGGCAAGATCTTC 1920
QY 1921 CTCGAGAGAGACGGCATATTTATGTGTGTGAGATGCAAGATATGCGCAAGATGTA 1980

DB 1918 CTCGAGAGAGACGGCATATTTATGTGTGAGATGCAAGAAATATGCGCAAGATGTA 1977
QY 1981 CATGATGCCCTTGTGCAATATATTAAGCAAGAGGTTGGAGTTGAAAACCTAGAACATG 2040
DB 1978 CATGATGCCCTTGTGCAATATATTAAGCAAGAGGTTGGAGTTGAAAACCTAGAACATG 2037
QY 2041 AAAACCTGCGCACTTTAAAGAAAGAAACCGCTACCTTCAGAGATTTGGTCAATA 2097
DB 2038 AAAACCTGCGCACTTTAAAGAAAGAAACCGCTACCTTCAGAGATTTGGTCAATA 2094

RESULT 6
US-09-371-347-47
; Sequence 47, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE;
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 2093
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-47

Query Match 85.5%; Score 1793; DB 10; Length 2093;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 ATGAGAGAGTTCTGTACTATATGCTACACAGACAGGACAGCAAAAGCCATCGCAGAA 60
DB 1 ATGAGAGAGTTCTGTACTATATGCTACACAGACAGGACAGCAAAAGCCATCGCAGAA 60
QY 61 GAAATGTGTGACAAAGCTGTGTACATGATTTTCTGCAAGATCTTCACTGTATATGTA 120
DB 61 GAAATGTGTGACAAAGCTGTGTACATGATTTTCTGCAAGATCTTCACTGTATATGTA 120
QY 121 TCCGATTAAGTATGACCTTAAACCGAAACAGCTCCCTGTTGTGTGTGTTCTACACG 180
DB 121 TCCGATTAAGTATGACCTTAAACCGAAACAGCTCCCTGTTGTGTGTGTTCTACACG 180
QY 181 GGCACCGGAGACCCACCCGACAGAGCCCGCAAGTTGTTAAAGAAATACAGAACCAACA 240
DB 181 GGCACCGGAGACCCACCCGACAGAGCCCGCAAGTTGTTAAAGAAATACAGAACCAACA 240
QY 241 CTGCGGTGATTTCTTCTCACTGCTGCGGTATGAGTTACTGAGTCTCGGTATTCAGAA 300
DB 241 CTGCGGTGATTTCTTCTCACTGCTGCGGTATGAGTTACTGAGTCTCGGTATTCAGAA 300
QY 301 TACACCTACTTTTGGCAATGGGGGAAATTAAGTAAACGACTTCAAGAGCTGGAGCC 360
DB 301 TACACCTACTTTTGGCAATGGGGGAAATTAAGTAAACGACTTCAAGAGCTGGAGCC 360
QY 361 CGGATTTCTATGACACTGACATGAGATGATGATGATGATGATGATGATGATGATGATG 420
DB 361 CGGATTTCTATGACACTGACATGAGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 CCGTGTATGCTGACTGTGCGCAAGCCCTCAAGAAAGCATTTTAAGTCAAGCAGAGACAA 480
DB 421 CCGTGTATGCTGACTGTGCGCAAGCCCTCAAGAAAGCATTTTAAGTCAAGCAGAGACAA 480
QY 481 GAGAGATTAAGTGGGCACTCCCGGTGATCACTGCATCTTGAAGACAGACCTTGG 540

481 GAGGAGTAAGTGGCGATCCGGTGGCAATCCTGATCTTGAAGACAGACCTTGTG 540
481 GAGGAGTAAGTGGCGATCCGGTGGCAATCCTGATCTTGAAGACAGACCTTGTG 540
541 AAGTCAGAGCTGTACATATTTGAATCTCAAGTCAGAGCTGTGATTCGATTCAGGA 600
541 AAGTCAGAGCTGTACATATTTGAATCTCAAGTCAGAGCTGTGATTCGATTCAGGA 600
601 AGAAGAGATTCGTGAGTGTGGAAGCAAAATGACAGTGAACCAACCAATGTTTGA 660
601 AGAAGAGATTCGTGAGTGTGGAAGCAAAATGACAGTGAACCAACCAATGTTTGA 660
661 ATGGAAGCTTTGAGTGTGCTCACTTACCGCTTGGTACCCCACTGTCAGAGCTCTG 720
661 ATGGAAGCTTTGAGTGTGCTCACTTACCGCTTGGTACCCCACTGTCAGAGCTCTG 720
721 AATATTCCTGGTTTACCCCGAATATTTACAGGTATGATGAGAGTCTGTTGGCCAG 780
721 AATATTCCTGGTTTACCCCGAATATTTACAGGTATGATGAGAGTCTGTTGGCCAG 780
781 GAGGAAGCCCAAGTATCTGTGATCTTCAAGATCAGATCTGATTTTCAAGTTCAGAA 840
781 GAGGAAGCCCAAGTATCTGTGATCTTCAAGATCAGATCTGATTTTCAAGTTCAGAA 840
841 GAGTTCAACTTACTAGCAATGATGCAATAAACCACTGCTGGTGAATTTGGAAT 900
841 GAGTTCAACTTACTAGCAATGATGCAATAAACCACTGCTGGTGAATTTGGAAT 900
901 TCAAAATCAGACTTTTCTTCACTAGAGCTGAGATCTTCAAGCTGATCTGCTTCAAGT 960
901 TCAAAATCAGACTTTTCTTCACTAGAGCTGAGATCTTCAAGCTGATCTGCTTCAAGT 960
961 GATTCTGAGGTACAAAGCCTTACTCAAAAGCTGCAAGCTTGAAGTAAAGAGACCTGC 1020
961 GATTCTGAGGTACAAAGCCTTACTCAAAAGCTGCAAGCTTGAAGTAAAGAGACCTGC 1020
1021 GTGCTTTGAAATTAAGGAGACACAAAGAAAGAGACTTACCTTACCCGACATATA 1080
1021 GTGCTTTGAAATTAAGGAGACACAAAGAAAGAGACTTACCTTACCCGACATATA 1080
1081 CTTGCGGAGATGTTCTCTCAAGTCAATTTTACCTGCTGTTGAAATCCGAGCAATTC 1140
1081 CTTGCGGAGATGTTCTCTCAAGTCAATTTTACCTGCTGTTGAAATCCGAGCAATTC 1140
1141 AAAAGGCAATTTTGGGAGCCCTTGTGATATCAAGTCAAGTCTGAAAAGCCGAGG 1200
1141 AAAAGGCAATTTTGGGAGCCCTTGTGATATCAAGTCAAGTCTGAAAAGCCGAGG 1200
1201 CTAAGGAGCTGTGCAATTAACAAAGGAGCCGATATAGCCGCTTTTGAACAGATGCC 1260
1201 CTAAGGAGCTGTGCAATTAACAAAGGAGCCGATATAGCCGCTTTTGAACAGATGCC 1260
1261 TGTGCTGCTGTGATGATCTCTCTGCTGCTTCCCTTCTTGCCAGCCACCACTCACTC 1320
1261 TGTGCTGCTGTGATGATCTCTCTGCTGCTTCCCTTCTTGCCAGCCACCACTCACTC 1320
1321 CTGCTGGAACATCTTCTTAACTTCAACCCAGACCAATATGCTGTGCAAGCTCAAGTTA 1380
1321 CTGCTGGAACATCTTCTTAACTTCAACCCAGACCAATATGCTGTGCAAGCTCAAGTTA 1380
1381 TTTCAACCAGGAAGCTCAATTTGTCTTCAACTTGTGAATTTCTGTCTACGCGACA 1440
1381 TTTCAACCAGGAAGCTCAATTTGTCTTCAACTTGTGAATTTCTGTCTACGCGACA 1440
1441 ACAGAGTCTGTGGAAGGAGATATGACAGCTGCTGCTGCTGTTGTTGCTTCACTT 1500
1441 ACAGAGTCTGTGGAAGGAGATATGACAGCTGCTGCTGCTGTTGTTGCTTCACTT 1500
1501 CTTGAGCCAAACATATCATGATCCCATGAGAAGACGCGGAAAGCCCTGAGCTCTTAAGATA 1560
1501 CTTGAGCCAAACATATCATGATCCCATGAGAAGACGCGGAAAGCCCTGAGCTCTTAAGATA 1560
1561 TCCATCTCTCTCGAACAACAATTTCTTCACTTACCAATGACCCCTCAATCCCATC 1620
1561 TCCATCTCTCTCGAACAACAATTTCTTCACTTACCAATGACCCCTCAATCCCATC 1620

1561 TCCATCTCTCTCGAACAACAATTTCTTCACTTACCAATGACCCCTCAATCCCATC 1620
1621 ATATGAGTGGGTCCAGGAACCGGCATAGCCCTTTATTTGGTTCCTACAAATAGAG 1680
1621 ATATGAGTGGGTCCAGGAACCGGCATAGCCCTTTATTTGGTTCCTACAAATAGAG 1680
1681 AAATCCGAAGACAAACCCAGATGGAATTTTGAAGCAATGTGTTTGTGCTGC 1740
1681 AAATCCGAAGACAAACCCAGATGGAATTTTGAAGCAATGTGTTTGTGCTGC 1740
1741 AGGCATTAAGGATGGGATTAATCTATTCAAGAAAGACTCAGACATTTCTTAAGCATGG 1800
1741 AGGCATTAAGGATGGGATTAATCTATTCAAGAAAGACTCAGACATTTCTTAAGCATGG 1800
1797 ATCTTAAGGATTAAGGATTTATCTATTCAAGAAAGACTCAGACATTTCTTAAGCATGG 1796
1797 ATCTTAAGGATTAAGGATTTATCTATTCAAGAAAGACTCAGACATTTCTTAAGCATGG 1796
1801 ATCTTAAGGATTAAGGATTTATCTATTCAAGAAAGACTCAGACATTTCTTAAGCATGG 1860
1801 ATCTTAAGGATTAAGGATTTATCTATTCAAGAAAGACTCAGACATTTCTTAAGCATGG 1860
1861 CCAGCAAGATATGACAAACATTCAGCTTCAATGCGCAGAGCTGCGAGAAATCTTC 1920
1861 CCAGCAAGATATGACAAACATTCAGCTTCAATGCGCAGAGCTGCGAGAAATCTTC 1920
1857 CCAGCAAGATATGACAAACATTCAGCTTCAATGCGCAGAGCTGCGAGAAATCTTC 1916
1857 CCAGCAAGATATGACAAACATTCAGCTTCAATGCGCAGAGCTGCGAGAAATCTTC 1916
1921 CTCAGGAAGAGCCCATATTTATGTTGTGAGATGCAAAAGATATGCGCAAGATGTA 1980
1921 CTCAGGAAGAGCCCATATTTATGTTGTGAGATGCAAAAGATATGCGCAAGATGTA 1980
1917 CTCAGGAAGAGCCCATATTTATGTTGTGAGATGCAAAAGATATGCGCAAGATGTA 1976
1917 CTCAGGAAGAGCCCATATTTATGTTGTGAGATGCAAAAGATATGCGCAAGATGTA 1976
1981 CATGATGCCCTTGTGCAATTAATTAAGCAAGGTTGAGTTGAAATAGCAATG 2040
1981 CATGATGCCCTTGTGCAATTAATTAAGCAAGGTTGAGTTGAAATAGCAATG 2040
1977 CATGATGCCCTTGTGCAATTAATTAAGCAAGGTTGAGTTGAAATAGCAATG 2036
1977 CATGATGCCCTTGTGCAATTAATTAAGCAAGGTTGAGTTGAAATAGCAATG 2036
2041 AAAACCTGGCCACTTTAAAGAAAGAAACGCTACCTTCAAGATATTTGCTATTA 2097
2041 AAAACCTGGCCACTTTAAAGAAAGAAACGCTACCTTCAAGATATTTGCTATTA 2097
2037 AAAACCTGGCCACTTTAAAGAAAGAAACGCTACCTTCAAGATATTTGCTATTA 2093
2037 AAAACCTGGCCACTTTAAAGAAAGAAACGCTACCTTCAAGATATTTGCTATTA 2093

RESULT 7
US-10-741-600-692
; Sequence 692, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ. ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO: 692
; LENGTH: 3256
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-692

Query Match 50.6%; Score 1062; DB 21; Length 3256;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2012; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

67 TGTGAGCAAGCTGTGTAATGATTTTGTGAGATCTTCACTGATATTTAGTAATCCGAT 126
160 TGTGAGCAAGCTGTGTAATGATTTTGTGAGATCTTCACTGATATTTAGTAATCCGAT 219
127 AAGTATGACCTTAAACCGAAACAGCTCTCTGTTGTGTTGTTCTACAGGCGACC 186
220 AAGTATGACCTTAAACCGAAACAGCTCTCTGTTGTGTTGTTCTACAGGCGACC 279
187 GGAAGCCCAACCGGACAGAGCCGCAAGTTTGAAGAAATACAGAACCAACCTGCGG 246
280 GGAAGCCCAACCGGACAGAGCCGCAAGTTTGAAGAAATACAGAACCAACCTGCGG 339
247 GTTGAATTTCTTGTCTACCTGCGGTATGAGTTATCTGGTCTCGGTATTCAGAAATCACC 306
340 GTTGAATTTCTTGTCTACCTGCGGTATGAGTTATCTGGTCTCGGTATTCAGAAATCACC 399

307 TACTTTGCAATGGGGAGAGATTAATTGATTAACGACTTCAAGAGCTTGGAGCCCGGCAAT 366
400 TACTTTTGCATATGGGGAGAGATTAATTGATTAACGACTTCAAGAGCTTGGAGCCCGGCAAT 459
367 TTCTATGACACTGACATGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426
460 TTCTATGACACTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 519
427 ATTGCTGACACTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 486
520 ATTGCTGACACTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 579
487 ATTAAGTGGGCACTCCCGGGGCACTACCTGATGATGATGATGATGATGATGATGATGATGAT 546
580 ATTAAGTGGGCACTCCCGGGGCACTACCTGATGATGATGATGATGATGATGATGATGATGAT 639
547 GAGCTGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 606
640 GAGCTGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 699
607 GATTCGAGCTTTGAGCAAAATGCAATGACGACGACGACGACGACGACGACGACGACGACGAC 666
700 GATTCGAGCTTTGAGCAAAATGCAATGACGACGACGACGACGACGACGACGACGACGACGAC 759
667 GACTTGAATGCTCACTTACCGGTTGGATACCGGCTGCTCAAGAGCTTCTGATGATGAT 726
760 GACTTGAATGCTCACTTACCGGTTGGATACCGGCTGCTCAAGAGCTTCTGATGATGAT 819
727 CCTGCTTACCCCGCAAAATTTTACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 786
820 CCTGCTTACCCCGCAAAATTTTACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 879
787 AGCGAATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 846
880 AGCGAATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 939
847 CAATCTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 906
940 CAATCTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 999
907 ACAGACTTTTCTCATGAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 966
1000 ACAGACTTTTCTCATGAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1059
967 GAGGTACAAAGCTTCTCAAAAGCTGCAAGCTTGAAGATTAAGAGAGAGAGAGAGAGAGAGAGAG 1026
1060 GAGGTACAAAGCTTCTCAAAAGCTGCAAGCTTGAAGATTAAGAGAGAGAGAGAGAGAGAGAGAG 1119
1027 TTGAAAATTAAGGACACACAAAGAAAGAAAGAGCTTACCTTACCCGACATTAATCTGCG 1086
1120 TTGAAAATTAAGGACACACAAAGAAAGAAAGAGCTTACCTTACCCGACATTAATCTGCG 1179
1087 GATGTTCTCTCAGTTCATTTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1146
1180 GATGTTCTCTCAGTTCATTTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1239
1147 GCAATTTTGGAGCCCTTGTGACATTAACGATGACGATGATGATGATGATGATGATGATGATGAT 1206
1240 GCAATTTTGGAGCCCTTGTGACATTAACGATGACGATGATGATGATGATGATGATGATGATGAT 1299
1207 GAGCTGACATTAACAAAGGGGAGCGGATTAAGCGCTTGTAGAGATGCTGCTGCGC 1266
1300 GAGCTGACATTAACAAAGGGGAGCGGATTAAGCGCTTGTAGAGATGCTGCTGCGC 1359
1267 TGCTTGTGATCT 1326
1360 TGCTTGTGATCT 1419
1327 GAACATCTTCTTAACCTTCAACCCAGACATTAATGCTGACAGCTCAAGTTTATTTTCAAC 1386
1420 GAACATCTTCTTAACCTTCAACCCAGACATTAATGCTGACAGCTCAAGTTTATTTTCAAC 1479

1387 CCAGAAAAGCTCCATTTTGTCTTCAACATTTGGAATTTCTGTACTGCAACAGAG 1446
1480 CCAAGAAAGCTCCATTTTGTCTTCAACATTTGGAATTTCTGTACTGCAACAGAG 1539
1447 GTTTCGCGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1506
1540 GTTTCGCGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1599
1507 CCAACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1566
1600 CCAACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1659
1567 TCTCTCGAACAACAAATTTCTTCACTTACAGATGATGATGATGATGATGATGATGATGATGAT 1626
1660 TCTCTCGAACAACAAATTTCTTCACTTACAGATGATGATGATGATGATGATGATGATGATGAT 1719
1627 GTGGTCCAGAAACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1686
1720 GTGGTCCAGAAACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1779
1687 CAAGAACAAACCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1746
1780 CAAGAACAAACCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1839
1747 AAGATAGGATTTATCTATTCAGAAAGAGCTCAGACATTTCTTAAGCATGAGATCTTA 1806
1840 AAGATAGGATTTATCTATTCAGAAAGAGCTCAGACATTTCTTAAGCATGAGATCTTA 1899
1807 ACTCATTAAGATTTCTTCTTCAAGAGATGCTCTGTTGGGAGAGAGAGAGAGAGAGAGAGAG 1866
1900 ACTCATTAAGATTTCTTCTTCAAGAGATGCTCTGTTGGGAGAGAGAGAGAGAGAGAGAGAG 1959
1867 AAGTATGTCAGAACAAACCTCAGCTTCAAGAGATGCTCTGTTGGGAGAGAGAGAGAGAGAG 1926
1960 AAGTATGTCAGAACAAACCTCAGCTTCAAGAGATGCTCTGTTGGGAGAGAGAGAGAGAGAG 2019
1927 GAGAACGCGCATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1986
2020 GAGAACGCGCATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2079
1987 GCCCTTGTGCAATTAATTAAGCAAGAGGTTGAGATTAAGAACTAGAACATTAAGAACT 2046
2080 GCCCTTGTGCAATTAATTAAGCAAGAGGTTGAGATTAAGAACTAGAACATTAAGAACT 2139
2047 CTGGCCACTTTTAAAGAGAGAAAGAGCTTACCTTACAGATTTTGTGCTATTA 2097
2140 CTGGCCACTTTTAAAGAGAGAAAGAGCTTACCTTACAGATTTTGTGCTATTA 2190

RESULT 8
US-10-741-600-693
; Sequence 693, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 693
; LENGTH: 3274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-693

Query Match 50.6%; Score 1062; DB 21; Length 3274;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2012; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
67 TGTGAGACAGTGTGTACATGATTTTCTGACAGATCTTCACTGTATTAAGTAATCCGAT 126

178 TGTGAGAGAGCTGTGGTACATGATTTTCTGCAGATCTTCACTGTATTAGTGAATCCGAT 237
127 AAGTATGACCTAAAAACCGAAGACGCTCTTGTGTGTGTGTCTACACGGGACC 186
238 AAGTATGACCTAAAAACCGAAGACGCTCTTGTGTGTGTGTCTACACGGGACC 237
187 GGAGACCCACCGACACAGCCCGGAAATTTGTTAAGAAATACAGAACCAACCTGCG 246
298 GGAGACCCACCGACACAGCCCGGAAATTTGTTAAGAAATACAGAACCAACCTGCG 357
247 GTTGAATTTCTTGTCTGACCTGCGGTATGAGGTACTGGGTCTCGGTGATTCAGATACAC 306
358 GTTGAATTTCTTGTCTGACCTGCGGTATGAGGTACTGGGTCTCGGTGATTCAGATACAC 417
307 TACTTTGCAATGGGGGAAAGATTAATGATTAACGATTCAGAGCTTGAGCCCGCAT 366
418 TACTTTGCAATGGGGGAAAGATTAATGATTAACGATTCAGAGCTTGAGCCCGCAT 477
367 TTTCTATGACACTGACATGACAGATGACTGTGTAGTGTAAACCTTGTGTGAGCCGTG 426
478 TTTCTATGACACTGACATGACAGATGACTGTGTAGTGTAAACCTTGTGTGAGCCGTG 537
427 ATTGCTGACACTGTGGCCAGCCCTCAGAAAGCATTTTAGTCAAGCAGAGGACAAAGAGAG 486
538 ATTGCTGACACTGTGGCCAGCCCTCAGAAAGCATTTTAGTCAAGCAGAGGACAAAGAGAG 597
487 ATAAAGTGGGCACTCCCGGTGGATCACTGATCTTGAAGACAGACCTTGTGAAGTCA 546
598 ATAAAGTGGGCACTCCCGGTGGATCACTGATCTTGAAGACAGACCTTGTGAAGTCA 657
547 GAGTGTCTACATGATTAATCTCAAGTGTGAGCTTGTGATTCAGATTAATTCAGAGAAAG 606
658 GAGTGTCTACATGATTAATCTCAAGTGTGAGCTTGTGATTCAGATTAATTCAGAGAAAG 717
607 GATCTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATTCATTTGTAATTGA 666
718 GATCTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATTCATTTGTAATTGA 777
667 GACTTTGAGTCTCTCACTTACCCGTTGGGTACCCCACTCTCAAGCCCTCTGGAATATT 726
778 GACTTTGAGTCTCTCACTTACCCGTTGGGTACCCCACTCTCAAGCCCTCTGGAATATT 837
727 CTTGTGTACCCCGCAAAATTTTACAGTATCTGACAGAGTCTTGTGACAGAGAA 786
838 CTTGTGTACCCCGCAAAATTTTACAGTATCTGACAGAGTCTTGTGACAGAGAA 897
787 AGCCAAATATCTGTGACTTGCAGAGATCCAGTTTTCAGTGGCAATTTCAAAAGGAGT 846
898 AGCCAAATATCTGTGACTTGCAGAGATCCAGTTTTCAGTGGCAATTTCAAAAGGAGT 957
847 CAATTAATCTGAGATGATGCAATTAACCACTGTGTGTGATTTGAATTTGAATTTCAAT 906
958 CAATTAATCTGAGATGATGCAATTAACCACTGTGTGTGATTTGAATTTGAATTTCAAT 1017
907 ACAGACTTTTCTATGAGCTGTGAGATGCTTGCAGCTGATCTGCTTAAAGATTTCT 966
1018 ACAGACTTTTCTATGAGCTGTGAGATGCTTGCAGCTGATCTGCTTAAAGATTTCT 1077
967 GAGGTACAAAGCTTACTCAAAAGCTGAGCTTGAAGATTAAGAGAGAGAGAGAGAGAG 1026
1078 GAGGTACAAAGCTTACTCAAAAGCTGAGCTTGAAGATTAAGAGAGAGAGAGAGAGAG 1137
1027 TTGAAATTAAGGAGACACAAAGAAAGAGAGCTTACCTTACCCAGCATATACCTGCG 1086
1138 TTGAAATTAAGGAGACACAAAGAAAGAGAGCTTACCTTACCCAGCATATACCTGCG 1197
1087 GAGGTCTCTCCAGCTTACTTAACTGTGTGTGAAATTCAGAGAAATTTCTTAAAG 1146
1198 GAGGTCTCTCCAGCTTACTTAACTGTGTGTGAAATTCAGAGAAATTTCTTAAAG 1257
1147 GCATTTTGGAGGCTTGTGACTATACAGTGAAGTGTGAAAGAGAGAGAGAGAGAG 1206

1258 GCATTTTTCAGAGCCCTTGTGACTATACAGTGAAGTGTGAAAAGCCAGGCTACAG 1317
1207 GAGCTGTGAGTAAACAAAGGGGAGGCGGATTAATAGCCCTTGTGACAGATGCTGTGCC 1266
1318 GAGCTGTGAGTAAACAAAGGGGAGGCGGATTAATAGCGCTTGTGACAGATGCTGTGCC 1377
1267 TGTGTGTGAGATCTCTCTGCTTCTTCTGCTTCTTGTGACAGCACTCAAGTCTCTGCTC 1326
1378 TGTGTGTGAGATCTCTCTGCTTCTTCTGCTTCTTGTGACAGCACTCAAGTCTCTGCTC 1437
1327 GAACATCTTCTCTTAACTTCAACCCAGACCATATTCGTGTGACAGCTCAAGTTATTTTAC 1386
1438 GAACATCTTCTCTTAACTTCAACCCAGACCATATTCGTGTGACAGCTCAAGTTATTTAC 1497
1387 CCAGAAAGCTCATTGTTGTTCTTCAACATTTGTGAAATTTCTGTCTACCTGCAACAGAG 1446
1498 CCAGAAAGCTCATTGTTGTTGTTCTTCAACATTTGTGAAATTTCTGTCTACCTGCAACAGAG 1557
1447 GTTCTGCGAAGGAGATTAATGATACAGCTGCTGCGCTTGTGTGCTTCAAGTCTTCCAG 1506
1558 GTTCTGCGAAGGAGATTAATGATACAGCTGCTGCGCTTGTGTGCTTCAAGTCTTCCAG 1617
1507 CCAGAAATATGATCATCCATGAGACAGCGGGAAGCCCTGAGCTCTTAAGATATCATC 1566
1618 CCAGAAATATGATCATCCATGAGACAGCGGGAAGCCCTGAGCTCTTAAGATATCATC 1677
1567 TCTCTGTGAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATCATATAG 1626
1678 TCTCTGTGAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATCATATAG 1737
1627 GTTGTGTCAGAAACCGGCAATGCGGCTTATTTGGTTCCTTCAACATGAGAGAAATC 1686
1738 GTTGTGTCAGAAACCGGCAATGCGGCTTATTTGGTTCCTTCAACATGAGAGAAATC 1797
1687 CAAGAAACCAACCCAGATGGAATTTTGAAGCAATGTGTGTTTGTGCTGACAGGAT 1746
1798 CAAGAAACCAACCCAGATGGAATTTTGAAGCAATGTGTGTTTGTGCTGACAGGAT 1857
1747 AAGATATGAGATTAATTTATTCAGAAAGAGCTCAGACATTTCTTAAAGATGGAATCTTA 1806
1858 AAGATATGAGATTAATTTATTCAGAAAGAGCTCAGACATTTCTTAAAGATGGAATCTTA 1917
1807 ACTCATTAAGATTTCTTCTCAAGAGATGCTCCTGTTGGGAGAGAGAGCCAGCA 1866
1918 ACTCATTAAGATTTCTTCTCAAGAGATGCTCCTGTTGGGAGAGAGAGCCAGCA 1977
1867 AAGTATGTAAGAGACAAATCCAGCTTCAATGSCAGACAGGTGSCAGAAATCCTCTCAG 1926
1978 AAGTATGTAAGAGACAAATCCAGCTTCAATGSCAGACAGGTGSCAGAAATCCTCTCAG 2037
1927 GAGAACGGCCATATTTATGTGTGTGAGATGCAAGATTAAGCAAGATTTACATGAT 1986
2038 GAGAACGGCCATATTTATGTGTGTGAGATGCAAGATTAAGCAAGATTTACATGAT 2097
1987 GCCCTGTGCAATTAATTAAGCAAGAGTTGAGTTGAAATTAAGCAATTAAGCAATTAAG 2046
2098 GCCCTGTGCAATTAATTAAGCAAGAGTTGAGTTGAAATTAAGCAATTAAGCAATTAAG 2157
2047 CTGAGCACTTTAAAGAAAGAAAGAAAGCTTACAGATTTTGTGATTA 2097
2158 CTGAGCACTTTAAAGAAAGAAAGAAAGCTTACAGATTTTGTGATTA 2208

RESULT 9
US-10-029-386-6369
; Sequence 6369, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 6369
LENGTH: 591
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008727.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.45
OTHER INFORMATION: NT HIT: AF121205.1, EVALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUE 3.30e+00
OTHER INFORMATION: EST_HUMAN HIT: A0132586.1, EVALUE 0.00e+00
US-10-029-386-6369

Query Match 15.7%; Score 330; DB 16; Length 591;
Best Local Similarity 99.7%; Pred. No. 1.2e-169;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGTTGAGCCCTGATTCGCTGCGCCAGCCCTCAGAAAGCATT 460
DB 38 GTTTAGAACTTGTGTTGAGCCCTGATTCGCTGCGCCAGCCCTCAGAAAGCATT 97
QY 461 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCCGGCGCATCCTGGCAT 520
DB 98 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCCGGCGCATCCTGGCAT 157
QY 521 CCTTGAAGCAGACCTTGTGAAGTCAAGCTGCTACATTAATCTCAAGTCAAGCTTC 580
DB 158 CCTGAGAGCAGACCTTGTGAAGTCAAGCTGCTACATTAATCTCAAGTCAAGCTTC 217
QY 581 TGAAGTTCATGATTTCAGAGAAAGAAAGATTCTGAGTTTGAAGCAAAATGCAAGTAA 640
DB 218 TGAAGTTCATGATTTCAGAGAAAGAAAGATTCTGAGTTTGAAGCAAAATGCAAGTAA 277
QY 641 GCAACCAATCCAAATGTTGATTGAAGACTTTGAGTCTTCACTTACCCGTTGGGTACCC 700
DB 278 GCAACCAATCCAAATGTTGATTGAAGACTTTGAGTCTTCACTTACCCGTTGGGTACCC 337
QY 701 CACTCTCACAAGCCTCTGTAATATTCCTGTTTACCCCAAGATATTTTACAGTACATC 760
DB 338 CACTCTCACAAGCCTCTGTAATATTCCTGTTTACCCCAAGATATTTTACAGTACATC 397
QY 761 TGCAGAGTCTCTTGGCCAGG 781
DB 398 TGCAGAGTCTCTTGGCCAGG 418

RESULT 10
US-10-029-386-20100
Sequence 20100, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AEMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20100
LENGTH: 379
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008727.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.45
OTHER INFORMATION: NT HIT: g114729757, EVALUE 0.00e+00

OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUE 1.80e+00
OTHER INFORMATION: EST_HUMAN HIT: A0132586.1, EVALUE 0.00e+00
US-10-029-386-20100

Query Match 15.6%; Score 328; DB 16; Length 379;
Best Local Similarity 99.7%; Pred. No. 1.5e-168;
Matches 378; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 402 TTTAGAACTTGTGTTGAGCCGTTGATTCGCTGCGCCAGCCCTCAGAAAGCATT 461
DB 1 TTTAGAACTTGTGTTGAGCCGTTGATTCGCTGCGCCAGCCCTCAGAAAGCATT 60
QY 462 TAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCCGTGGCATCCTGCATC 521
DB 61 TAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCCGTGGCATCCTGCATC 120
QY 522 CTTGAAGCAGACCTTGTGAAGTCAAGCTGCTACCATTTGAATCTCAAGTCAAGCTTCT 581
DB 121 CTTGAAGCAGACCTTGTGAAGTCAAGCTGCTACCATTTGAATCTCAAGTCAAGCTTCT 180
QY 582 GAGATTCGATGATTCAAGAGAAAGATTCGAGTTTGAAGCAAAATGCAAGTAAAG 641
DB 181 GAGATTCGATGATTCAAGAGAAAGATTCGAGTTTGAAGCAAAATGCAAGTAAAG 240
QY 642 CAACCAATCCAAATGTTGATTGAAGACTTTGAGTCTTCACTTACCCGTTGGGTACCC 701
DB 241 CAACCAATCCAAATGTTGATTGAAGACTTTGAGTCTTCACTTACCCGTTGGGTACCC 300
QY 702 ACTTTCACAAGCCTCTGTAATATTCCTGTTTACCCCAAGATATTTACAGTACATCT 761
DB 301 ACTTTCACAAGCCTCTGTAATATTCCTGTTTACCCCAAGATATTTACAGTACATCT 360
QY 762 GCAGAGTCTCTTGGCCAG 780
DB 361 GCAGAGTCTCTTGGCCAG 379

RESULT 11
US-10-029-386-1735
Sequence 1735, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AEMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 1735
LENGTH: 591
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC021609.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
OTHER INFORMATION: NT HIT: AF121205.1, EVALUE 0.00e+00
OTHER INFORMATION: EST_HUMAN HIT: A0132586.1, EVALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUE 3.30e+00
US-10-029-386-1735

Query Match 13.3%; Score 279; DB 16; Length 591;
Best Local Similarity 99.5%; Pred. No. 1.2e-141;
Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGGTGAAGCCCTGTGATTCCTGACTCTGGCCAGCCCTCAGAAAGCATT 460
DB 38 GTTTAGAACTTGTGGTGAAGCCCTGTGATTCCTGACTCTGGCCAGCCCTCAGAAAGCATT 97
QY 461 TTGAGTCAACAGAGAGCAAGAGAGATTAAGTGGCCGACCTCCGGTGGCATCCTGCAGT 520
DB 98 TTGAGTCAACAGAGAGCAAGAGAGATTAAGTGGCCGACCTCCGGTGGCATCCTGCAGT 157
QY 521 CCTTGAAGAGAGAGCTTGTGAAGTCAAGAGCTGCTACACATTGAATCTCAAGTGAAGTTT 580
DB 158 CCTGAGAGAGAGAGCTTGTGAAGTCAAGAGCTGCTACACATTGAATCTCAAGTGAAGTTT 217
QY 581 TGAAGTTCGATGATTCAGAGAGAGAGATTCGAGGTTTGAAGCAAAATGCAAGTGAACA 640
DB 218 TGAAGTTCGATGATTCAGAGAGAGAGATTCGAGGTTTGAAGCAAAATGCAAGTGAACA 277
QY 641 GCAACCAATCCAAATGTTGTAATGAAGATTCGAGTCTCACTTACCCGTTGGTACCCC 700
DB 278 GCAACCAATCCAAATGTTGTAATGAAGATTCGAGTCTCACTTACCCGTTGGTACCCC 337
QY 701 CACTTCACAAGGCTCTCTGAATATTCCTGTTTACCCCAAGAAATTTTACAGGTACATC 760
DB 338 CACTTCACAAGGCTCTCTGAATATTCCTGTTTACCCCAAGAAATTTTACAGGTACATC 397
QY 761 TGCAGAGTCTCTTGGCCAGG 781
DB 398 TGCAGAGTCTCTTGGCCAGG 418

RESULT 12
US-10-029-386-15435
; Sequence 15435, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 3428
; SOFTWARE: Annumax Sequence Listing Engine vers. 1.1
; SEQ ID NO 15435
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021609.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
; OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALU0 1.80e+00
; OTHER INFORMATION: EST HUMAN HIT: AU132586.1, EVALU0 0.00e+00
; OTHER INFORMATION: NT HIT: g114729757, EVALU0 0.00e+00
US-10-029-386-15435

Query Match 13.2%; Score 277; DB 16; Length 379;
Best Local Similarity 99.5%; Pred. No. 1.5e-140;
Matches 377; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 402 TTTTGAACCTTGTGGTGAAGCCCTGTGATTCCTGACTCTGGCCAGCCCTCAGAAAGCATT 461
DB 1 TTTTGAACCTTGTGGTGAAGCCCTGTGATTCCTGACTCTGGCCAGCCCTCAGAAAGCATT 60
QY 462 TAGGTCAAGAGAGAGCAAGAGAGATTAAGTGGCCGACCTCCGGTGGCATCCTGCATC 521
DB 61 TAGGTCAAGAGAGAGCAAGAGAGATTAAGTGGCCGACCTCCGGTGGCATCCTGCATC 120

QY 522 CTTGAGAGAGAGCTTGTGAAGTCAAGAGCTGCTACACATTGAATCTCAAGTGAAGTTT 581
DB 121 CTTGAGAGAGAGCTTGTGAAGTCAAGAGCTGCTACACATTGAATCTCAAGTGAAGTTT 180
QY 582 GAGATTTCGATGATTCAGAGAGAGAGATTCGAGGTTTGAAGCAAAATGCAAGTGAACA 641
DB 181 GAGATTTCGATGATTCAGAGAGAGAGATTCGAGGTTTGAAGCAAAATGCAAGTGAACA 240
QY 642 CAACCAATCCAAATGTTGTAATGAAGATTCGAGTCTCACTTACCCGTTGGTACCCC 701
DB 241 CAACCAATCCAAATGTTGTAATGAAGATTCGAGTCTCACTTACCCGTTGGTACCCC 300
QY 702 ACTTCACAAGGCTCTCTGAATATTCCTGTTTACCCCAAGAAATTTTACAGGTACATC 761
DB 301 ACTTCACAAGGCTCTCTGAATATTCCTGTTTACCCCAAGAAATTTTACAGGTACATC 360
QY 762 GCAGAGTCTCTTGGCCAG 780
DB 361 GCAGAGTCTCTTGGCCAG 379

RESULT 13
US-10-741-600-17757
; Sequence 17757, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17757
; LENGTH: 43985
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-17757

Query Match 12.7%; Score 266; DB 21; Length 43985;
Best Local Similarity 99.5%; Pred. No. 2.1e-134;
Matches 366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGGTGAAGCCCTGTGATTCCTGACTCTGGCCAGCCCTCAGAAAGCATT 460
DB 14836 GTTTAGAACTTGTGGTGAAGCCCTGTGATTCCTGACTCTGGCCAGCCCTCAGAAAGCATT 14895
QY 461 TTGAGTCAACAGAGAGCAAGAGAGATTAAGTGGCCGACCTCCGGTGGCATCCTGCAGT 520
DB 14896 TTGAGTCAACAGAGAGCAAGAGAGATTAAGTGGCCGACCTCCGGTGGCATCCTGCAGT 14955
QY 521 CCTTGAAGAGAGCTTGTGAAGTCAAGAGCTGCTACACATTGAATCTCAAGTGAAGTTT 580
DB 14956 CCTTGAAGAGAGCTTGTGAAGTCAAGAGCTGCTACACATTGAATCTCAAGTGAAGTTT 15015
QY 581 TGAAGTTCGATGATTCAGAGAGAGAGATTCGAGGTTTGAAGCAAAATGCAAGTGAACA 640
DB 15016 TGAAGTTCGATGATTCAGAGAGAGAGATTCGAGGTTTGAAGCAAAATGCAAGTGAACA 15075
QY 641 GCAACCAATCCAAATGTTGTAATGAAGATTCGAGTCTCACTTACCCGTTGGTACCCC 700
DB 15076 GCAACCAATCCAAATGTTGTAATGAAGATTCGAGTCTCACTTACCCGTTGGTACCCC 15135
QY 701 CACTTCACAAGGCTCTCTGAATATTCCTGTTTACCCCAAGAAATTTTACAGGTACATC 760
DB 15136 CACTTCACAAGGCTCTCTGAATATTCCTGTTTACCCCAAGAAATTTTACAGGTACATC 15195
QY 761 TGCAGAG 768
DB 15196 TGCAGAG 15203

RESULT 14
US-10-029-386-633/c
Sequence 633, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 633
LENGTH: 525
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC021609.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.48
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.58
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.52
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.57
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.79
OTHER INFORMATION: SWISSPROT HIT: P37039, EVALUE 1.00e-06
OTHER INFORMATION: EST HUMAN HIT: BF346446.1, EVALUE 1.00e-98
OTHER INFORMATION: NT HIT: AF121212.1, EVALUE 0.00e+00
US-10-029-386-633

Query Match 9 0%; Score 188; DB 16; Length 525;
Best Local Similarity 100.0%; Pred. No. 1.1e-91;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1765 TTCAGAAAGAGCTCAGACATTTCTTAAGCATGGAGTTAACTCATTAAGGTTTC 1824
DB 234 TTCAGAAAGAGCTCAGACATTTCTTAAGCATGGAGTTAACTCATTAAGGTTTC 175
QY 1825 TTCTCAAGAGATGCTCTGTGGGAGAGAAAGCCCAAGCAAGTATGTACAGCAAC 1884
DB 174 TTCTCAAGAGATGCTCTGTGGGAGAGAAAGCCCAAGCAAGTATGTACAGCAAC 115
QY 1885 ATCCAGCTTCATGCGCAGAGGTGGGGAATCTCTCCAGAGAAAGCCCATTTAT 1944
DB 114 ATCCAGCTTCATGCGCAGAGGTGGGGAATCTCTCCAGAGAAAGCCCATTTAT 55
QY 1945 GTGTGTGG 1952
DB 54 GTGTGTGG 47

RESULT 15

US-10-029-386-14338/c

Sequence 14338, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

SEQ ID NO 14338

LENGTH: 175

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: MAP TO AC021609.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.48
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.58
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.52
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.57
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.79
OTHER INFORMATION: SWISSPROT HIT: O61608, EVALUE 4.00e-04
OTHER INFORMATION: EST HUMAN HIT: AA085543.1, EVALUE 7.00e-94
OTHER INFORMATION: NT HIT: G13325067, EVALUE 5.00e-94
US-10-029-386-14338

Query Match 8 3%; Score 175; DB 16; Length 175;

Best Local Similarity 100.0%; Pred. No. 1.5e-84;

Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1770 AAAAGCTCAGACATTTCTTAAGCATGGAGTTAACTCATTAAGGTTTCCTTC 1829
DB 175 AAAAGCTCAGACATTTCTTAAGCATGGAGTTAACTCATTAAGGTTTCCTTC 116
QY 1830 AAGAGTGTCTCTGTGGGAGAGAAAGCCCAAGCAAGTATGTACAGCAACATCCA 1889
DB 115 AAGAGTGTCTCTGTGGGAGAGAAAGCCCAAGCAAGTATGTACAGCAACATCCA 56
QY 1890 GCTTCATGCGCAGAGGTGGGGAATCTCTCCAGAGAAAGCCCATTTAT 1944
DB 55 GCTTCATGCGCAGAGGTGGGGAATCTCTCCAGAGAAAGCCCATTTAT 1

Search completed: August 27, 2005, 17:33:22
Job time : 903.401 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 23:18:31 ; Search time 4546.04 Seconds
(without alignments)
17558.328 Million cell updates/sec

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Perfect score: 2097
Sequence: 1 atgagagaggttcgtact.....ttcagatattgtgcataa 2097

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : EST:*

1: gb_est1:*\n2: gb_est2:*\n3: gb_hic:*\n4: gb_est3:*\n5: gb_est4:*\n6: gb_est5:*\n7: gb_est6:*\n8: gb_gsa1:*\n9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1592	75.9	3100	3	BC062577 Homo sapi
2	1007	48.0	3143	3	BC035977 Homo sapi
3	740	35.3	874	4	BM801462 AGENCOURT
4	719	34.3	908	5	BX348674 BX348674
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6	586	27.9	852	5	BO431497 AGENCOURT
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9	543	25.9	877	1	AU124440 AU124440
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11	507	24.2	834	5	BU941078 AGENCOURT
12	470	22.4	521	6	CB164340 K-EST0225
13	461	22.0	776	6	CB997527 AGENCOURT
14	455	21.7	822	1	AU132586 AU132586
15	448	21.4	591	2	AW965709 EST377782
16	446	21.3	818	6	CD559384 AGENCOURT
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20	406	19.4	710	5	BU570323 AGENCOURT
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29	337	16.1	818	7	CP995233 AGENCOURT
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31	335	16.0	413	2	BF810479 RCS-CI014
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36	308	14.7	667	7	CR770923 DKE2463N
37	308	14.7	767	7	CR557482 DKE2463N
38	302	14.4	440	4	BG877205 QV3-HT046
39	293	14.0	481	7	CR549172 DKE2459J
40	292	13.9	528	2	BE301292 ba8pb07.x
41	290	13.8	395	4	BM838530 K-EST0114
42	272	13.0	301	1	AL704780 DKE2463N
43	264	12.6	366	6	CB298361 220019.re
44	257	12.3	366	2	BF808461 QV1-CI017
45	257	12.3	368	1	AA355001 EST63417

ALIGNMENTS

RESULT 1
LOCUS BC062577
DEFINITION Homo sapiens cDNA clone IMAGE:5189058, containing frame-shift errors.
ACCESSION BC062577
VERSION BC062577.1 GI:38511756
KEYWORDS HTc.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS Strausberg, R.L., Feingold, R.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Bluetow, K.H., Schejter, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uebelin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Rana, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullen, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richardson, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, U., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Kravitski, M.I., Skalek, U., Smalley, D.B., Scherker, A., Schein, J.E., Jones, S.J. and Marra, M.A.
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE
PUBMED 22388257
REFERENCE 12477932
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (24-Nov-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NHL-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

REMARK
COMMENT

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.ncm@nih.gov
Ahter, N., Ayle, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Boufield, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,
Madero, Q. L., Masello, C., Maskeri, B., Mastrian, S. D., McCloskey, J. C.,
McDowell, J., Pearson, R., Stancirip, S., Thomas, P. J., Touchman, J. W.,
Tsurgeon, C., Vogt, J. L., Walker, M. A., Wetherby, K. D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E. D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LIML at: <http://image.liml.gov>
Series: IRAC Plate: 135 Row: e Column: 21
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA 91: 4505278
This clone has the following problem: frame shifted.

FEATURES

source

1. 3100
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
283 GGTCTCGGTGATTGAGATACCTTCTTTCAGTGGGGAAGATATGATTAACGA 342
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343 CTTCAAGCTTGAAGCCCGCATTTCTATGACACTGACATGACATGACTGTGTAGT 402
232 CTTCAAGCTTGAAGCCCGCATTTCTATGACACTGACATGACATGACTGTGTAGT 291
403 TTGAACTTGTGTGAGCGGTGATTTGCTGCACTCTGCGCAGCCCTCAGAAAGCATTTT 462
292 TTGAACTTGTGTGAGCGGTGATTTGCTGCACTCTGCGCAGCCCTCAGAAAGCATTTT 351
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412 TCGAGGACAGACTTGTGAAGTCAAGCTGCTACATTTGAATTTCAAGTCAGCTTCTG 471
583 AGATTGATGATTCAGAGAAAGATTTGAGGTTTGAAGCAAAATGACGTGAAGC 642
472 AGATTGATGATTCAGAGAAAGATTTGAGGTTTGAAGCAAAATGACGTGAAGC 531
643 AACCAATTCATGTTGTAATTTGAAGCTTGAAGTCTTCACTTACCGGTGGTACCCCA 702
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703 CTCTCAAGGCTCTTGAATTTCTGTTTACCCCAAGAAATTTTACAGTACATCTG 762
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763 CAGAGTCTCTTGGCCAGAGAAAGCAAGTATCTGTGACTTCAAGAGATTCAGTTT 822
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QY 823 CAAATGCAATTTCAAAAGCAGTTCACTTACTAGATGATGCCATTAACCACTCTG 882
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QY 883 CAGTGAATTTGAGCACTTCAAAATGAGCTTTCTATCAGCTGGAGATGCTTCAG 942
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QY 1423 TTTCTGCTCACTGCGCAACAGAGGTTTGGCGGAAGGAGTATGTAACGGCTGGCGCC 1482
DB 1311 TTTCTGCTCACTGCGCAACAGAGGTTTGGCGGAAGGAGTATGTAACGGCTGGCGCC 1370
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QY	121	TCCGATTAAGTATGACTTAATAAACCGAAGACAGCTCTCTGTGTGTGTGTGTCTTAACAG	180
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QY	661	ATTGAAAGCTTTGAGTCTCTCACTTACCCGTTCCGTTACCCCACTCTCAACAAGCTCTCTG	720
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DEFINITION AGENCOURT_6459212 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5560477
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ACCESSION BM801462
VERSION BM801462.1 GI:19118285
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 874)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
JOURNAL Email: sgabds-remail.nih.gov
COMMENT Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
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Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 35.3%; Score 740; DB 4; Length 874;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 740; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 TCGGATATGATGACCTTAATAACGGAACAGCTCCTGTGTGTTGGTTTCTTACACAG 180
DB 170 TCGGATATGATGACCTTAATAACGGAACAGCTCCTGTGTGTTGGTTTCTTACACAG 229
QY 181 GGACCGGAGACCAACCGGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
DB 230 GGACCGGAGACCAACCGGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 289
QY 241 CTCGCGGTTGATTTCTTCTGCTCACTGCGGTATGAGGTTCTCGGTTCTCGGTATTCAGAA 300
DB 290 CTCGCGGTTGATTTCTTCTGCTCACTGCGGTATGAGGTTCTCGGTTCTCGGTATTCAGAA 349
QY 301 TACACCTACTTTTGCATGGGGGGAAGTATTTGATTAAGCACTTCAAGAGCTTGAGGCC 360
DB 350 TACACCTACTTTTGCATGGGGGGAAGTATTTGATTAAGCACTTCAAGAGCTTGAGGCC 409
QY 361 CGGCAATTTCTATGACACTGACATGACATGATGCTGTAGGTTTGAAGCTTGTGTTGAG 420
DB 410 CGGCAATTTCTATGACACTGACATGACATGATGCTGTAGGTTTGAAGCTTGTGTTGAG 469
QY 421 CGTGATTTGCTGAGACTGTGGCCAGCCCTCAGAAAGCATTTTAAAGTCAAGCAGAGCAAA 480

DB 470 CCGTGATTTGCTGAGACTGTGGCCAGCCCTCAGAAAGCATTTTAAAGTCAAGCAGAGCAAA 529
QY 481 GAGAGATATGAGGCGCACTCCCGGTGAGCATCACTGATCTTGTAGAGACAGACTTGTG 540
DB 530 GAGAGATATGAGGCGCACTCCCGGTGAGCATCACTGATCTTGTAGAGACAGACTTGTG 589
QY 541 AAGTCAGACTGCTACACATTTGATATTCATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 590 AAGTCAGACTGCTACACATTTGATATTCATGATGATGATGATGATGATGATGATGATGATGAT 649
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QY 661 ATTGAAGCTTTGAGTCTTCACTTACCCGTTGGTATCCCACTCTCAGAGCTTCTG 720
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DB 770 AATATTTCTGTTTACCCCC 789

RESULT 4
BX348674 908 bp mRNA linear EST 08-APR-2004
LOCUS BX348674 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS00C010Y11 5-PRIME, mRNA sequence.
ACCESSION BX348674
VERSION BX348674.1 GI:30375301
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 908)
Li, W.-B., Gruber, C., Jessee, J. and Polyes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, web : www.genoscope.cns.fr
Note: segre@genoscope.cns.fr, web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3392.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CS0BAG062B02_CS00490_1&c=3392.f

FEATURES
source Location/Qualifiers
1..908
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS00C010Y11"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_id="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 34.3%; Score 719; DB 5; Length 908;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 674 AGTCTCACTTACCGTGGTACCCCACTCAGCAAGCTTCTGAATATTCCTGGTT 733

DB 28 AGTCTCACTACCCGTTGGTACCCCACTCTCAACAGCTCTGTGAATATTCCTGT 87
QY 734 TACCCCAATATTTTACAGTACATCTGACAGAGTCTTTGGCCAGAGAAAGCAAG 793
DB 88 TACCCCAATATTTTACAGTACATCTGACAGAGTCTTTGGCCAGAGAAAGCAAG 147
QY 794 TATCTGTGACTTACAGAGATCCAGTTTTCAGTGCCATTTCAAGAGATTTCACTTA 853
DB 148 TATCTGTGACTTACAGAGATCCAGTTTTCAGTGCCATTTCAAGAGATTTCACTTA 207
QY 854 CTACAGATGATCCATTAATAACCACTCTGCTGTAGATTTGAATTTCAATATACACT 913
DB 208 CTACAGATGATCCATTAATAACCACTCTGCTGTAGATTTGAATTTCAATATACACT 267
QY 914 TTTTCCATAGCTGTAGATGCTTTCAGAGTATCTGCTTAACTGATTTCTGAGTAC 973
DB 268 TTTTCCATAGCTGTAGATGCTTTCAGAGTATCTGCTTAACTGATTTCTGAGTAC 327
QY 974 AAAGCTTACTCCAAAGCTGACAGCTTGAAGATTAAGAGACAGCTGCTTTTGAATA 1033
DB 328 AAAGCTTACTCCAAAGCTGACAGCTTGAAGATTAAGAGACAGCTGCTTTTGAATA 387
QY 1034 TAAAGGACAGACAAAGAAAGAAAGAGTACCTTACCCAGCATATACCTGCGGATTT 1093
DB 388 TAAAGGACAGACAAAGAAAGAAAGAGTACCTTACCCAGCATATACCTGCGGATTT 447
QY 1094 CTCTCCAGTTCAATTTTACCTGTGTCTTGAATTCGAGCAATCTTAAAGAGCATTTT 1153
DB 448 CTCTCCAGTTCAATTTTACCTGTGTCTTGAATTCGAGCAATCTTAAAGAGCATTTT 507
QY 1154 TCGAGACCTTGTGACTATACAGTGAAGTCTTAAAGAGAGCTTACAGAGCTGT 1213
DB 508 TCGAGACCTTGTGACTATACAGTGAAGTCTTAAAGAGAGCTTACAGAGCTGT 567
QY 1214 GCAGTAAACAGGGGAGCGAGTATATAGCGCTTTGACAGATGCTGTGCTGTGT 1273
DB 568 GCAGTAAACAGGGGAGCGAGTATATAGCGCTTTGACAGATGCTGTGCTGTGT 627
QY 1274 TGGATCTCTCTCTGCTTTCCCTTTCTTGGCAGCCACACTCACTCTCTGCTGAACT 1333
DB 628 TGGATCTCTCTCTGCTTTCCCTTTCTTGGCAGCCACACTCACTCTCTGCTGAACT 687
QY 1334 TTCTTAACTTCAACCAAGCATATTCGTGCAAGCTCAAGTTATTTCAACCCAGGA 1392
DB 688 TTCTTAACTTCAACCAAGCATATTCGTGCAAGCTCAAGTTATTTCAACCCAGGA 746

RESULT 5
CN260357 646 bp mRNA linear EST 16-MAY-2004
LOCUS 17000424179730 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN260357
VERSION CN260357.1 GI:47276771
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fiek, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkoweki, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Genon Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@genon.com
Insert Length: 646 Std Error: 0.00.

FEATURES

source

Location/Qualifiers

1..646
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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"
/clone_id="GRN ES"
/note="oligo dt primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

ORIGIN

Query Match 29.7%; Score 623; DB 7; Length 646;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 623; Conservative 0;

QY 987 AAGACTGACGCTTGAAGATTAAGAGAGACAGCTGCTTTTGAATAATTAAGCAGACAC 1046
DB 24 AAGACTGACGCTTGAAGATTAAGAGAGACAGCTGCTTTTGAATAATTAAGCAGACAC 83
QY 1047 AAAGAAAGAAAGAGCTTACCTTACCCAGCATATACCTGCGGATTTCTCTCACTTAT 1106
DB 84 AAAGAAAGAAAGAGCTTACCTTACCCAGCATATACCTGCGGATTTCTCTCACTTAT 143
QY 1107 TTTTACCTGCTGTCTTGAATTCGAGCAATCTTAAAGAGCATTTTTCGAGCCCTGT 1166
DB 144 TTTTACCTGCTGTCTTGAATTCGAGCAATCTTAAAGAGCATTTTTCGAGCCCTGT 203
QY 1167 GGAATATACAGTGAAGTCTGAAAGAGAGAGCTTACAGAGCTGTGAGTAAACAG 1226
DB 204 GGAATATACAGTGAAGTCTGAAAGAGAGAGCTTACAGAGCTGTGAGTAAACAG 263
QY 1227 GCGAGCCGATTATAGCCGCTTTGACAGATGCTGTGCTGTGTGATCTCTCT 1286
DB 264 GCGAGCCGATTATAGCCGCTTTGACAGATGCTGTGCTGTGTGATCTCTCTCT 323
QY 1287 CGCTTCCCTTCTGCGAGCCACACTGCTGCTGCTGCTGAAACATCTTAACTTCA 1346
DB 324 CGCTTCCCTTCTGCGAGCCACACTGCTGCTGCTGCTGAAACATCTTAACTTCA 383
QY 1347 ACCAGAACATATATGCTGTGACAGCTCAAGTTATTTACCAAGAAAGCTCATTTGT 1406
DB 384 ACCAGAACATATATGCTGTGACAGCTCAAGTTATTTACCAAGAAAGCTCATTTGT 443
QY 1407 CTTCACATTTGGAATTTCTGTCTTACTGCAACACAGAGTTCTGCGAAGGAGTATG 1466
DB 444 CTTCACATTTGGAATTTCTGTCTTACTGCAACACAGAGTTCTGCGAAGGAGTATG 503
QY 1467 TACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1526
DB 504 TACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 563
QY 1527 TGAAGACAGCGGAAAGCCCTGCTCTTAAGATTCATCTCTCTGAAACAAATTC 1586
DB 564 TGAAGACAGCGGAAAGCCCTGCTCTTAAGATTCATCTCTCTGAAACAAATTC 623
QY 1587 TTTTCACTTACCAAGTACCTCT 1609
DB 624 TTTTCACTTACCAAGTACCTCT 646

RESULT 6
BQ431497 852 bp mRNA linear EST 24-MAY-2002
LOCUS 17000424179730 GRN_ES Homo sapiens cDNA clone IMAGE:6158144
DEFINITION AGENCOURT 7894690 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6158144
ACCESSION BQ431497
VERSION BQ431497
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

QY	241	TTGCGGGTAAATTTCTTTGGCTCACTGGGGATATGGGTAACTGGGCTCGGTGATTCAGAA	300
Db	293	CTGCCGGTAAATTTCTTTGCTCACTGGGGATATGGGTAACTGGGCTCGGTGATTCAGAA	352
QY	301	TACACCTACTTTTSCAATGGGGGAGATTAATTGATTAACGACTTCAAGACTTGGAGCC	360
Db	353	TACACCTACTTTTSCAATGGGGGAGATTAATTGATTAACGACTTCAAGACTTGGAGCC	412
QY	361	CGGCAATTTCTATGACATCGACATATGCATATGACTGTATAGTTTAGAATTGTGTGTTAG	420
Db	413	CGGCAATTTCTATGACATCGACATATGACTGTATAGTTTAGAATTGTGTGTTAG	472
QY	421	CCGTGATATGCTGAGCTCTGGCCAGACCCTCAGAAAGCAATTTTAGTCAAGCAGAGACA	480
Db	473	CCGTGATATGCTGAGCTCTGGCCAGACCCTCAGAAAGCAATTTTAGTCAAGCAGAGACA	532
QY	481	GAGGAGATTAAGTGGGCGCACTCCCGGTGGCATCACTGTGACTCTTGAGAGACAGACTTGTG	540
Db	533	GAGGAGATTAAGTGGGCGCACTCCCGGTGGCATCACTGTGACTCTTGAGAGACAGACTTGTG	592
QY	541	AAGTCAGAGCTGCTACATCAATTGAATCTCAAGTCGAGCTTCTGAGATTGATGATTCAGAA	600
Db	593	AAGTCAGAGCTGCTACATCAATTGAATCTCAAGTCGAGCTTCTGAGATTGATGATTCAGAA	652
QY	601	AGAAAGATTCGAGGTTT	619
Db	653	AGAAAGATTCGAGGTTT	671

RESULT 8				
AU279788				
LOCUS	AU279788	565 bp	mRNA	linear
DEFINITION	AU279788	CHONS2 Homo sapiens cDNA clone CHONS200148 5', mRNA	CHONS200148 5', mRNA	EST 31-JUL-2003

ACCSSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AU279788	AU279788	GI:28299015	EST.	Homo sapiens
				Homo sapiens (human)

REFERENCE 1 (bases 1 to 565)
AUTHORS Imabayashi, H., Mori, T., Gojo, S., Kiyono, T., Sugiyama, T., Irie, R., Isegai, T., Hata, J., Tomoya, Y. and Umezawa, A.
TITLE Redifferentiation of dedifferentiated chondrocytes and chondrogenesis of human bone marrow stromal cells via chondrosphere formation with expression profiling by large-scale cDNA analysis
JOURNAL Exp. Cell Res. 288 (1), 35-50 (2003)

COMMENT Contact: Takao Isogai

Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel.: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomic@hri.co.jp
HRI human cDNA Project, Sugiyama, T.; Wakamatsu, A.; Irie, R.;
Umezawa, A.; Fukuma, M.; Kueskari, S.; Hata, J.; Ihiki, S.; Yamamoto, J.;
Isono, Y.; Saito, K.; Nakamura, Y.; Masuko, Y.; Nagai, K.; Isogai, T.
HRI human cDNA project, cDNA library construction & 5'-end one
pass sequencing: Helix Research Institute.

FEATURES	Location/Qualifiers
SOURCE	1. .565

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CHONS200148"
/cell_type="chondrocytes"
/clone_id="CHONS2"
/note="Vector: pME18SFL3"
ORIGIN

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Query Match	26.9%;	Score 565;	DB 1;	Length 565;
Best Local Similarity	100.0%;	Pred. No. 2.1e-298;		
Matches 565;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

819 TTTTCAAGTGCCAATTTTCAAAGCAGTTCAACTTACTAGCAATGATGTCATATAAAACAC 878
 1 TTTTCAAGTGCCAATTTTCAAAGCAGTTCAACTTACTAGCAATGATGTCATATAAAACAC 60

879 TCTGCTGTAGAATTGGACATTTCAAATACAGACTTTTCTATCAGCCTGGAGATCCTT 938

939 CAGCGTATTCGCCCTAACAGTATTCAGGTACAAGCTACTCCAAAGACTGCAGCT 998

121 CAGCGTATCTGCCCTTAACAGTATTTCTGAGGTACAAAGCCTACTCCAAAGACTGCAGCT 180

181 TGAAGATAAAAGAGAGCACTGCGTCTTTTGAATAATAAAGCAGACACAAAGAGAAAGG 240

1059 AGCTACCTTACCCAGCATATACTGCGGAGTGTCTCTCAGTTCAATTTTACCTGTTG 1118

1119 TCCTGAAATCCGAGCAATTCCTAAAAGGCAATTTTGGCAGCCCTTGTCGACTATACCAAG 1178

301 TCTGAATCCGAGCAATTCCTAAAGCAATTTTGGGAGCCCTTGAGACTATACCAG 360

1175 GACAGTGC TGAAGACG CAGGCTAC GAGAGT GTCAGT AAAACAGAGGG CAGCCAA TTA 1235
361 TGACAGTCTG AAAACG CAGGCTAC GAGAGT GTG CAGTAA ACAGGGG CAGCCGATTA 420

1239 TAGCCGCTTGTACAGATGCTGTGCTGTGTGATCTCCTCGCTTCCCTTC 1298

1299 TTGGCAGGCCACCACTCAGTCTCTGCTGGAACATCTTCTTAACTTCAACCCAGACCATTA 1315
421 TAGCCGCTTGTACGAGATGCCCTGATGCCCTCTTGTATGATCTCCCTCCCTGCTTCCCTTTC 480

481 TTGCCAGCCACCACTAGTCTCTGCTCGACATCTTCTAACTTCAACCCAGACATA 540

541 TTGGTGTGCAAGCTCAAGTTTATTT 565
1359 TTTCGTGTCAGCTCAAGTTTATTT 1383

RESULT 9

	877 bp	mRNA	linear	EST	01-AUG-2002
AU124440					
LOCUS					
SPRINTON					
AU124440					
NT2RM4					
Homo sapiens cDNA clone NT2RM4000010 5' mRNA					

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sequence.
ACCESSION      GT:10949156
AUI2440        AUI24440 1
BERSTON

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KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 877)

AUTHORS
Oda, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J.,
Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and
Teraishi, M.

TITLE	Author(s)
HRI human cDNA project	Oota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Sato, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Goshima, Y., Yamamoto, T., Terauchi, M.

JOURNAL
COMMENT
Unpublished (2000)
Contact: Takao Isegai
Genetics Laboratory

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel.: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hi.co.jp

RESULT 11
 BU941078 834 bp mRNA linear EST 18-OCT-2002
 LOCUS AGENCOURT_10540067 NIH_MGC_128 Homo sapiens cDNA clone
 DEFINITION IMAGE:6712893 5', mRNA sequence.
 ACCESSION BU941078 GI:24129897
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 834)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: NCI
 CDNA Library Preparation: Michael Brownstein Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLCM3022 row: e column: 21
 High quality sequence stop: 586.
 Location/Qualifiers
 1. 834
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_image="IMAGE:6712893"
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 /lab_host="DH10B (71-phage-resistant)"
 /clone_lib="NIH MGC 128"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggcccatcggcc);
 Site 2: SfiI (ggccggccggcc); Double-stranded cDNA was
 prepared from a pool of 40 cell line poly(A) RNAs (bladder
 - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
 kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
 salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
 adaptors were used in cloning as follows:
 5'-ATGCGATGCTATCAGCAGAGTGGCGCATTCGCGCG-3' and
 5'-ATCTAGAGCGCCGAGCGCGCGCATTCGCGCG-3'. Full-length
 enriched library was constructed using the Clontech
 Creator SMART kit and size-selected to contain the >2 kb
 size fraction (other fractions present in NIH_MGC_126 and
 NIH_MGC_127). Library created in the laboratory of T.
 Uedlin, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC
 Library."

ORIGIN

Query Match 24.2%; Score 507; DB 5; Length 834;
 Best Local Similarity 99.7%; Pctd. No. 1.8e-266;
 Matches 607; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

379 GGACATGACATGATCTGTGAGTTTGAACCTGTGAGCGCGTGTGAGCTC 438
 Db 3 GGACATGACATGATCTGTGAGTTTGAACCTGTGAGCGCGTGTGAGCTC 62
 Qy 439 TGGCAGCCCTCGAAGACATTTTAACTCAAGCAGACCAAGAGAGATTAATGCGCA 498
 Db 63 TGGCAGCCCTCGAAGACATTTTAACTCAAGCAGACCAAGAGAGATTAATGCGCA 122
 Qy 499 CTCGCCGTGACATCTGATCTTGAAGAGACATCTTGAAGTCAAGAGCTGTACAC 558
 Db 123 CTCGCCGTGACATCTGATCTTGAAGAGACATCTTGAAGTCAAGAGCTGTACAC 182
 Qy 559 ATTGAATCTCAAGTCAGCTTCTGAGATTCGATTCAGAGAAAGATTCGAGGTT 618

Db 183 ATTGAATCTCAAGTCAGCTTCTGAGATTCGATTCAGAGAAAGATTCGAGGTT 242
 Qy 619 TTGAAGCAAAATGACGTGAACAGCAACCAATCCATGTTGTAATGAAGCTTGATGCC 678
 Db 243 TTGAAGCAAAATGACGTGAACAGCAACCAATCCATGTTGTAATGAAGCTTGATGCC 302
 Qy 679 TCACTTACCCGTTGGTACCCCACTCTCAAGAGCTCTCTGAATATTCCTGTTTACC 738
 Db 303 TCACTTACCCGTTGGTACCCCACTCTCAAGAGCTCTCTGAATATTCCTGTTTACC 362
 Qy 739 CCAGAAATATTTACAGTACATCTGCAGAGTCTTTGGCCAGAGAGAAACCAATATCT 798
 Db 363 CCAGAAATATTTACAGTACATCTGCAGAGTCTTTGGCCAGAGAGAAACCAATATCT 422
 Qy 799 GTGACTTACGATTCAGATTTTCAAGTCCCAATTTCAAGAGCTTCAACTACTACG 858
 Db 423 GTGACTTACGATTCAGATTTTCAAGTCCCAATTTCAAGAGCTTCAACTACTACG 482
 Qy 859 AATGATGCCATTAACCACTCTGCTGTGAGATTTGACATTTCAATACAGACTTTTCC 918
 Db 483 AATGATGCCATTAACCACTCTGCTGTGAGATTTGACATTTCAATACAGACTTTTCC 542
 Qy 919 TATCAGCTTGAAGATCCTTCAAGCTGATCTGCCCTTACAGTATTCGAGGTACAAAC 978
 Db 543 TATCAGCTTGAAGATCCTTCAAGCTGATCTGCCCTTACAGTATTCGAGGTACAAAC 602
 Qy 979 CTACTCCAA 987
 Db 603 CTACTCCAA 611

RESULT 12
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 LOCUS K-EST0225498 L17N670205n1 Homo sapiens cDNA clone
 DEFINITION L17N670205n1-39-F02 5', mRNA sequence.
 ACCESSION CBI64340
 VERSION CBI64340.1 GI:28150466
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 521)
 Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
 Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
 Kim, Y.S.
 TITLE 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 39 row: F column: 02
 High quality sequence stop: 521.
 Location/Qualifiers
 1. 521
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_image="L17N670205n1-39-F02"
 /sex="F"
 /lab_host="Top10P"
 /clone_lib="L17N670205n1"
 /note="Organ: Liver; Vector: pRTT3-Pac; Site 1: EcoRI;
 Site 2: NotI; The library was contributed by the Soares
 laboratory and it was constructed as described by Bonaldo,
 M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
 6(9): 791-806. RNA was prepared from harvested cell
 culture."

ORIGIN
Query Match 22.4%; Score 470; DB 6; Length 521;
Best Local Similarity 99.8%; Pred. No. 3.9e-246;
Matches 520; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1540 AAGCCCTGGCTCTTAAGATATCATCTCTCCGAAACAACAATTTTCCACTTACCA 1599
DB 1 AAGCCCTGGCTCTTAAGATATCATCTCTCCGAAACAACAATTTTCCACTTACCA 60

QY 1600 GATGACCCCTCAATCCCATCATATATGTTGGTCCAGAAACCGCATAGCCCGTTATT 1659
DB 61 GATGACCCCTCAATCCCATCATATATGTTGGTCCAGAAACCGCATAGCCCGTTATT 120

QY 1660 GGGTCTCTCAACAATAGAGAACTCCCAAGAACACACCAGATGAAATTTTGGAGCA 1719
DB 121 GGGTCTCTCAACAATAGAGAACTCCCAAGAACACACCAGATGAAATTTTGGAGCA 180

QY 1720 ATGTGTTGTTTGTGCTGCTGAGCAATAGATAGGATTTATCTATTCAGAAAAGAGCTC 1779
DB 181 ATGTGTTGTTTGTGCTGAGCAATAGATAGGATTTATCTATTCAGAAAAGAGCTC 240

QY 1780 AGACATTTCTTAAGCATATGGAATCTTAATCAATTAAGGTTTCTTCTCAAGATGCT 1839
DB 241 AGATATTTCTTAAGCATATGGAATCTTAATCAATTAAGGTTTCTTCTCAAGATGCT 300

QY 1840 CCGTGGGGAGAGAGAAAGCCCGCAAGATATGTACAGAACATCCAGCTTCATGGC 1899
DB 301 CCGTGGGGAGAGAGAAAGCCCGCAAGATATGTACAGAACATCCAGCTTCATGGC 360

QY 1900 CACAGAGTGGCGAAATCCCTCCAGAGAAACGGCCATTTATGTGTGTGAGATGCA 1959
DB 361 CACAGAGTGGCGAAATCCCTCCAGAGAAACGGCCATTTATGTGTGTGAGATGCA 420

QY 1960 AAGAATATGCGCAAGATGTATCATATGATGCTTGTGTGCAATTAATTAAGCAAGAGTTGA 2019
DB 421 AAGAATATGCGCAAGATGTATCATATGATGCTTGTGTGCAATTAATTAAGCAAGAGTTGA 480

QY 2020 GTTGAATACTAGAGCATGAAACCTTGCCCATTTTAA 2060
DB 481 GTTGAATACTAGAGCATGAAACCTTGCCCATTTTAA 521

RESULT 13
CB97527 776 bp mRNA linear EST 01-MAY-2003
LOCUS AGENCOURT13620640 NIH MGC 148 Homo sapiens cDNA clone
DEFINITION IMAGE:30338684 5', mRNA sequence.
CB97527
VERSION CB97527.1 GI:30292047
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukayrova; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteleia; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 776)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: csaps-remail.nih.gov
Tissue Procurement: Dr. Stefan Hanson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: NDAM365 row: 1 column: 21
High quality sequence stop: 564.
Location/Qualifiers
1..776

FEATURES
Source

ORIGIN
Query Match 22.0%; Score 461; DB 6; Length 776;
Best Local Similarity 99.5%; Pred. No. 3.7e-241;
Matches 611; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAGAGGTTCTGTACTATATGCTACACAGAGGAGCAAGCCATCGCAGAA 60
DB 88 ATGAGAGGTTCTGTACTATATGCTACACAGAGGAGCAAGCCATCGCAGAA 147

QY 61 GAAATATGAGCAAGCTGTGTACATGATTTTCTGACATCTTCACTGTATTAGTAA 120
DB 148 GAAATATGAGCAAGCTGTGTACATGATTTTCTGACATCTTCACTGTATTAGTAA 207

QY 121 TCCGATATGATGATCTTAAACCCGAAACAGCTCTTGTGTGTGTTTCTACACG 180
DB 208 TCCGATATGATGATCTTAAACCCGAAACAGCTCTTGTGTGTGTTTCTACACG 267

QY 181 GGCACCGGAGACCCACCCGACAGAGCCGCAAGTTGTTAAGAAATPACGAACA 240
DB 268 GGCACCGGAGACCCACCCGACAGAGCCGCAAGTTGTTAAGAAATPACGAACA 327

QY 241 CTGCGGTTGATTTCTTGTCTCACTGCGTATGAGTTACTGGGTCTCGGTGATTCAGAA 300
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QY 361 CGGCAATTTCTATGACCTGGACATGAGATGATGTTGATGATTTAGAACTTGTGTTGAG 420
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DB 508 CCGTGATTTCTGATGATCTGGCCAGCCCTCAGAAACATTTTGTCAAGCAGAGCAAA 567

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QY 541 AAGTCAGAGCTGTACATGATTAATCAAGTGAAGCTTGTGATTCGATTCAGGA 600
DB 628 AAGTCAGAGCTGTACATGATTAATCAAGTGAAGCTTGTGATTCGATTCAGGA 687

QY 601 AGAAGGATTTCTGA 614
DB 688 AGAAGGATTTCTGA 701

RESULT 14
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DEFINITION sequence.

ACCESSION AU132586
VERSION AU132586.1 GI:10929240
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 822)
Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y., Saito, K., Yamamoto, J.,
Nishikawa, T., Nakamura, Y., Nagai, T., Sugano, S., Masuno, Y. and
Isogai, T.
TITLE HRI human cDNA project (Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y.,
Saito, K., Yamamoto, J., Nishikawa, T., Nakamura, Y., Nagai, T.,
Sugano, S., Masuno, Y., Isogai, T.)
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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cells after 2-weeks retinoic acid (RA) induction"
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Best Local Similarity 99.6%; Pred. No. 7.4e-238;
Matches 555; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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DB 182 GGTCTCGGATTCAGATTAACCTTCTTGGCAATGGGGGAAGTAATGTAACGA 241
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DB 242 CTTCAAGACCTTGAAGCCCGCATTTCTATGACATGACATGACAGATGACTGTAGGT 301
QY 403 TTAGAACTTGTGTTAGCCGTGATGCTGTCGACCTGCGCAAGCCCTCAAGAAACATTTT 462
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DB 362 AGGTCAAGAGAGGAAGAAGAGATTAAGTGGGCACTCCCGTGACATCACTGATCC 421
QY 523 TTGAGAGACAGACCTTGAAGTCAAGCTGCTACATTTGAATCTGAAGTCAAGCTTCTG 582
DB 422 TCGAGAGACAGACCTTGAAGTCAAGCTGCTACATTTGAATCTGAAGTCAAGCTTCTG 481
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DERIVATION AW965709
ACCESSION AW965709.1 GI:8155545
VERSION AW965709.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 591)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and
Quackenbush, J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@igr.org
Plate: 218
Seq primer: Reverse.
FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
/clone_1lb="MAGE resequences, MAGI"
/note="Vector: pBluescriptSkm"
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Best Local Similarity 100.0%; Pred. No. 5e-234;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1192 AAGCGAGGCTACAGAGCTGTGCAAGTAACAAGGGGACGCCGATTAATAGCGCTTTGTA 1251
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QY 1252 CGAGATGCTGTGCTGCTGTTGATCTCTCTGCTTCCCTTCTTCCAGGACCA 1311
DB 61 CGAGATGCTGTGCTGCTGTTGATCTCTCTGCTTCCCTTCTTCCAGGACCA 120
QY 1312 CTCAGTCTCTCTCGAATCATCTTCTTAACCTTCAACCCAGACATATTCGTGTGAAC 1371
DB 121 CTCAGTCTCTCTCGAATCATCTTCTTAACCTTCAACCCAGACATATTCGTGTGAAC 180
QY 1372 TCAAGTTTATTCACCCAGAAAGCTCCATTTTGTCTTCAACATTTGGAATTTCTGTCT 1431
DB 181 TCAAGTTTATTCACCCAGAAAGCTCCATTTTGTCTTCAACATTTGGAATTTCTGTCT 240
QY 1432 ACTGCACAACAGAGGTTCTGCGAAGGAGATGATGACAGGCTGAGCTTGTGTT 1491
DB 241 ACTGCACAACAGAGGTTCTGCGAAGGAGATGATGACAGGCTGAGCTTGTGTT 300
QY 1492 GCTTCAGTCTTCAACCAATACATGATCCATGGAAGACAGCGGGAAGCCCTGAGCT 1551
DB 301 GCTTCAGTCTTCAACCAATACATGATCCATGGAAGACAGCGGGAAGCCCTGAGCT 360

Qy 1552 CCTAAGATATCCATCTCTCTCGAACAACAATTCTTCCACTTACCAATGACCCCTCA 1611
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Qy 1612 ATCCCCATCATATGTTGGTCCAGGAA 1639
Db 421 ATCCCCATCATATGTTGGTCCAGGAA 448

Search completed: August 27, 2005, 15:58:33
Job time : 4548.04 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 19:17:21 ; Search time 6007.21 Seconds
(without alignments)
16914.771 Million cell updates/sec

Title: US-09-371-347A-41

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2046	97.6	3241	6	COJ26091 Sequence
2	2046	97.6	3259	6	ARI44976 Sequence
3	2046	97.6	3259	6	AX050463 Sequence
4	2046	97.6	3259	9	AF025794 Homo sapi
5	2046	97.6	3291	9	AF121214 Homo sapi
6	1995	95.1	3310	9	BC054816 Homo sapi
7	1338	63.8	2933	11	BV177620 Homo sapi
8	1338	63.8	2933	11	BV178010 Homo sapi
9	386	18.4	330	6	BD077780 5' EST of
10	381	18.2	1353	9	AF121205 Homo sapi
11	330	15.7	109626	9	AC010346 Homo sapi
12	330	15.7	110756	9	AC025174 Homo sapi
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14	279	13.3	167237	2	AC021609 Homo sapi
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17	188	9.0	1034	9	AF121212 Homo sapi
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	21	161	7.7	158199	2	AC022921 Homo sapi
	22	158	7.5	1256	9	AF121208 Homo sapi
	23	158	7.5	2475	6	AR454615 Sequence
	24	158	7.5	2475	6	AX375651 Sequence
	25	155	7.4	2011	9	AF121208 Homo sapi
	26	146	7.0	2214	9	AF121208 Homo sapi
	27	125	6.0	969	9	AF121208 Homo sapi
	28	121	5.8	1119	9	AF121208 Homo sapi
	29	119	5.7	1200	9	AF121208 Homo sapi
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	33	60	2.9	60	6	CO539377 Sequence
	34	54	2.6	54	6	AX611839 Sequence
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	37	48	2.3	48	6	AX611835 Sequence
	38	47	2.3	48	6	AX611841 Sequence
	39	47	2.2	183	6	CO670532 Sequence
	40	44	2.1	650	9	AF121209 Homo sapi
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	42	38	1.8	38	6	AX611837 Sequence
	43	38	1.8	63	6	AX611834 Sequence
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ALIGNMENTS

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DEFINITION	COJ26091				
ACCESSION	COJ26091.1	GI:42288134			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE					
AUTHORS	Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.				
TITLE	Kite, such as nucleic acid arrays, comprising a majority of humenexons or transcripts, for detecting expression and other uses thereof				
JOURNAL	Patent: WO 02068579-A 12025 06-SEP-2002;				
FEATUES	PE Corporation (NY) (US)				
source	1. 3241				
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	/db_xref="taxon:9606"				
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QY	121	TCGATTAAGTAACTTAAGAAAGCAAGCTCTTGTGTGTGTTCTTACACAG	180		
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RESULT 2
ARI44976
LOCUS ARI44976 3259 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 23 from patent US 6210950.
ACCESSION ARI44976
VERSION ARI44976.1 GI:15106843
KEYWORDS
SOURCE
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3259)
AUTHORS Johnson, W.G. and Stenroos, E.Scott.
TITLE Methods for diagnosing, preventing, and treating developmental disorders due to a combination of genetic and environmental factors
JOURNAL Patent: US 6210950-A 23 03-APR-2001;
FEATURES
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ORIGIN /mol_type="unassigned DNA"

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB ATGAGAGAGGTTCTGTACTATATGCTACACAGCAGGAGCAGGCAAAAGCCATCGAGAA 139
61 GAAATATGTAGAGCAGCTGTGTACATGTATTTCTGCAGATCTTCACTGTATTAGTGA 120
DB GAAATATGTAGAGCAGCTGTGTACATGTATTTCTGCAGATCTTCACTGTATTAGTGA 199
140 GAAATATGTAGAGCAGCTGTGTACATGTATTTCTGCAGATCTTCACTGTATTAGTGA 199
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DB TCCGATATGATGACCTTAATAAACCGAAACAGCTCTCTTGTGTGTGTCTTACAG 259
200 TCCGATATGATGACCTTAATAAACCGAAACAGCTCTCTTGTGTGTGTCTTACAG 259
QY 181 GGCACCGGAGACCCACCGACACAGCCCGCAAGTTGTTAAGGAAATACAGAACAA 240
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241 CTGCCGGTGAATTTCTTGTCTCACTGCGGTATGGGTACTGSGTCTCGGTATTCAGAA 300
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440 CGGCATTTCTATGACACTGGACATGAGATGACTGTGTAGAGTTAGAACTGTGTGAG 499
QY 421 CGGTGATTTGCTGAGACTGTGCGCAGCCCTCAGAAAGCAATTTAGTCAAGCAGAGCA 480
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560 GAGAGATATAGTGGCGCACTCCCGGTGGCATCACTGACATCTTGAAGACAGACTTTG 619
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VERSION	AX050463.1				
KEYWORDS	GI:12226668				
SOURCE	.				
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.				
REFERENCE	1				
AUTHORS	Johnson, W.G. and Stenroos, E.S.				
TITLE	Methods for diagnosing, preventing, and treating developmental disorders due to a combination of genetic and environmental factors				
JOURNAL	Patent: WO 0071754-A 23 30-NOV-2000;				
	University of Medicine and Dentistry of New Jersey (US)				
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RESULT 4

AF025794

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

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 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
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 Cloning and mapping of a cDNA for methionine synthase reductase, a flavoprotein defective in patients with homocystinuria
 Proc. Natl. Acad. Sci. U.S.A. 95 (6), 3059-3064 (1998)
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LOCUS AF121214 Homo sapiens methionine synthase reductase (MTRR) mRNA, complete
DEFINITION cds.
ACCESSION AF121214
VERSION AF121214.1 GI:6561338
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Leclerc, D., Odievre, M., Wu, Q., Wilson, A., Huizenga, J.J., Rozen, R.,
Scherer, S.W., and Gravel, R.A.
TITLE Molecular cloning, expression and physical mapping of the human
methionine synthase reductase gene
JOURNAL Gene 240 (1), 75-88 (1999)
MEDLINE 20033550
PubMed 10564814
REFERENCE
AUTHORS 2 (bases 1 to 3291)
Leclerc, D., Odievre, M., Wu, Q., Wilson, A., Huizenga, J.J.,
Johns, T., Shoudridge, E.A., Rosenblatt, D.S., Scherer, S.W., Rozen, R.
and Gravel, R.A.
TITLE Direct Submision
JOURNAL Submitted (18-JAN-1999) Human Genetics, Montreal Children's
Hospital, 4060 Ste-Catherine West, Montreal, Quebec H3Z 2Z3, Canada
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RESULT 6

BC054816 3310 bp mRNA linear PRI 16-SEP-2003
LOCUS Homo sapiens 5-methyltetrahydrofolate-homocysteine
DEFINITION methyltransferase reductase, mRNA (CDNA clone IMAGE:5205285),
partial cds.

ACCESSION BC054816 GI:33392775
VERSION BC054816.1

KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 3310)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, E., Brownstein, M.J., Ueda, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J.,
Aramson, R.D., Mullaly, S.J., Bosak, S., McEwan, P.J.,
Morken, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vallalun, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Helton, E., Kettelman, W., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 3310)
AUTHORS Strauberg, R.
TITLE Direct Submission
JOURNAL Submitted (03-JUL-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbe-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhi.nih.gov
Akher, N., Ayle, K., Beckstrom-Stenberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-D., Karlins, E., Kwong, P., Lurie, P., Legaspi, R.,
Maduro, Q.L., Masello, C., Masker, B., Mestrian, S.D., McLooney, J.C.,
McDowell, J., Pearson, R., Stantrop, S., Thomas, P.J., Touchman, J.W.,
Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
Series: IRAP Plate: 115 Row: d Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4505278.

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1733 AAATCTCAAGAACCAACCCAGATGAAATTTTGAAGCAATGTGTGTTTGTGCTGC 1792
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1793 AGGCATTAAGGATTAAGATTAATCTTACAGAAAGAGCTCAACATTTCTTAAAGCATGCG 1852
1801 ATCTTAATCTCAATTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1860
1853 ATCTTAATCTCAATTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1912
1861 CCAGCAAGATATGTAACAAGACATCCAGCTTCAATGAGCAGAGTGGCGAGATCTCTC 1920
1913 CCAGCAAGATATGTAACAAGACATCCAGCTTCAATGAGCAGAGTGGCGAGATCTCTC 1972
1921 CTTCAGAGAACGCGCATTTTATGTGTGTGAGATGCAAGAAATATGSCCAAGATGTA 1980
1973 CTTCAGAGAACGCGCATTTTATGTGTGTGAGATGCAAGAAATATGSCCAAGATGTA 2032
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2033 CATGATGCTCTGTGTGAATTAATTAAGCAAGAGTGTGAGTTGAAAAATTAAGAGCAATG 2092
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RESULT 7
BV177620/c 2933 bp DNA linear STS 10-JUN-2004
LOCUS BV177620
DEFINITION egm95800 Human DNA (Sequenc) Homo sapiens STS genomic, sequence
tagged site.
ACCESSION BV177620
VERSION BV177620.1 GI:48013757
KEYWORDS STS.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2933)
AUTHORS Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
TITLE Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
JOURNAL Regions
COMMENT Genome Res. (2004) In press
Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 2933.
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1778; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
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Db 2846 CAATGGGGGAAGTAATTTAATTAACGACTTCAAGACTTGAAGCCCGGCAATTTCTATGA 2787
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Db 2786 CACTGACATGACAGATGACTGTGTAGGTTTAAACCTTGTGGTTGAGCCGTGATGCTGG 2727
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Db 2666 CGCACTCCCGGTGGCATCACTGATCTTGAAGAGAGAGACTTGTGAAGTCAAGACTGCT 2607
QY 555 ACAATTGAATCTCAAGTGAAGCTTCTGAGATTGATGATTCAGAGAAAGAAAGATTCTGA 614
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Db 1946 CAGTAAACAAAGGGGACGCGATTAAGCCGCTTGTAGAGAGATGCTGTGCTGTGTT 1887
QY 1275 GGAATCTCTCTGCTTTCCTTCTTTCGACCACTGATCTCTGCTGCAACTCT 1334
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QY 1335 TCCCTAACTTCAACCCAGACCAATTCGATGAGTGAAGTCAAGTTTATTCACCGAGAAA 1394
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QY 1455 GAAAGGATATGATACAGGCTGCTGCTGCTTGTGTTGCTTCAAGTTCTTCAAGCAAAAT 1514
Db 1706 GAAAGGATATGATACAGGCTGCTGCTGCTTGTGTTGCTTCAAGTTCTTCAAGCAAAAT 1647
QY 1515 ACATGATCCCAATGAAGAGAGAGC-GGGAAAGCCCTGCTCTTAAGATATTCATCTCTC 1573
Db 1646 ACATGATCCCAATGAAG 1587
QY 1574 GAAACAACAATTTCTTCACTTACAGATGACCCCTCAATCCCATCATATATGATGCTG 1633
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Db 1467 AACACCCAGATGGAATTTTGGAGCAATGAGTTGTTTGGCTGAGGAGATTAAGATA 1408
QY 1754 GGGATTAATCATTCAGAAAAGAGCTCAGANATTTCTTAAGCATGGGATTTTAATCATC 1813
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QY 1874 TACAAGACAACATCAGCTTCAATGACAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAG 1933
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QY 1934 GCCATATTTATGTGTGTGAGATGCAAGAAATATGAGCAAGATGATCATGATGCTCTTG 1993
Db 1227 GCCATATTTATGTGTGTGAGATGCAAGAAATATGAGCAAGATGATCATGATGCTCTTG 1168

QY 1994 TGCATAATAAAGCAAGAGTTGAGTGAAGAAAACTAGAGCAATGAAACCCTGCGCA 2053
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DB 1107 CTTTAAAGAGAAAAAGCTTACCTTCAGGATTTTGTGATTA 1064

RESULT 8
BV178010/c 2933 bp DNA linear STS 10-JUN-2004
LOCUS sqm97986 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
DEFINITION tagged site.
ACCESSION BV178010 GI:48014252
VERSION BV178010.1 GI:48014252
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2933)
Nelson,R.M., Marnellob,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
Cantor,C.R. and Braun,A.
Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
Genome Res. (2004) In press

JOURNAL
COMMENT Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 2933.

FEATURES
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ORIGIN
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Query Match 63.8%; Score 1338; DB 11; Length 2933;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1778; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 315 CAATGGGGGAGATTAATGATTAACGACTTCAAGAGCTTGGAGCCCGCATTTCTATGA 374
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QY 375 CACTGACATGACGATGACGTGTAGTGTAGAACTTGTGTGAGCCGATGCTGCTG 434
DB 2786 CACTGACATGACGATGACGTGTAGTGTAGAACTTGTGTGAGCCGATGCTGCTG 2727
QY 435 ACTCTGGCCAGCCCTCAGAAAGCAATTTAGTCAAGCAGAGCAAGAGAGATTAAGTG 494
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QY 1694 AACACCCAGATGAATTTTGAAGCAATGAGTGTGTTTGGCTGAGGCAATAGATTA 1753
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QY	1934	GCCATATTATATGTGTGTGGAGATATGCAAGAACTAATGGCAAGATGTAATATATCCTTG	1993
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Db	1167	TGCAAAATATATAGCAAAAGAGGTGGAGTTGAAAACTAGAAAGCATGAAAACTCTGGCCA	1108
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RESULT 9	BD077780	390 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD077780				
DEFINITION	5'EST of secretory protein in brain.				
ACCESSION	BD077780				
VERSION	BD077780.1	GI:2262383			
KEYWORDS	JP 2001512015-A/65.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 390)				
TITLE	Edwards,J.B.D.M., Ducleert,A. and Lacroix,B.				
JOURNAL	5'EST of secretory protein in brain				
	Patent: JP 2001512015-A 65 21-AUG-2001;				
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COMMENT	OS	Homo sapiens (human)			
	PN	JP 2001512015-A/65			
	PD	21-AUG-2001			
	PF	31-JUL-1998 JP 2000505293			
	PR	01-AUG-1997 US 08/905223			
	PI	JEAN BAPTISTE DUMAS MILNE EDWARDS, AYMERIC DUCLEERT, BRUNO LACROIX			
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Matches 386;	Conservative	0;	Mismatches	0;	Indels
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QY	1030	AAATTAAGGCAGACACAAAGAAAGAGAGTACTTACCCAGCATATATCTTCGGGA	1088		
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QY	1090	TGTTCTCTCAGATTCAATTTTAACTGGTGTCTTGAATCCGACAATTCCTAAAGGCA	1149
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QY	1210	CTGCGAGTAAACAAGGGGAGCGAGTAAAGCCGCTTTGTACAGATGCGCTGCTGC	1269
Db	243	CTGTGAGTAAACAAGGGGAGCGAGTAAAGCCGCTTTGTACAGATGCGCTGCTGC	302
QY	1270	TGTGTGATCTCCTCTCGCTTTCCTTTCTTGCGAGCAGCACTCACTCTTCGCTCGAA	1329
Db	303	TGTGTGATCTCCTCTCGCTTTCCTTTCTTGCGAGCAGCACTCACTCTTCGCTCGAA	362
QY	1330	CATCTTCTTAACTCTCAACCCAGACC	1355
Db	363	CATCTTCTTAACTCTCAACCCAGACC	388

RESULT	10
LOCUS	F121202S04 1353 bp DNA linear PRI 14-DEC-1999
DEFINITION	Homo sapiens methionine synthase reductase (MTRR) gene, exon 5.
ACCESSION	AF121205
VERSION	AF121205.1 GI:6572530
KEYWORDS	.
SOURCE	4 of 12
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1353) Leclerc,D., Odievre,M., Wu,Q., Wilson,A., Huizenga,J.J., Rozen,R., Scherrer,S.W. and Gravel,R.A. Molecular cloning, expression and physical mapping of the human methionine synthase reductase gene Gene 240 (1), 75-88 (1999)
AUTHORS	
TITLE	
JOURNAL	
MEDLINE	20033550
PUBMED	10564814
REFERENCE	2 (bases 1 to 1353) Leclerc,D. Direct Submission Submitted (20-JAN-1999) Human Genetics, Montreal Children's Hospital, 4060 Ste-Catherine West, Montreal, Quebec H3Z 2Z3, Canada
FEATURES	Location/Qualifiers 1..1353 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="5" /map="5p15.2-p15.3; between W1755 and D5S1957" 358..736 /gene="MTRR" /number=5
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Dd	417 TTAGGTCAAGAGAGACAAGAGAGATAATGTGGCGCACTCCCGGTGGCATCACCTGCAT 476
Oy	521 CCTTAGAGACAGACCTTGTGAAGTCAGAGCTGCTACACATTGAATTCACATCGAGCTTC 580

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Qy 581 TGAATTCATGATGATTCAGAGAAAGAAATTCAGGTTTGAAGCAAAATGACAGTAACA 640
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LOCUS Homo sapiens chromosome 5 clone C17B-H1_201852, complete sequence.
AC010346 GI:11336705
DEFINITION HTG.
ACCESSION Homo sapiens (human)
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
DOE Joint Genome Institute and Stanford Human Genome Center.
REFERENCE
AUTHORS Unpublished
TITLE 2 (bases 1 to 109626)
DOE Joint Genome Institute.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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DOE Joint Genome Institute and Stanford Human Genome Center.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (10-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
JOURNAL Drive, Walnut Creek, CA 94598, USA
On Nov 10, 2000 this sequence version replaced gi:9256196.
COMMENT Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
SFS Content:
WI-9255 G05749.

FEATURES

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Db 88571 GTTTAGAACTTGTGTTGAGCCGTGATTCCTGAGACTTGCCAGCCCTCAGAAAGCAT 88630
Qy 461 TTGAGTCACAGACAGACAGAGAGATTAAGTGGCGCATCTCCGGTGGCATCACTGCAT 520
Db 88631 TTGAGTCACAGACAGACAGAGAGATTAAGTGGCGCATCTCCGGTGGCATCACTGCAT 88690

Qy 521 CCTTGAAGACAGACCTTGTGAAGTCAAGAGCTGCTACATTTGAATCTCAAGTCAGCTTC 580
Db 88691 CCTTGAAGACAGACCTTGTGAAGTCAAGAGCTGCTACATTTGAATCTCAAGTCAGCTTC 88750
Qy 581 TGAATTCATGATGATTCAGAGAAAGAAATTCAGGTTTGAAGCAAAATGACAGTAACA 640
Db 88751 TGAATTCATGATGATTCAGAGAAAGAAATTCAGGTTTGAAGCAAAATGACAGTAACA 88810
Qy 641 GCAACCAATCCAAATGTTGAATTAATTAAGACTTTGAGTCTCACTTACCCGTTGGTAACCC 700
Db 88811 GCAACCAATCCAAATGTTGAATTAATTAAGACTTTGAGTCTCACTTACCCGTTGGTAACCC 88870
Qy 701 CACTCTCACAAGCCTCTCTGAATATTCCTGTTTACCCCAAGATTTTACAGTATC 760
Db 88871 CACTCTCACAAGCCTCTCTGAATATTCCTGTTTACCCCAAGATTTTACAGTATC 88930
Qy 761 TGCAGAGTCTCTTGGCCAGG 781
Db 88931 TGCAGAGTCTCTTGGCCAGG 88951

RESULT 12
AC025174 110756 bp DNA linear PRI 28-MAR-2002
LOCUS Homo sapiens chromosome 5 clone CTD-2072124, complete sequence.
AC025174
DEFINITION HTG.
ACCESSION Homo sapiens (human)
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE 1 (bases 1 to 110756)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
DOE Joint Genome Institute and Stanford Human Genome Center.
REFERENCE
AUTHORS Unpublished
TITLE 2 (bases 1 to 110756)
DOE Joint Genome Institute.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 110756)
DOE Joint Genome Institute.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 110756)
DOE Joint Genome Institute and Stanford Human Genome Center.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (28-MAR-2002) DOE Joint Genome Institute, 2800 Mitchell
JOURNAL Drive, Walnut Creek, CA 94598, USA
On Mar 28, 2002 this sequence version replaced gi:19224767.
COMMENT Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.

FEATURES

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/chromosome="5"
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Best Local Similarity 99.7%; Pred. No. 1.6e-168; Indels 0; Gaps 0;
Matches 380; Conservative 0; Mismatches 1;
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Db	20040	GTATTGAACTTTGGTGTGACCCCGGATTCGTGACCTCGGCCAGCCCTCAGAAAGCANT	20093
Qy	461	TTAGGTAAAGCAGAGCAAGAGAGATTAAGTGGCCGACTCCCGGTGGCATCACTGGCAT	520
Db	20100	TTTAGTTCAMCAGAGGCAAGAGAGATTAAGTGGCCGACTCCCGGTGGCATCACTGGCAT	20159
Qy	521	CCTTGAGGACAGACCTTGTGAAGTCAGAGGTGCTACACATTGAAATCTCAAGTCGAGCTTC	580
Db	20160	CTTCGAGGACAGACCTTGTGAAGTCAGAGGTGCTACACATTGAAATCTCAAGTCGAGCTTC	20219
Qy	581	TGAGATTGATGATTCAGAGAAAGGATTCAGAGGTTTGAAGCAAAATGCAGTGACAA	640
Db	20220	TGAGATTGATGATTCAGAGAAAGGATTCAGAGGTTTGAAGCAAAATGCAGTGACAA	20279
Qy	641	GCAACCAATCAATGTTGTATTTGAAAGACTTGAAGTCCTCACTTACCCTGGTGATACCC	700
Db	20280	GCAACCAATCAATGTTGTATTTGAAAGACTTGAAGTCCTCACTTACCCTGGTGATACCC	20339
Qy	701	CACCTCAGAAAGCCTCCTGAATTCCTGGTTCATCCCGAGAAATTTTACAGGTACATC	760
Db	20340	CACCTCAGAAAGCCTCCTGAATTCCTGGTTCATCCCGAGAAATTTTACAGGTACATC	20399
Qy	761	TGCAGAGATCTCTTGGCCAGG	781
Db	20400	TGCAGAGATCTCTTGGCCAGG	20420
RESULT 13	AC022921	158199 bp	DNA linear HTG 12-MAR-2000
LOCUS	AC022921	Homo sapiens clone RP11-1388P20, WORKING DRAFT SEQUENCE, 12	
DEFINITION	AC022921	unordered pieces.	
ACCESSION	AC022921.2	GI:7229868	
VERSION	AC022921.2	GI:7229868	
KEYWORDS	HTG; HTGS PHASE1; HTGS _DRAFT.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 158199)		
TITLE	Birren,B., Linton,L., Nuebaum,C. and Lander,E.		
JOURNAL	Homo sapiens, clone RP11-1388P20		
REFERENCE	2 (bases 1 to 158199)		
AUTHORS	Birren,B., Linton,L., Nuebaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barra,N., Beckert,J., Bida,F., Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G., Castle,A., Choepel,J., Collangelo,M., Collins,S., Collimore,A., Cooke,P., DeArrelano,K., Dewar,K., Domino,M., Doyle,M., Fenebor,J., Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galsgan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Landers,T., Lehoczy,J., Levine,R., Iien,C., Liu,G., Locke,K., Macdonald,P., Margulis,N., McEwan,P., McGurk,A., McKernan,K., McPheters,R., Melgrim,J., Meneus,L., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K., Pierre,N., Pisanl,C., Pollars,V., Raymond,C., Riley,R., Rothman,D., Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J., Zimmet,A. and Zody,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (07-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
COMMENT	On Mar 12, 2000 this sequence version replaced gi:6921909. All repeats were identified using RepeatMasker: smtl, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html		
	----- Genome Center		
	Center: Whitehead Institute/ MIT Center for Genome Research		
	Center code: WITB		
	Web site: http://www-seq.wi.mit.edu		
	Contact: sequence_submissions@genome.wi.mit.edu		

	Project Information
	Center project name: L6314
	Center Clone name: L38_P_20
	Summary Statistics
	Sequencing Vector: M13; M77815; 100% of reads
	Chemistry: Dye-terminator Big Dye; 100% of reads
	Assembly program: Phrap; version 0.960731
	Consensus quality: 152636 bases at least Q40
	Consensus quality: 155474 bases at least Q30
	Consensus quality: 156388 bases at least Q20
	Insert size: 178000; agarose-fp
	Insert size: 157099; sum-of-contigs
	Quality coverage: 4.4 in Q20 bases; agarose-fp
	Quality coverage: 5.0 in Q20 bases; sum-of-contigs

	* NOTE: This is a 'working draft' sequence. It currently
	* consists of 12 contigs. The true order of the pieces
	* is not known and their order in this sequence record is
	* arbitrary. Gaps between the contigs are represented as
	* runs of N, but the exact sizes of the gaps are unknown.
	* This record will be updated with the finished sequence
	* as soon as it is available and the accession number will
	* be preserved.
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	1 1283: contig of 1283 bp in length
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	1284 1383: gap of 100 bp
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	1384 4203: contig of 2820 bp in length
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	4204 4503: gap of 100 bp
	*
	4304 6786: contig of 2483 bp in length
	*
	6787 6886: gap of 100 bp
	*
	6887 9683: contig of 2797 bp in length
	*
	9684 9783: gap of 100 bp
	*
	9784 12802: contig of 3119 bp in length
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	12903 13002: gap of 100 bp
	*
	13003 16429: contig of 3427 bp in length
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	16430 16529: gap of 100 bp
	*
	16530 25501: contig of 8672 bp in length
	*
	25502 25501: gap of 100 bp
	*
	25502 36759: contig of 11458 bp in length
	*
	36760 36859: gap of 100 bp
	*
	36860 53921: contig of 17062 bp in length
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	53922 54021: gap of 100 bp
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	54022 72054: contig of 18033 bp in length
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	72055 72154: gap of 100 bp
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	72155 102527: contig of 30373 bp in length
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	102528 102627: gap of 100 bp
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	/note="assembly_fragment"
misc_feature	4304..6786
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misc_feature	6887..9683
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	9784..12902
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misc_feature	13003..16429
	/note="assembly_fragment"
misc_feature	16530..25201
	/note="assembly_fragment"
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	/note="assembly_fragment"

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ORIGIN
Query Match      13.3%; Score 279; DB 2; Length 158199;
Best Local Similarity 99.5%; Pred. No. 1,3e-140;
Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTTAAGACTTGTGTTGAGCCGTGATTCCTGACTCTGGCCAGCCCTTGAAGACATT 460
DB 3446 GTTTAAGACTTGTGTTGAGCCGTGATTCCTGACTCTGGCCAGCCCTTGAAGACATT 3505
QY 461 TTAGTCAAGCAGAGGCAAGAGAGATAGTGGCGCACTCCGGTGGCATCCTGACAT 520
DB 3506 TTAGTCAAGCAGAGGCAAGAGAGATAGTGGCGCACTCCGGTGGCATCCTGACAT 3565
QY 521 CCTTGAAGCAGAGCCTTGTGAGTCAAGCTGCTACACATTGAATCTCAAGTCGACTTC 580
DB 3566 CCTGAGAGCAGAGCCTGCTGAGTCAAGCTGCTACACATTGAATCTCAAGTCGACTTC 3625
QY 581 TGAGATTGATGATTCAGAGAAAGAGATTCTGAGGTTTGAAGCAAAATGCAGTGAACA 640
DB 3626 TGAGATTGATGATTCAGAGAAAGAGATTCTGAGGTTTGAAGCAAAATGCAGTGAACA 3685
QY 641 GCACCAATCCATGTTGTAATGAAGACTTGAATCCTCACTTACCCGTTGGTACCCC 700
DB 3686 GCACCAATCCATGTTGTAATGAAGACTTGAATCCTCACTTACCCGTTGGTACCCC 3745
QY 701 CACTCTCAGAGCCTCTCTGATATTCCTGTTTACCCCGAATATTTACAGGTACATC 760
DB 3746 CACTCTCAGAGCCTCTCTGATATTCCTGTTTACCCCGAATATTTACAGGTACATC 3805
QY 761 TGCAGAGTCTCTTGGCCAGG 781
DB 3806 TGCAGAGTCTCTTGGCCAGG 3826

RESULT 14
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LOCUS      Homo sapiens clone RP11-259D10, WORKING DRAFT SEQUENCE, 6 unordered
DEFINITION      pieces.
AC021609      AC021609.3      GI:7230210
VERSION      HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 167237)
Biren,B., Linton,L., Nuebaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Bede,P.,
Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G., Castle,A.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
Dearellano,K., Dewar,K., Dominko,M., Doyle,M., Fenesfor,J.,
Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heatford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kam,L., Kartas,A., Klein,J.,
Landers,T., Lenoczky,J., Levine,R., Liu,C., Liu,G., Locke,K.,
Macdonald,P., Margulis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrum,J., Menus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,

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TITLE
JOURNAL
COMMENT
Roy,A., Santor,R., Severy,P., Spencer,B., Strange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A., and Zody,M.
Direct Submission
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 12, 2000 this sequence version replaced gi:689697.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green,P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: http://www-seg.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 259 D 10
Center clone name: 259 D 10
----- Summary Statistics
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 161183 bases at least Q40
Consensus quality: 164380 bases at least Q30
Consensus quality: 165590 bases at least Q20
Insert size: 164000; agarose-fp
Insert size: 166737; sum-of-ctnigs
Quality coverage: 5.1 in Q20 bases; sum-of-ctnigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 3656: contig of 3656 bp in length
* 3657 3756: gap of 100 bp
* 3757 9436: contig of 5680 bp in length
* 9437 9536: gap of 100 bp
* 9537 27768: contig of 18222 bp in length
* 27769 27868: gap of 100 bp
* 27869 52058: contig of 24190 bp in length
* 52059 80100: gap of 100 bp
* 80101 80200: contig of 27942 bp in length
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ORIGIN

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 Best Local Similarity 99.5%; Pred. No. 1.3e-140;
 Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTTGTTGAGCCGTGATTTGCTGACCTTGCCAGCCCTCAGAAAGCATT 460
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 DB 62083 GTTTAGAACTTTGTTGAGCCGTGATTTGCTGACCTTGCCAGCCCTCAGAAAGCATT 62142

QY 461 TTGAGTCAGACAGACAGACAGAGAGATTAAGTGGCGGACCTCCCGTGACATCCTTCAT 520
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 DB 62143 TTGAGTCAGACAGACAGACAGAGATTAAGTGGCGGACCTCCCGTGACATCCTTCAT 62202

QY 521 CCTTGAAGACAGACCTTTGTGAAGTCAGAGCTGCTACACATTGAATCTCAAGTCAGCTTC 580
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 DB 62203 CCTTGAAGACAGACCTTTGTGAAGTCAGAGCTGCTACACATTGAATCTCAAGTCAGCTTC 62262

QY 581 TGAGATTCGATGATTCAGAAAGAAAGATTTCTGAGGTTTGAAGCAAAATGCACTGAACA 640
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 DB 62263 TGAGATTCGATGATTCAGAAAGAAAGATTTCTGAGGTTTGAAGCAAAATGCACTGAACA 62322

QY 641 GCAACCAATCAATGTTGTAATTGAAGACTTGAAGCTGCTACCTACCCGTTGGTACCCC 700
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 DB 62323 GCAACCAATCAATGTTGTAATTGAAGACTTGAAGCTGCTACCTACCCGTTGGTACCCC 62382

QY 701 CACTTCACAGACCTCTCTGATATTCCTGTTTACCCCGAGATATTTACAGGTATC 760
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 DB 62383 CACTTCACAGACCTCTCTGATATTCCTGTTTACCCCGAGATATTTACAGGTATC 62442

QY 761 TGCAGAGGTCTCTTGGCCAG 781
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 DB 62443 TGCAGAGGTCTCTTGGCCAG 62463

RESULT 15
 AC091945 177596 bp DNA linear HTG 09-JUN-2001
 LOCUS AC091945 Homo sapiens chromosome 5 clone RP11-35616, WORKING DRAFT SEQUENCE,
 DEFINITION 27 unordered pieces.
 AC091945
 VERSION AC091945.1 GI:14333881
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS DOE Joint Genome Institute.
 TITLE Unpublished
 JOURNAL 2 (bases 1 to 177596)
 REFERENCE DOE Joint Genome Institute.
 AUTHORS Direct Submission
 JOURNAL Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 COMMENT
 -----Genome Center
 Center: Joint Genome Institute
 Center Code: JGI
 Web site: http://www.jgi.doe.gov

 Project Information
 Center Project Name: 543267
 Center Clone Name: RP11-35616

 Summary Statistics
 Consensus quality: 152700 bases at least Q40
 Consensus quality: 168451 bases at least Q30
 Consensus quality: 170419 bases at least Q20
 Estimated insert size: 226080; agarose-fp estimation
 Estimated insert size: 174966; sum-of-contigs estimation
 Quality coverage: 7.75 in Q20 bases; agarose-fp estimation
 Quality coverage: 10.01 in Q20 bases; sum-of-contigs estimation.

NOTE: This is a 'working draft' sequence. It currently
 * consists of 27 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of 'N', but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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 1208 1307: gap of unknown length
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 5654 7030: contig of 1377 bp in length
 7031 7130: gap of unknown length
 7131 9069: contig of 1939 bp in length
 9070 9159: gap of unknown length
 9160 11452: contig of 2283 bp in length
 11453 11552: gap of unknown length
 11553 16002: contig of 4450 bp in length
 16003 16102: gap of unknown length
 16103 21083: contig of 4981 bp in length
 21084 21883: gap of unknown length
 21884 26893: contig of 5710 bp in length
 26894 26993: gap of unknown length
 26994 30087: contig of 2994 bp in length
 30088 32949: gap of unknown length
 32950 33049: gap of unknown length
 33050 38757: contig of 5708 bp in length
 38758 38857: gap of unknown length
 38858 45202: contig of 6345 bp in length
 45203 45302: gap of unknown length
 45303 50911: contig of 5609 bp in length
 50912 51012: gap of unknown length
 51012 55880: contig of 4865 bp in length
 55881 55980: gap of unknown length
 55981 63189: contig of 7209 bp in length
 63190 63289: gap of unknown length
 63290 66332: contig of 6343 bp in length
 66333 69733: gap of unknown length
 69734 76377: contig of 6645 bp in length
 76378 76477: gap of unknown length
 76478 83051: contig of 6574 bp in length
 83052 83151: gap of unknown length
 83152 94929: contig of 11778 bp in length
 94930 95029: gap of unknown length
 95030 104346: contig of 9317 bp in length
 104347 104446: gap of unknown length
 104447 115275: contig of 10829 bp in length
 115276 115376: gap of unknown length
 115377 123488: contig of 8113 bp in length
 123489 123588: gap of unknown length
 123589 133172: contig of 9584 bp in length
 133173 133272: gap of unknown length
 133273 145495: contig of 12223 bp in length
 145496 145595: gap of unknown length
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FEATURES
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ORIGIN

Query Match 13.3%; Score 279; DB 2; Length 177596;
 Best Local Similarity 99.5%; Pred. No. 1.3e-140;

Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 461 TTAGGTCAAGCAGAGGACAAGAGAGATTAAGTGGCGCACTCCCGGTGGCATCACTGCAT 520
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Db 83584 TTAGGTCAAGCAGAGGACAAGAGAGATTAAGTGGCGCACTCCCGGTGGCATCACTGCAT 83643
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QY 521 CCTTGGAGCAGACCTTGTGAAGTCAAGCTGCTACACATTAATCTCAAGTGCAGCTTC 580
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Db 83644 CCTCGAGGACAGACCTGTGAAGTCAAGCTGCTACACATTAATCTCAAGTGCAGCTTC 83703
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QY 701 CACTCTCAAGGCTCTCTGAATATTCCTGTTTACCCTCCAGAAATTTTACAGGTACATC 760
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QY 761 TGCAGGAGTCTCTTGGCCAGG 781
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Db 83884 TGCAGGAGTCTCTTGGCCAGG 83904
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 13:32:20 ; Search time 733.49 Seconds
(without alignment)
16924.161 Million cell updates/sec

Title: US-09-371-347A-41

Perfect score: 2097
Sequence: 1 atgagggaggttcctact.....ctcagatattgtgcataa 2097

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq16Dec04:*
1: geneseqn1980s:*
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12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2094	99.9	2094	11	ADM43209 Human met
2	2046	97.6	3259	5	AA65070 DNA encod
3	2046	97.6	3259	5	AA65070 DNA encod
4	2046	97.6	3259	5	AA65070 DNA encod
5	2043	97.4	2094	11	ADM43206 Human bch
6	1995	95.1	3270	13	ADM43208 Human wll
7	1992	95.0	2094	11	ADM43212 Human met
8	1944	92.7	3259	3	AA58935 DNA encod
9	1800	85.8	2091	11	ADM43216 Human met
10	1800	85.8	2091	11	ADM43216 Human met
11	1701	81.1	3256	3	AA58977 A human m
12	1640	78.2	3255	3	AA58976 A human m
13	1062	50.6	3256	13	ADG39029 Human SNP
14	1062	50.6	3274	13	ADG39030 Human SNP
15	1007	48.0	3189	4	ACM42470 Human dia
16	805	38.4	1986	4	AA61064 CDNA enco
17	427	20.4	1663	4	AA61062 CDNA enco
18	366	18.4	390	2	AA61062 CDNA enco
19	330	15.7	591	12	ACH73174 Human gen
20	328	15.6	379	12	ACH86905 Human gen

21	279	13.3	591	12	ACH68540 Human gen
22	277	13.2	379	12	ACH82240 Human gen
23	225	10.7	503	5	AA65069 DNA encod
24	188	9.0	525	12	ACH67438 Human gen
25	175	8.3	175	12	ACH81143 Human gen
26	158	7.5	2475	6	AD32365 Human jun
27	158	7.5	2475	13	AD161720 Human gen
28	137	6.5	525	12	ACH73117 Human gen
29	124	5.9	175	12	ACH68848 Human gen
30	65	3.1	244	3	AA242736 Human 5'
31	60	2.9	60	6	ABN36264 Human bpl
32	52	2.5	1835	5	AA65071 DNA encod
33	51	2.4	51	4	AA178548 Human b11
34	30	1.4	1681	11	AD131127 Human CDN
35	26	1.2	26	3	AA58955 PCR prime
36	26	1.2	26	3	AA58939 PCR prime
37	26	1.2	26	6	ABX09549 Arteriosc
38	26	1.2	26	6	AA143713 Ptegestat
39	26	1.2	26	11	ADM43205 Human met
40	26	1.2	26	11	ADM43189 Human met
41	25	1.2	25	3	AA58952 PCR prime
42	25	1.2	25	3	AA58937 PCR prime
43	25	1.2	25	3	AA58947 PCR prime
44	25	1.2	25	11	ADM43187 Human met
45	25	1.2	25	11	ADM43202 Human met

ALIGNMENTS

RESULT 1	ADM43209	standard; CDNA; 2094 BP.
ID	ADM43209	standard; CDNA; 2094 BP.
XX	ADM43209;	
AC	03-JUN-2004 (first entry)	
DT	Human methionine synthase reductase CDS G66A variant.	
XX	Human; sb; Methionine synthase reductase polypeptide; HsMTRR; cancer;	
KW	cardiovascular disease; neural tube defect; hyperhomocysteinemia;	
KW	chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	Key	Location/Qualifiers
FT	CDS	1..2094
FT		/*tag= a
FT		/product= "HsMTRR"
FT		/partial
FT		/note= "No stop codon shown"
FT	variation	replace(66,G)
FT		/*tag= b
FT	variation	/standard_name= "Single_nucleotide_polymorphism"
FT		replace(110,A)
FT		/*tag= c
FT		/standard_name= "Single_nucleotide_polymorphism"
PN	US2003082676-A1.	
XX	01-MAY-2003.	
PD		
XX	10-AUG-1999;	99US-00371347.
XX		
XX	16-JAN-1998;	98US-0071622P.
PR	15-JAN-1999;	99US-00232028.
XX		
PA	(GRAV/) GRAVEL R. A.	
PA	(ROZE/) ROZEN R.	
PA	(LECL/) LECLERC D.	
PA	(WILS/) WILSON A.	
PA	(ROSE/) ROSENBLATT D.	

XX Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
PI
XX WPI; 2003-5/76610/54.
DR
DR P-PSDB; ADM43211.
XX
XX
PT New substantially pure nucleic acid encoding a mammalian methionine
PT synthase reductase polypeptide, useful for diagnosing, preventing or
PT treating conditions associated with altered methionine synthase activity,
PT e.g. cancer.

Claim 3; SEQ ID NO 41; 26pp; English.

The invention relates to a substantially pure nucleic acid that encodes a mammalian methionine synthase reductase polypeptide, HmSTR, or that hybridizes at high stringency to a nucleic acid appearing as ADW43208 or ADW43309. Also included are a non-human animal where one or both genetic alleles encoding the methionine synthase reductase polypeptide are mutated, an antibody that specifically binds the above methionine synthase reductase polypeptide, a method of detecting the presence of the above polypeptide, a method for detecting sequence variants for methionine synthase reductase in a mammal, methods of treating or preventing cancer (or cardiovascular disease or neural tube defects) in a subject, methods of screening for a compound that modulates methionine synthase reductase biological activity and a method for detecting an increased risk of developing a neural tube defect in a mammalian embryo or foetus. The nucleic acid is useful in diagnosing, preventing or treating conditions associated with altered methionine synthase activity, such as cancer, cardiovascular disease or neural tube defects, or in screening for a compound that modulates methionine synthase reductase biological activity. Naturally occurring variants of the polypeptide are also associated with hyperhomocysteinemia. The gene for HmSTR is located on chromosome 5p15.2-p15.3. The present sequence is the coding sequence of a variant human HmSTR cDNA.

SQ Sequence 2094 BP; 592 A; 489 C; 480 G; 533 T; 0 U; 0 Other;

Query Match	Score	DB	Length
99.9%	2094	11	2094

Matches 2094; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATAGAGAGGTTCTGTGTACTAATGTGTAACAAGCAGGGAACGGCAATGGCAAA	60
Dp	1	ATAGAGAGGTTCTGTGTACTAATGTGTAACAAGCAGGGAACGGCAATGGCAAA	60
Qy	61	GAATATGTGAGCAAGCTGTGTACATGAGATTTCTGAGATCTCACTGTATTAGTAA	120
Dp	61	GAATATGTGAGCAAGCTGTGTACATGAGATTTCTGAGATCTCACTGTATTAGTAA	120
Qy	121	TCCGATTAAGTATGACTTAATAAACCGAAACAGCTCCTCTTGTGTGTGTGTTTCAACA	180
Dp	121	TCCGATTAAGTATGACTTAATAAACCGAAACAGCTCCTCTTGTGTGTGTGTTTCAACA	180
Qy	181	GGCACCAGAGACCCACCCGACACAGCCGGCAAGTTGTTAAGGAATACAGAACCAAA	240
Dp	181	GGCACCAGAGACCCACCCGACACAGCCGGCAAGTTGTTAAGGAATACAGAACCAAA	240
Qy	241	CTGCCGGTGAATTTCTTTGCTCACTGCGGTATGGGTTACTGGGTCGGTGATTCGAA	300
Dp	241	CTGCCGGTGAATTTCTTTGCTCACTGCGGTATGGGTTACTGGGTCGGTGATTCGAA	300
Qy	301	TACACCTACTTTTGCAATGGGGGGAAGATATTGATTAACCACTTCAGACTTGGAGCC	360
Dp	301	TACACCTACTTTTGCAATGGGGGGAAGATATTGATTAACCACTTCAGACTTGGAGCC	360
Qy	361	CGGCAATTTCTATGACACTGACCATGTGAGATGACTGTGTATGAACTGTGGTTGAG	420
Dp	361	CGGCAATTTCTATGACACTGACCATGTGAGATGACTGTGTATGAACTGTGGTTGAG	420
Qy	421	CCGTGATTTGCTGGACTCTGCGCAGCCCTCAAGAAACATTTTAGGTCAGACAGACAA	480
Dp	421	CCGTGATTTGCTGGACTCTGCGCAGCCCTCAAGAAACATTTTAGGTCAGACAGACAA	480

QY	481	AAGAGATTAAGTGGCGCACTCCGGGTGGCATACCTGCACTCTTGAGACAGACCTTGTG	540
Db	481	GAGAGATTAAGTGGCGCACTCCGGGTGGCATACCTGCACTCTTGAGACAGACCTTGTG	540
QY	541	AAGTCAGAGCTGCATACATTTGAATCTCAAGTCGAGCTTCTGAGATTGATTCATTCAGAA	600
Db	541	AAGTCAGAGCTGCATACATTTGAATCTCAAGTCGAGCTTCTGAGATTGATTCATTCAGAA	600
QY	601	AGAAAGATTTCTGAGTTTGGAGCAAAATGCAGTGAACAGCAACCAATCCATGTTGTGA	660
Db	601	AGAAAGATTTCTGAGTTTGGAGCAAAATGCAGTGAACAGCAACCAATCCATGTTGTGA	660
QY	661	ATTGAAGACTTTGAGTCCCTCACTTAAACCCGTTCCGTACCCCACTCTCAAGAGCTCTCTG	720
Db	661	ATTGAAGACTTTGAGTCCCTCACTTAAACCCGTTCCGTACCCCACTCTCAAGAGCTCTCTG	720
QY	721	AATATTCCTGGTTTAAACCCCGAATATTTTACAGGTACATCTGCAGAGAGTCTCTTGGCAG	780
Db	721	AATATTCCTGGTTTAAACCCCGAATATTTTACAGGTACATCTGCAGAGAGTCTCTTGGCAG	780
QY	781	GAGAAAAGCCAAAGTATCTGACTTCAGCAAGATCAAGTCTTTCAGAGTCCCAATTTTCAAG	840
Db	781	GAGAAAAGCCAAAGTATCTGACTTCAGCAAGATCAAGTCTTTCAGAGTCCCAATTTTCAAG	840
QY	841	GCACTTCACTTACTACGAATGATGCCATATAAAAACACTGCTGCTGATGAATTTGAGACTT	900
Db	841	GCACTTCACTTACTACGAATGATGCCATATAAAAACACTGCTGCTGATGAATTTGAGACTT	900
QY	901	TCAATATCAGACTTTTCTCTATCAGCTCGAGATCCCTTACGCGTGAATCTGCCCTAACGT	960
Db	901	TCAATATCAGACTTTTCTCTATCAGCTCGAGATCCCTTACGCGTGAATCTGCCCTAACGT	960
QY	961	GATTCCTGAGGTACAAAGCCTTACTCACAAGACTGCAAGCTTGAAGATTAAGAAGACACTGC	1020
Db	961	GATTCCTGAGGTACAAAGCCTTACTCACAAGACTGCAAGCTTGAAGATTAAGAAGACACTGC	1020
QY	1021	GTCCTTTTGAATAATTAAGGCGAGACACAAGAAGAAAGAGACTACTTACCCCGACATATA	1080
Db	1021	GTCCTTTTGAATAATTAAGGCGAGACACAAGAAGAAAGAGACTACTTACCCCGACATATA	1080
QY	1081	CCTCGCGGAGTGTCTCCAGTTCATTTTAACTGGGTCTTGAATCCGAGCAATTCCT	1140
Db	1081	CCTCGCGGAGTGTCTCCAGTTCATTTTAACTGGGTCTTGAATCCGAGCAATTCCT	1140
QY	1141	AAAAAGCATTTTTCGAGCCCTTGTGACTATACAGTACAGTGTCTGAAGACGCGAGG	1200
Db	1141	AAAAAGCATTTTTCGAGCCCTTGTGACTATACAGTACAGTGTCTGAAGACGCGAGG	1200
QY	1201	CTACAGAGCTGTGCAGTAAACAAGGGGCGAGCCGATTATAGCCGCTTTGTATCGAGATGCC	1260
Db	1201	CTACAGAGCTGTGCAGTAAACAAGGGGCGAGCCGATTATAGCCGCTTTGTATCGAGATGCC	1260
QY	1261	TGTGCCGTGTGTGGATCTCCCTCCGTGCCCTTCCCTCTTGCGACGCCACATCAGCTC	1320
Db	1261	TGTGCCGTGTGTGGATCTCCCTCCGTGCCCTTCCCTCTTGCGACGCCACATCAGCTC	1320
QY	1321	CTGCTCGAACACTTCTCTTAAACTTCAACCCAGACCAATATCGTGTGCAACTCAGTTTA	1380
Db	1321	CTGCTCGAACACTTCTCTTAAACTTCAACCCAGACCAATATCGTGTGCAACTCAGTTTA	1380
QY	1381	TTTTCACCCAGAAAGCTTCATTTTGTCTTCAACATGTGTGAATTTCTGTCTACGTGCACA	1440
Db	1381	TTTTCACCCAGAAAGCTTCATTTTGTCTTCAACATGTGTGAATTTCTGTCTACGTGCACA	1440
QY	1441	ACAAAGGTTCTGCGGAAAGGAGATATGACAGGCTGTGCGCTTGTGTGCTTCAGTT	1500
Db	1441	ACAAAGGTTCTGCGGAAAGGAGATATGACAGGCTGTGCGCTTGTGTGCTTCAGTT	1500
QY	1501	CTTACAGCAAAACAATACATGCCATCCATGAAAGACAGCGGAAAGGCCCTGCTCCTTAAGATA	1560
Db	1501	CTTACAGCAAAACAATACATGCCATCCATGAAAGACAGCGGAAAGGCCCTGCTCCTTAAGATA	1560
QY	1561	TCCATCTCTCCGACACAATAATCTTTCACCTTACAGATGACCCCTCAATCCCATC	1620

Db	1561	TCGATCTCTCCTCGAACAACAAATTTCTTTCACATTAACGATGACCCCTCAATCCCATC	1620
Qy	1621	ATAATGGTGGTCCAGAACCCGGCATAGCCCCGTTTATTTGGGTTCTACACATAGAGAG	1680
Db	1621	ATATATGGTGGTCCAGGAACCCGGCATAGCCCCGTTTATTTGGGTTCTACACATAGAGAG	1680
Qy	1681	AAACTCCAGAACCAACCCCGATGGAATTTTGGAGCATATGTGGTGTTTTTGGCTGC	1740
Db	1681	AAACTCCAGAACCAACCCCGATGGAATTTTGGAGCAATGTGGTGTTTTTGGCTGC	1740
Qy	1741	AGGCATAGAGTAGGGATTAATCTAATTGAGAAAGAGCTCAGACATTTCTTAAGCATGG	1800
Db	1741	AGGCATAGAGTAGGGATTAATCTAATTGAGAAAGAGCTCAGACATTTCTTAAGCATGG	1800
Qy	1801	ATCTTAACTCATCTAAAGTTCCTTTCAGAGAGTGTCTCTGTTGGGAGAGGAAGCC	1860
Db	1801	ATCTTAACTCATCTAAAGTTCCTTTCAGAGAGTGTCTCTGTTGGGAGAGGAAGCC	1860
Qy	1861	CCAGCAAAAGTATGTACAGAACACATCCAGCTTCATGGCCAGCAGTGGCGAGATCTC	1920
Db	1861	CCAGCAAAAGTATGTACAGAACACATCCAGCTTCATGGCCAGCAGTGGCGAGATCTC	1920
Qy	1921	CTCCAGAGGAACGGCCATATTATGTGTGAGAGTGCAGAAAGATATATGGCCAAAGATGTA	1980
Db	1921	CTCCAGAGGAACGGCCATATTATGTGTGAGAGTGCAGAAAGATATATGGCCAAAGATGTA	1980
Qy	1981	CATGATGCCCTTGTGCAATATATAGCAAAAGGTTGAGGTTGAAAACTAGAAAGCAATG	2040
Db	1981	CATGATGCCCTTGTGCAATATATAGCAAAAGGTTGAGGTTGAAAACTAGAAAGCAATG	2040
Qy	2041	AAAAACCCTGGCACTTTTAAAGAGAAAAAGCTACCTTCAGAGATTTTGGTCA	2094
Db	2041	AAAAACCCTGGCACTTTTAAAGAGAAAAAGCTACCTTCAGAGATTTTGGTCA	2094

RESULT 2

ID AAS65070 standard; cDNA; 3259 BP.

AC AAS65070 ;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #874

KM Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss

OS Homo sapiens

PN WO200175067-A2

PD 11-OCT-2001

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217

XX
XX
XX) WYCEO TNG
DZ

XX	DT	LT	TRNG	YR
DT	DT	LT	TRNG	YR

XX WPT: 2001-639362/73

DK P-PSDB; ABG00883.
XX

PT diagnosis: forensic, identification of mutations

PT responsible for general status and blooddiversity.

PS Claim 1; SEQ ID NO 874; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polynucleotide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAs664197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

SQ Sequence 3255 BP; 944 A; 695 C; 674 G; 946 T; 0 U; 0 Other;

Query match	97.6%	Score 2046;	DB 5;	Length 3259;
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Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGAGGAGTTTCTGTACTATATGCTACACAGCAGGACAGGCAAGGCCATCGCAGAA 60

Db 80 ATGAGGAGGTTTCTGTTACTATATGCTACACAGCAGGACAGGCAGGCCATCCAGAA 13

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D6 200 TCCGATTAAGTATGACCTAAACCAGAACAAGCTCCTCTGTGTGTGGTTCACCACT

181 GGCACCGAGACCCACCCGACACAGCCCGCAGGTGTGTAAAGAAATACAGAACCAACA 24

Db 260 GGCACCGAGACCCACCCGACACAGCCCGCAGTTTGTAAGGAAACACGAAACCAACA 31

241 CIGCCGTAATTCCTTCACCTGCGAAGGTAACGGATCTCGGAACTCAAGAA 30

D6 320 CTGCTGGTGAATTCTTGGCTTACCTGCGTATGGGTAACGGGCTCGGGATTCAGGAACTAGGAA

QY
301 TACCCIIAIIIGCAATGGGGAAGATAATTTGTATTATCCTAACIICATGAGACIICGAGACC

[illegible]

2011-12-15 14:30:00

22

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2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 104

THE UNIVERSITY OF CHICAGO

QUESTION

730

QY 661 ATTGAGACTTTGAGTCTCTCACTTACCCTGCGTACCCCACTCTCAAGCCTCTCTG 720
DB 740 ATTGAGACTTTGAGTCTCTCACTTACCCTGCGTACCCCACTCTCAAGCCTCTCTG 729
QY 721 AATATTCCTGGTTAAACCCCAAGATATTTACAGGTACATCGAGAGAGTCTCTGGCAG 780
DB 800 AATATTCCTGGTTAAACCCCAAGATATTTACAGGTACATCGAGAGAGTCTCTGGCAG 859
QY 781 GAGGAAAGCCAGATATCTGTGACTTCAGCAGATCCAGTTTTCAGAGTCCAAATTTCAAG 840
DB 860 GAGGAAAGCCAGATATCTGTGACTTCAGCAGATCCAGTTTTCAGAGTCCAAATTTCAAG 919
QY 841 GCGATTCACTTACTAGAAATGATGCCATTAATAACCACTGCTGCTGATGAAATTTGAGACT 900
DB 920 GCGATTCACTTACTAGAAATGATGCCATTAATAACCACTGCTGCTGATGAAATTTGAGACT 979
QY 901 TCAAAATACAGACTTTTCTATCAGCCTGAGAGATCCTTACAGCCTGATCTGCCCTTAACAT 960
DB 980 TCAAAATACAGACTTTTCTATCAGCCTGAGAGATCCTTACAGCCTGATCTGCCCTTAACAT 1039
QY 961 GATTCTGAGGTACAAAGCCTTACTCMAAAGCTGAGCTTGAAGATTAAGAGAGCACTGC 1020
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QY 1021 GTCTTTTGAATAATTAAGGAGAGACAAAGAAAGAGACTTACCTTACCAGCATATA 1080
DB 1100 GTCTTTTGAATAATTAAGGAGAGACAAAGAAAGAGACTTACCTTACCAGCATATA 1159
QY 1081 CCTGCGGAGATGTTCTCTCCAGTTCACTTGTGATGCTGTAAGATCCGAGCAATTCCT 1140
DB 1160 CCTGCGGAGATGTTCTCTCCAGTTCACTTGTGATGCTGTAAGATCCGAGCAATTCCT 1219
QY 1141 AAAAAGGCATTTTTCGAGCCCTTGTGACTATAACAAGTACAGTGTGAAAAAGCCGAG 1200
DB 1220 AAAAAGGCATTTTTCGAGCCCTTGTGACTATAACAAGTACAGTGTGAAAAAGCCGAG 1279
QY 1201 CTACAGAGCTGTGCACTTAATAACAAGGAGCCGATTAATAGCCCTTTTATACAGATGCC 1260
DB 1280 CTACAGAGCTGTGCACTTAATAACAAGGAGCCGATTAATAGCCCTTTTATACAGATGCC 1339
QY 1261 TGTGCTGCTGTTGATGATCTCTCTGCTTCTCTGCTTCTGCGCAGCCAGCACTCAATCTC 1320
DB 1340 TGTGCTGCTGTTGATGATCTCTCTGCTTCTCTGCTTCTGCGCAGCCAGCACTCAATCTC 1399
QY 1321 CTGCTGCAACATCTTCTTAACTTCAACCCAGACCATATTCGTGTGAGCTCAAGTTTA 1380
DB 1400 CTGCTGCAACATCTTCTTAACTTCAACCCAGACCATATTCGTGTGAGCTCAAGTTTA 1459
QY 1381 TTTTCAACCAAGAAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTCTGTCTACCTGCCA 1440
DB 1460 TTTTCAACCAAGAAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTCTGTCTACCTGCCA 1519
QY 1441 ACAGAGGTTCTGCGGAGAGAGTATGTACAGGCTGCGCTTGTGTTGTTGTTGCTTCACT 1500
DB 1520 ACAGAGGTTCTGCGGAGAGAGTATGTACAGGCTGCGCTTGTGTTGTTGTTGCTTCACT 1579
QY 1501 CTTCAGCCAAACATATGATGCCATTCATGAGAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
DB 1580 CTTCAGCCAAACATATGATGCCATTCATGAGAGACGCGGAAAGCCCTGCTCTTAAGATA 1639
QY 1561 TCCATCTCTCTCTGCAACCAAAATTTTTCATTAACATGACCCCTCAATCCCATC 1620
DB 1640 TCCATCTCTCTCTGCAACCAAAATTTTTCATTAACATGACCCCTCAATCCCATC 1699
QY 1621 AATAATGAGGTTCAGAGAACCGGATAGCCCGTTTATTTGGGTTCTTACAACATAGAGAG 1680
DB 1700 AATAATGAGGTTCAGAGAACCGGATAGCCCGTTTATTTGGGTTCTTACAACATAGAGAG 1759
QY 1681 AAATCTCAAGAAACAACCCAGATGAAATTTTGGAGCAATGTGTTTGTGCTGC 1740
DB 1760 AAATCTCAAGAAACAACCCAGATGAAATTTTGGAGCAATGTGTTTGTGCTGC 1819
QY 1741 AGGCAATAGGATAGGATATCTATTCAAGAAAGAGCTCAGACATTTCTTAAGCATGGG 1800

DB 1820 AGGCAATAGGATAGGATATCTATTCAAGAAAGAGCTCAGACATTTCTTAAGCATGGG 1879
QY 1801 ATCTTAATCATTAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGAGAGAGCC 1860
DB 1880 ATCTTAATCATTAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGAGAGAGCC 1939
QY 1861 CCAGCAAGATATGATACAGACCAATCATCAGCTTCATGGCCAGCAGGTGGCAGAAATCTC 1920
DB 1940 CCAGCAAGATATGATACAGACCAATCATCAGCTTCATGGCCAGCAGGTGGCAGAAATCTC 1999
QY 1921 CTCAGAGAGAGGCGCATATTTATGTTGTGAGATGCAAGAAATATGGCCAGATGTA 1980
DB 2000 CTCAGAGAGAGGCGCATATTTATGTTGTGAGATGCAAGAAATATGGCCAGATGTA 2059
QY 1981 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGGTTGAGTTGAAAACTAGAAAGCATG 2040
DB 2060 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGGTTGAGTTGAAAACTAGAAAGCATG 2119
QY 2041 AAAACCTGGCCACTTTAAAGAAAGAAACGCTACCTTCAGATATTTGTCTATA 2097
DB 2120 AAAACCTGGCCACTTTAAAGAAAGAAACGCTACCTTCAGATATTTGTCTATA 2176

RESULT 3
AAC91226
ID AAC91226 standard; DNA; 3259 BP.
XX
XX AAC91226;
AC
XX
XX 20-MAR-2001 (first entry)
DT
XX
XX Human schizophrenia related gene SEQ ID NO: 23.
DE
XX
XX Human: schizophrenia; developmental disorder; spina bifida cystica;
KM Tourette's syndrome; bipolar illness; autism; conduct disorder;
KM attention deficit disorder; obsessive compulsive disorder;
XX chronic multiple tic syndrome; learning disorder; polymorphism; ds.
XX
OS Homo sapiens.
XX
XX NC0200071754-A1.
PN
XX
XX 30-NOV-2000.
PD
XX
XX 24-MAY-2000; 2000MO-US014354.
PF
XX
XX 25-MAY-1999; 99US-00318448.
PR
XX
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
PA
XX
XX Johnson WG, Stenroos ES;
PI
XX
XX WPI; 2001-025174/03.
DR
XX
XX
XX Diagnosing a developmental disorder, e.g. schizophrenia, by forming
PT datasets (DS) of genetic (e.g. genotypes of folate metabolism alleles)
PT and environmental variables affecting an individual and then comparing
PT these DS with reference DS.
XX
XX
XX Disclosure; Page 142-143; 156pp; English.
PS
XX
XX The present invention provides a novel method of estimating the
CC susceptibility of an individual to a developmental disorder using genetic
CC and environmental variables. The method can be used in the diagnosis,
CC prevention and treatment of disorders such as schizophrenia, spina bifida
CC cystica, Tourette's syndrome, bipolar illness, autism, conduct disorders,
CC attention deficit disorder, obsessive compulsive disorder, chronic
CC multiple tic syndrome and learning disorders such as dyslexia
XX
XX Sequence 3259 BP; 944 A; 695 C; 674 G; 946 T; 0 U; 0 Other;
SQ

Query Match 97.6%; Score 2046; DB 5; Length 3259;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 ATGAGAGAGTTTCTGTACTATATGCTACACAGCAGGAGACGCAAAAGCCATCGCAGAA 60
DB |||
DB 80 ATGAGAGAGTTTCTGTACTATATGCTACACAGCAGGAGACGCAAAAGCCATCGCAGAA 139
QY 61 GAAATATGAGCAGCTGTGTACATGATTTCTGAGATCTTCACTGATTTAGTGA 120
DB |||
DB 140 GAAATATGAGCAGCTGTGTACATGATTTCTGAGATCTTCACTGATTTAGTGA 199
QY 121 TCCGATATGATGACCTTAAACCGGAAAGAGCTCTCTGTTGTGTGTTCTACAG 180
DB |||
DB 200 TCGATATATGATGACCTTAAACCGGAAAGAGCTCTCTGTTGTGTGTTCTACAG 259
QY 181 GGCACCGGAGACCCGACACAGCCGCGAGTTGTTAGAAATACAGAACCA 240
DB 260 GGCACCGGAGACCCGACACAGCCGCGAGTTGTTAGGAAATACAGAACCA 319
QY 241 CTGCGGTTGATTTCTTGTCTACCTGCGGTATGGGTTACTGGGTCTCGGTATTCAGAA 300
DB |||
DB 320 CTGCGGTTGATTTCTTGTCTACCTGCGGTATGGGTTACTGGGTCTCGGTATTCAGAA 379
QY 301 TACACTACTTTTGCATATGAGGAGAGATATTTGATTAACGACTTCAAGAGCTTGAGCC 360
DB 380 TACACTACTTTTGCATATGAGGAGAGATATTTGATTAACGACTTCAAGAGCTTGAGCC 439
QY 361 CGGACTTTCTATGACACTGACATGACATGACTGTGTAGAGTTTAAAGCTTGTGTGAG 420
DB 440 CGGACTTTCTATGACACTGACATGACATGACTGTGTAGAGTTTAAAGCTTGTGTGAG 499
QY 421 CCGTGTATGCTGAGACTCTGCGCCGCTCAGAAACATTTTATGATCAAGAGAGACAA 480
DB 500 CCGTGTATGCTGAGACTCTGCGCCGCTCAGAAACATTTTATGATCAAGAGAGACAA 559
QY 481 GAGAGATATAGTGGCCGACTCCCGGTGGCATCACTGACCTTCTGAGAGACAGACTTGTG 540
DB 560 GAGAGATATAGTGGCCGACTCCCGGTGGCATCACTGACCTTCTGAGAGAGACAGACTTGTG 619
QY 541 AAGTCAGAGCTGTACACATTTGATATCTCAAGTCGAGCTTCTGAGATTCAGATTCAGAA 600
DB 620 AAGTCAGAGCTGTACACATTTGATATCTCAAGTCGAGCTTCTGAGATTCAGATTCAGAA 679
QY 601 AGAAAGATTTCTGAGTTTGAAGCAAAATGCAAGTAAACGAAACCAATCCAAATGTTGA 660
DB 680 AGAAAGATTTCTGAGTTTGAAGCAAAATGCAAGTAAACGAAACCAATCCAAATGTTGA 739
QY 661 ATTGAAGACTTGAAGTCTCACTTACCCGTTCCGTTACCCCACTCTCAAGAGCTCTG 720
DB 740 ATTGAAGACTTGAAGTCTCACTTACCCGTTCCGTTACCCCACTCTCTCAAGAGCTCTG 799
QY 721 AATATTCCTGTGTACCCCGCAATATTTACAGATCATCTGACAGAGTCTCTGCGCAG 780
DB 800 AATATTCCTGTGTACCCCGCAATATTTACAGATCATCTGACAGAGTCTCTGCGCAG 859
QY 781 GAGGAAAGCCAGATATCTGTGACTTCAAGCAGATCCAGTTTCAAGTCCCAATTTCAAG 840
DB 860 GAGGAAAGCCAGATATCTGTGACTTCAAGCAGATCCAGTTTCAAGTCCCAATTTCAAG 919
QY 841 GCAGTCAACTTCTCAAGATGATGCAATTAACCACTCTGCTGATGAGATTTGACAT 900
DB 920 GCAGTCAACTTCTCAAGATGATGCAATTAACCACTCTGCTGATGAGATTTGACAT 979
QY 901 TCAATATACAGACTTTTCTATCAGCCTGAGATGCTTCAAGCCTGATCTGCCCTTAACAGT 960
DB 980 TCAATATACAGACTTTTCTATCAGCCTGAGATGCTTCAAGCCTGATCTGCCCTTAACAGT 1039
QY 961 GATTTGAGGTACAAAGCTTACTTCAAGAGCTGCAAGTTGAAGTAAAGAGAGCACTGC 1020
DB 1040 GATTTGAGGTACAAAGCTTACTTCAAGAGCTGCAAGTTGAAGTAAAGAGAGCACTGC 1099
QY 1021 GTCTTTTGAATTAAGGACAGACAAAGAAAGAGAGCTTACCCGACATATA 1080
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DB 1100 GTCTTTTGAATTAAGGACAGACAAAGAAAGAGAGCTTACCCGACATATA 1159
QY 1081 CCTGGGGAGATTTCTCTCAGTTCAATTTTACTGCTGCTGAATCCGAGCAATTCCT 1140
DB |||
DB 1160 CCTGGGGAGATTTCTCTCAGTTCAATTTTACTGCTGCTGAATCCGAGCAATTCCT 1219
QY 1141 AAAAAGCATTTTTTCGAGCCCTTGTGACATATACAGTGAAGTGTGAAAAGCGCAG 1200
DB 1220 AAAAAGCATTTTTTCGAGCCCTTGTGACATATACAGTGAAGTGTGAAAAGCGCAG 1279
QY 1201 CTACAGAGCTGTGACATTAACAGAGGAGCCGATTAATAGCCGCTTGTAGAGATGCC 1260
DB 1280 CTACAGAGCTGTGACATTAACAGAGGAGCCGATTAATAGCCGCTTGTAGAGATGCC 1339
QY 1261 TGTGCTGTGTGTGATCTCTCTGCTTCCCTCTGTCAGGACACGCTCAAGTCTC 1320
DB 1340 TGTGCTGTGTGTGATCTCTCTGCTTCCCTCTGTCAGGACACGCTCAAGTCTC 1399
QY 1321 CTGCTGAAACATCTTCTTAACTTCAACCCAGACATATCTGTGCAAGCTCAAGTTTA 1380
DB 1400 CTGCTGAAACATCTTCTTAACTTCAACCCAGACATATCTGTGCAAGCTCAAGTTTA 1459
QY 1381 TTTCACCCAGAAAGCTCCATTTTGTCTTCAATTTGAGAAATTTCTGTACTGACACA 1440
DB 1460 TTTCACCCAGAAAGCTCCATTTTGTCTTCAATTTGAGAAATTTCTGTACTGACACA 1519
QY 1441 ACAGAGTTCTGCGAGAGGAGATATGATAGGCTGTGCTGTGTGTGTTGCTTCAAGT 1500
DB 1520 ACAGAGTTCTGCGAGAGGAGATATGATAGGCTGTGCTGTGTGTGTTGCTTCAAGT 1579
QY 1501 CTTGAGCCAAACATACATCATCCCATGAAAGACAGGAGAAAGCCCTGCTCTTAAGATA 1560
DB 1580 CTTGAGCCAAACATACATCATCCCATGAAAGACAGGAGAAAGCCCTGCTCTTAAGATA 1639
QY 1561 TCCATCTCTCTGAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
DB 1640 TCCATCTCTCTGAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1699
QY 1621 ATATATGTGTGTTCAGAAACCGGATAGCCCGTTTATGTGGTTCTTAAACATAGAG 1680
DB 1700 ATATATGTGTGTTCAGAAACCGGATAGCCCGTTTATGTGGTTCTTAAACATAGAG 1759
QY 1681 AAATCTCAAGAAACAACACCAAGTGAATTTTGTGAGCATGTGTGTTTTTGTGCTGC 1740
DB 1760 AAATCTCAAGAAACAACACCAAGTGAATTTTGTGAGCATGTGTGTTTTTGTGCTGC 1819
QY 1741 AAGCATTAAGATTAAGGATTAATCTATTACAGAAAGAGCTCAGACATTTCTTAAGATGG 1800
DB 1820 AAGCATTAAGATTAAGGATTAATCTATTACAGAAAGAGCTCAGACATTTCTTAAGATGG 1879
QY 1801 ATCTTAATCTATTAAGGTTTCTTCTCAAGATGCTCTGTGTGGAGAGAGAGGCC 1860
DB 1880 ATCTTAATCTATTAAGGTTTCTTCTCAAGATGCTCTGTGTGGAGAGAGAGGCC 1939
QY 1861 CCAGCAAGATTAATGTAACAAGCAACATCAGCTTCAATGAGCAGAGGTGGAGATCTCTC 1920
DB 1940 CCAGCAAGATTAATGTAACAAGCAACATCAGCTTCAATGAGCAGAGGTGGAGATCTCTC 1999
QY 1921 CTCACAGAGAGAGGACATATTTATGTGTGTGAGATGCAAGAAATATGCGCAAGATGA 1980
DB 2000 CTCACAGAGAGAGGACATATTTATGTGTGTGAGATGCAAGAAATATGCGCAAGATGA 2059
QY 1981 CATGATGCCCTGTGTGCAATTAATTAAGCAAGAGGTTGAGTTGAAAACTAGAGCAATG 2040
DB 2060 CATGATGCCCTGTGTGCAATTAATTAAGCAAGAGGTTGAGTTGAAAACTAGAGCAATG 2119
QY 2041 AAAAAGCTGAGCACTTAAAGAGAAAGAGTAAAGTCAAGATATTTTGTGATATA 2097
DB 2120 AAAAAGCTGAGCACTTAAAGAGAAAGAGTAAAGTCAAGATATTTTGTGATATA 2176
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RESULT 4
ADM43206

ID	ADM43206	standard; cDNA; 3259 BP.
XX	XX	
AC	ADM43206;	
XX	XX	
DT	03-JUN-2004	(first entry)
XX	XX	
DE	Human full length cDNA encoding methionine synthase reductase.	
XX	XX	
KW	Human; <i>bs</i> ; gene; Methionine synthase reductase polypeptide; <i>HamTR</i> ;	
KW	cancer; cardiovascular disease; neural tube defect;	
KW	hyperhomocysteinemia; chromosome 5p15.2-p15.3; SNP;	
KW	single nucleotide polymorphism.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
FT	Key	Location/Qualifiers
FT	CDS	80..2176
FT		/*tag= a
FT		/product= "hamTRR"
FT	variation	/replace(145,A)
FT		/*tag= b
FT		/standard name= "Single_nucleotide_polymorphism"
FT	variation	/replace(189,A)
FT		/*tag= C
FT		/standard_name= "Single_nucleotide_polymorphism"
XX	XX	
PN	US2003082676-A1.	
XX	XX	
PD	01-MAY-2003.	
XX	XX	
XP	10-AUG-1999;	99US-00371347.
XX	XX	
PR	16-JAN-1998;	98US-0071622P.
PR	15-JAN-1999;	98US-00232028.
XX	XX	
PA	(GRAV/) GRAVEL R. A.	
PA	(ROZE/) ROZEN R.	
PA	(LECL/) LECLERC D.	
PA	(WILS/) WILSON A.	
PA	(ROSE/) ROSENBLATT D.	
XX	XX	
PI	Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;	
XX	XX	
DR	WPI; 2003-576610/54.	
DR	P-PSDB; ADM43207.	
XX	XX	
PT	New substantially pure nucleic acid encoding a mammalian methionine	
PT	synthase reductase polypeptide, useful for diagnosing, preventing or	
PT	treating conditions associated with altered methionine synthase activity,	
PT	e.g. cancer.	
XX	XX	
PS	Example 2; SEQ ID NO 24; 26pp; English.	
XX	XX	
CC	The invention relates to a substantially pure nucleic acid that encodes a	
CC	mammalian methionine synthase reductase polypeptide, <i>HamTR</i> , or that	
CC	hybridizes at high stringency to a nucleic acid appearing as ADM43208 or	
CC	ADM43209. Also included are a non-human animal where one or both genetic	
CC	alleles encoding the methionine synthase reductase polypeptide are	
CC	mutated, an antibody that specifically binds the above methionine	
CC	synthase reductase polypeptide, a method of detecting the presence of the	
CC	above polypeptide, a method for detecting sequence variants for	
CC	methionine synthase reductase in a mammal, methods of treating or	
CC	preventing cancer (or cardiovascular disease or neural tube defects) in a	
CC	subject, methods of screening for a compound that modulates methionine	
CC	synthase reductase biological activity and a method for detecting an	
CC	increased risk of developing a neural tube defect in a mammalian embryo	
CC	or foetus. The nucleic acid is useful in diagnosing, preventing or	
CC	treating conditions associated with altered methionine synthase activity,	
CC	such as cancer, cardiovascular disease or neural tube defects, or in	
CC	screening for a compound that modulates methionine synthase reductase	
CC	biological activity. Naturally occurring variants of the polypeptide are	
CC	also associated with hyperhomocysteinemia. The gene for <i>HamTR</i> is	
CC	located on chromosome 5p15.2-p15.3. The present sequence is full length	

CC	Sequence of the wild-type human hsmTRR cDNA.
XX	Sequence 3259 BP; 944 A; 695 C; 674 G; 946 T; 0 U; 0 Other;
Sequence	3259 BP; 944 A; 695 C; 674 G; 946 T; 0 U; 0 Other;
Query Match	97.6%; Score 2046; DB 11; Length 3259;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 2096;	Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 ATGAGGAGGTTTCTGTTACTATATATGCTACACAGCAGGGAACGCAAAAGGCCATGCGAA 60
DB	80 ATGAGGAGGTTTCTGTTACTATATATGCTACACAGCAGGGAACGCAAAAGGCCATGCGAA 139
QY	61 GAAATATGTGACGACGTGTGTATCATGTGATTTTCTGCACATCTTCACTGTATTAATGAA 120
DB	140 GAAATGTGTGACGACGTGTGTATCATGTGATTTTCTGCACATCTTCACTGTATTAATGAA 199
QY	121 TCCGATATGATATGACCTAAATAACCGAAACAGCTCCTCTGTGTGTGTGTTTCTACACG 180
DB	200 TCCGATATGATATGACCTAAATAACCGAAACAGCTCCTCTGTGTGTGTGTTTCTACACG 259
QY	181 GGCACCGGAGACCCACCCGACACAGCCTCGAGTTGTTAAGAAATACAAACAAACA 240
DB	260 GGCACCGGAGACCCACCCGACACAGCCTCGAGTTGTTAAGAAATACAAACAAACA 319
QY	241 CTGCGCGGTGATTTCTTTTGTCTACCTGCGGTATGGTTACTGGGTCCTCGGTATTCGAA 300
DB	320 CTGCGCGGTGATTTCTTTTGTCTACCTGCGGTATGGTTACTGGGTCCTCGGTATTCGAA 379
QY	301 TACACCTACCTTTTGCAATGGGGGGGGAATAATGATTAACGACTTCAGAGCTTGGAGCC 360
DB	380 TACACCTACCTTTTGCAATGGGGGGGGAATAATGATTAACGACTTCAGAGCTTGGAGCC 439
QY	361 CGGCAATTTCTATGACACTGAGACATGCAGATGACTGTGTAGGTTTAACTTGTGTGTAG 420
DB	440 CGGCAATTTCTATGACACTGAGACATGCAGATGACTGTGTAGGTTTAACTTGTGTGTAG 499
QY	421 CCGTGATTTGTGTGACCTCTGTGCGCAGCCCTCAGAAAGCAATTTTATAGTACAGAGACAA 480
DB	500 CCGTGATTTGTGTGACCTCTGTGCGCAGCCCTCAGAAAGCAATTTTATAGTACAGAGACAA 559
QY	481 GAGGAGATTAAGTGGCGACCTCCCGGTGGCATCATCTGSCATCCTTGAGAGACAGACTTGTG 540
DB	560 GAGGAGATTAAGTGGCGACCTCCCGGTGGCATCATCTGSCATCCTTGAGAGACAGACTTGTG 619
QY	541 AAGTCAGAGCTGTACACATTTGAATCTCAAGTCGAGCTTCTGAGATTCGATGATTCAGA 600
DB	620 AAGTCAGAGCTGTACACATTTGAATCTCAAGTCGAGCTTCTGAGATTCGATGATTCAGA 679
QY	601 AGAAAGGATTCGAGGTTTGAAGCAAAATGCAGTGAACAGCAACCAATCCAAATGTTGTA 660
DB	680 AGAAAGGATTCGAGGTTTGAAGCAAAATGCAGTGAACAGCAACCAATCCAAATGTTGTA 739
QY	661 ATTGAACAATTTGAGTCTCTCACTTACCCGTTCCGTAACCCCACTCTCAACAAAGCTCTCTG 720
DB	740 ATTGAACAATTTGAGTCTCTCACTTACCCGTTCCGTAACCCCACTCTCAACAAAGCTCTCTG 799
QY	721 AATATTCTCGGTTTACCCCGAGATATTTCACAGTACATCTGCAGAGTCTCTTGGCCAG 780
DB	800 AATATTCTCGGTTTACCCCGAGATATTTCACAGTACATCTGCAGAGTCTCTTGGCCAG 859
QY	781 GAGGAAAGCCAGATATCTGTGACTTCGACAGATCCAGATTTTTCAGATGCCAATTTCAAG 840
DB	860 GAGGAAAGCCAGATATCTGTGACTTCGACAGATCCAGATTTTTCAGATGCCAATTTCAAG 919
QY	841 GCAAGTTCACTTACATGCAATGATGACATTAATAACCACTCTGCTGTGTGAAATTTGACATT 900
DB	920 GCAAGTTCACTTACATGCAATGATGACATTAATAACCACTCTGCTGTGTGAAATTTGACATT 979
QY	901 TCAAAATACAGCTTTTCTCTATCAGCCTGGAGATCCTTCAACGCGTATCTGCGCTTACAGT 960
DB	980 TCAAAATACAGCTTTTCTCTATCAGCCTGGAGATCCTTCAACGCGTATCTGCGCTTACAGT 1039
QY	961 GATTCTGAGGTACAAAGCTTACTCCAAAGACTGACGCTTGAAAGATTAAGAGACACTGCG 1020

Db 1040 GATTCTGAGGTACAAAGCCCTACTCAAAGACTGCACTTGAAGATTAAGAGAGCACTGC 1099
 QY 1021 GTCTCTTTTAAAAATTAAGGACAGACAAAGAAAGAAAGAGCTACTTACCCCGCATATA 1080
 Db 1100 GTCTCTTTTAAAAATTAAGGACAGACAAAGAAAGAAAGAGCTACTTACCCCGCATATA 1159
 QY 1081 CTGCGGAGATGTTCTCTCAAGTTCAATTTTACCTGAGTGTCTTGAATTCGAGCAATTCCT 1140
 Db 1160 CTGCGGAGATGTTCTCTCAAGTTCAATTTTACCTGAGTGTCTTGAATTCGAGCAATTCCT 1219
 QY 1141 AAAAAGGCAATTTTGGAGCCCTTGTGACTATATACAGTGAAGTGTGAAAAGCCAGG 1200
 Db 1220 AAAAAGGCAATTTTGGAGCCCTTGTGACTATATACAGTGAAGTGTGAAAAGCCAGG 1279
 QY 1201 CTACAGAGACTGTGCAAGTAAACAAGGGGCAAGCCGATTAATAGCCGCTTTGTAGAGATGCC 1260
 Db 1280 CTACAGAGACTGTGCAAGTAAACAAGGGGCAAGCCGATTAATAGCCGCTTTGTAGAGATGCC 1339
 QY 1261 TGGGCTGCTGTGTGGATCTCCCTCGCTTCCCTTCCCTTCCAGCCACCACTCAAGTCTC 1320
 Db 1340 TGGGCTGCTGTGTGGATCTCCCTCGCTTCCCTTCCCTTCCAGCCACCACTCAAGTCTC 1399
 QY 1321 CTGCTCGAATCTTCTCTAACTTCAACCCAGACATATTCGTGTGCAAGCTCAAGTTTA 1380
 Db 1400 CTGCTCGAATCTTCTCTAACTTCAACCCAGACATATTCGTGTGCAAGCTCAAGTTTA 1459
 QY 1381 TTTCACCCGAGAAAGCTCAATTTTGTCTTCAACATTTGTGGAATTTCTGTCTACTGCCACA 1440
 Db 1460 TTTCACCCGAGAAAGCTCAATTTTGTCTTCAACATTTGTGGAATTTCTGTCTACTGCCACA 1519
 QY 1441 ACAGAGGTTCTGCGGAAAGGAGATATGATACAGGCTGGCTGGCTGTGTGCTTCAAGTT 1500
 Db 1520 ACAGAGGTTCTGCGGAAAGGAGATATGATACAGGCTGGCTGGCTGTGTGCTTCAAGTT 1579
 QY 1501 CTTCAGCCAAACATACATGATCTCCATGAGAAGAGGGGAAAGCCCTGCTCTTAAGATA 1560
 Db 1580 CTTCAGCCAAACATACATGATCTCCATGAGAAGAGGGGAAAGCCCTGCTCTTAAGATA 1639
 QY 1561 TCGATCTCTCTCTGAAACAACAATTTCTTTCATTTACAGATGACCCCTCAATCCCATC 1620
 Db 1640 TCGATCTCTCTCTGAAACAACAATTTCTTTCATTTACAGATGACCCCTCAATCCCATC 1699
 QY 1621 ATTAATGTGGTCCAGAAACCCGATAGCCCGTTATGTGGTCTTACAACTAAGAG 1680
 Db 1700 ATTAATGTGGTCCAGAAACCCGATAGCCCGTTATGTGGTCTTACAACTAAGAG 1759
 QY 1681 AAATCTCAAGAAACAACCCAGATGAAATTTTGAAGCAATGTGTGTTTTTGGCTGC 1740
 Db 1760 AAATCTCAAGAAACAACCCAGATGAAATTTTGAAGCAATGTGTGTTTTTGGCTGC 1819
 QY 1741 AGGCAATAGGATAGGATTAATCTATTCAAGAAAAGACTCAGACATTTCTTAAGATGGG 1800
 Db 1820 AGGCAATAGGATAGGATTAATCTATTCAAGAAAAGACTCAGACATTTCTTAAGATGGG 1879
 QY 1801 ATCTTAATCTAATTAAGGTTTCTCTCAAGAGATGCTCCGTGTGGGAGAGAGAGCC 1860
 Db 1880 ATCTTAATCTAATTAAGGTTTCTCTCAAGAGATGCTCCGTGTGGGAGAGAGAGCC 1939
 QY 1861 CCAGCAAAATATGTACAGAACATCAGCTTCATGSCCAGAGAGGTGGGAGATCTCTC 1920
 Db 1940 CCAGCAAAATATGTACAGAACATCAGCTTCATGSCCAGAGAGGTGGGAGATCTCTC 1999
 QY 1921 CTCACAGAGAACGGCATATTTATGTGTGTGAGATGCAAGAAATATGCGCAAGATGTA 1980
 Db 2000 CTCACAGAGAACGGCATATTTATGTGTGTGAGATGCAAGAAATATGCGCAAGATGTA 2059
 QY 1981 CATTGATGCTTGTGCAATTAATTAAGCAAAAGAGTTGAGTTGAAAACCTAGAAGCAATG 2040
 Db 2060 CATTGATGCTTGTGCAATTAATTAAGCAAAAGAGTTGAGTTGAAAACCTAGAAGCAATG 2119
 QY 2041 AAAACCTGCGCACTTTAAAAGAAAGAAAACGCTTACAGATATTTGTGTCATTA 2097

Db 2120 AAAACCTGCGCACTTTAAAAGAAAGAAAACGCTTACAGATATTTGTGTCATTA 2176
 RESULT 5
 ADM43208
 ID ADM43208 standard; cDNA; 2094 BP.
 XX
 AC ADM43208;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human wild-type methionine synthase reductase CDS.
 XX
 KW Human; ss; Methionine synthase reductase polypeptide; HsMTRR; cancer;
 KW cardiovascular disease; neural tube defect; hyperhomocysteinemia;
 KW chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2094
 FT /*tag= a
 FT /product= "HsMTRR"
 FT /partial
 FT /note= "No stop codon shown"
 FT variation /*tag= b
 FT /*standard_name= "Single_nucleotide_polymorphism"
 FT /*tag= c
 FT /*standard_name= "Single_nucleotide_polymorphism"
 XX
 PN US2003082676-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 10-AUG-1999; 99US-00371347.
 XX
 PR 16-JAN-1998; 98US-0071622P.
 PR 15-JAN-1999; 99US-00232028.
 XX
 PA (GRAV/) GRAVEL R A.
 PA (ROZE/) ROZEN R.
 PA (LECL/) LECLERC D.
 PA (WILS/) WILSON A.
 PA (ROSE/) ROSENBLATT D.
 XX
 PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
 XX
 DR WPI: 2003-576610/54.
 DR P-PSDB; ADM43207.
 XX
 PT New substantially pure nucleic acid encoding a mammalian methionine
 PT synthase reductase polypeptide, useful for diagnosing, preventing or
 PT treating conditions associated with altered methionine synthase activity,
 PT e.g. cancer.
 XX
 PS Claim 3; SEQ ID NO 1; 26pp; English.
 XX
 CC The invention relates to a substantially pure nucleic acid that encodes a
 CC mammalian methionine synthase reductase polypeptide, HsMTRR, or that
 CC hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
 CC ADM43209. Also included are a non-human animal where one or both genetic
 CC alleles encoding the methionine synthase reductase polypeptide are
 CC mutated, an antibody that specifically binds the above methionine
 CC synthase reductase polypeptide, a method of detecting the presence of the
 CC above polypeptide, a method for detecting sequence variants for
 CC methionine synthase reductase in a mammal, methods of treating or
 CC preventing cancer (or cardiovascular disease or neural tube defects) in a
 CC subject, methods of screening for a compound that modulates methionine
 CC synthase reductase biological activity and a method for detecting an
 CC increased risk of developing a neural tube defect in a mammalian embryo
 CC or foetus. The nucleic acid is useful in diagnosing, preventing or

CC treating conditions associated with altered methionine synthase activity,
 CC such as cancer, cardiovascular disease or neural tube defects, or in
 CC screening for a compound that modulates methionine synthase reductase
 CC biological activity. Naturally occurring variants of the polypeptide are
 CC also associated with hyperhomocysteinaemia. The gene for Hmtrr is
 CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
 CC sequence of the wild-type human hsmtrr cDNA.

XX Sequence 2094 BP; 591 A; 489 C; 481 G; 533 T; 0 U; 0 Other;

Query Match 97.4%; Score 2043; DB 11; Length 2094;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2093; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGAGGTTTCTGTTACTATATGTCTACACAGGAGGACAGGCAAGCCATCGAGAA 60
 DB 1 ATGAGAGGTTTCTGTTACTATATGTCTACACAGGAGGACAGGCAAGCCATCGAGAA 60
 QY 61 GAAATATGTAGCAAGCTGTGTATCATATGATTTTCTGCAGATCTTCACTGTATTTAGTGA 120
 DB 61 GAAATATGTAGCAAGCTGTGTATCATATGATTTTCTGCAGATCTTCACTGTATTTAGTGA 120
 QY 121 TCCGATTAAGTATGACCTTAAACCGAAGACGCTCTCTGTTGTGTGTTTCTACACAG 180
 DB 121 TCCGATTAAGTATGACCTTAAACCGAAGACGCTCTCTGTTGTGTGTTTCTACACAG 180
 QY 181 GGCACCGGAGACCCACCCGACACAGCCCGAGATTTGTTAAGAAATACAGAACCAACA 240
 DB 181 GGCACCGGAGACCCACCCGACACAGCCCGAGATTTGTTAAGAAATACAGAACCAACA 240
 QY 241 CTGCGGTTATTTCTTGTCTCACTGCGGTTATGGTTACTGGGTCCTGGTATTCAGAA 300
 DB 241 CTGCGGTTATTTCTTGTCTCACTGCGGTTATGGTTACTGGGTCCTGGTATTCAGAA 300
 QY 301 TACACCTACTTTTGGCAATGGGAGGAAATATGATTAAGCACTTCAAGAGCTTGAAGC 360
 DB 301 TACACCTACTTTTGGCAATGGGAGGAAATATGATTAAGCACTTCAAGAGCTTGAAGC 360
 QY 361 CGGCAATTTCTATGACACTGTGACATGACATGACATGCTGTAGATTTAGAACTTGTGTG 420
 DB 361 CGGCAATTTCTATGACACTGTGACATGACATGACATGCTGTAGATTTAGAACTTGTGTG 420
 QY 421 CCGTGAATTCCTGACCTCTGCGCAGCCCTCAGAAAGATTTTATAGTCAACAGAGGACAA 480
 DB 421 CCGTGAATTCCTGACCTCTGCGCAGCCCTCAGAAAGATTTTATAGTCAACAGAGGACAA 480
 QY 481 GAGGAGATTAAGTGGCGCACTCCCGGTGGCATCACTGTGATCTTTGAGGACAGACCTTGTG 540
 DB 481 GAGGAGATTAAGTGGCGCACTCCCGGTGGCATCACTGTGATCTTTGAGGACAGACCTTGTG 540
 QY 541 AAGTCAGAGCTGTACACATTTGAATCTCAAGTCAGAGCTTCTGATTCAGATTCAGGA 600
 DB 541 AAGTCAGAGCTGTACACATTTGAATCTCAAGTCAGAGCTTCTGATTCAGATTCAGGA 600
 QY 601 AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAAGCAACCAATCAATGTGTGA 660
 DB 601 AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAAGCAACCAATCAATGTGTGA 660
 QY 661 ATTGAAGACTTGTGACTCTCACTTACCGGTTCCGATCCCGCACTCTCAAGAGCTCTCTG 720
 DB 661 ATTGAAGACTTGTGACTCTCACTTACCGGTTCCGATCCCGCACTCTCAAGAGCTCTCTG 720
 QY 721 AATATTCCTGTTTACCCCGAATATTTACAGGTATCATGTGAGAGGTCTTTGGCCAG 780
 DB 721 AATATTCCTGTTTACCCCGAATATTTACAGGTATCATGTGAGAGGTCTTTGGCCAG 780
 QY 781 GAGGAAAGCCAGATATCTGTGACTTCAAGCATCACTTTTCAAGTCCCAATTTCAAAG 840
 DB 781 GAGGAAAGCCAGATATCTGTGACTTCAAGCATCACTTTTCAAGTCCCAATTTCAAAG 840
 QY 841 GCAGTTCAACTTACTAGCAATGATGCAATTAAGCACTGCTGATGATTTGAGATTT 900
 DB 841 GCAGTTCAACTTACTAGCAATGATGCAATTAAGCACTGCTGATGATTTGAGATTT 900

QY 901 TCMAATACAGACTTTTCTATACAGCTGTGATGCTTACGCTGATCTGCTTAAACAGT 960
 DB 901 TCMAATACAGACTTTTCTATACAGCTGTGATGCTTACGCTGATCTGCTTAAACAGT 960
 QY 961 GATTCGAGGTCAAGCCCTACCTCAAGACCTGACCTTGAAGATTAAGAGAGCACTGC 1020
 DB 961 GATTCGAGGTCAAGCCCTACCTCAAGACCTGACCTTGAAGATTAAGAGAGCACTGC 1020
 QY 1021 GTCCCTTTGAAATAAAGGACAGACCAAGAAAGAGAGCTTACCTCCAGCATATA 1080
 DB 1021 GTCCCTTTGAAATAAAGGACAGACCAAGAAAGAGAGCTTACCTCCAGCATATA 1080
 QY 1081 CTTGCGGATATGTTCTCTCAAGTTCATTTTACCTGCTGTGAATCCGAGCAATTCCT 1140
 DB 1081 CTTGCGGATATGTTCTCTCAAGTTCATTTTACCTGCTGTGAATCCGAGCAATTCCT 1140
 QY 1141 AAAAAGCAATTTTGGAGCCCTGTGGAATATACAGTGAACAGCTGTAAGAGCCAGG 1200
 DB 1141 AAAAAGCAATTTTGGAGCCCTGTGGAATATACAGTGAACAGCTGTAAGAGCCAGG 1200
 QY 1201 CTACAGAGCTGTGACATTAACAGAGGAGGACCGATTTATAGCCCTTGTACAGATGCC 1260
 DB 1201 CTACAGAGCTGTGACATTAACAGAGGAGGACCGATTTATAGCCCTTGTACAGATGCC 1260
 QY 1261 TGTGCTGCTTGTGATCTCTCTGCTTTCCTTCTTCCAGCCACCACTCACTGCTC 1320
 DB 1261 TGTGCTGCTTGTGATCTCTCTGCTTTCCTTCTTCCAGCCACCACTCACTGCTC 1320
 QY 1321 CTGCTGGAACATCTTCTTAACTTCAACCCAGACCAATTCGATGCAAGCTCAAGTTTA 1380
 DB 1321 CTGCTGGAACATCTTCTTAACTTCAACCCAGACCAATTCGATGCAAGCTCAAGTTTA 1380
 QY 1381 TTTCAACCAAGAAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTGTCTACCTGCCACA 1440
 DB 1381 TTTCAACCAAGAAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTGTCTACCTGCCACA 1440
 QY 1441 ACAAGGTTCTGCGGAGGAGATATGATACAGCTGCTGCTGCTTGTGTTGCTTCACTT 1500
 DB 1441 ACAAGGTTCTGCGGAGGAGATATGATACAGCTGCTGCTGCTTGTGTTGCTTCACTT 1500
 QY 1501 CTTCAAGCAAACTAATGATGATCCCATGAAGACAGGAGGAAAGCCCTGAGCTCTTAAGATA 1560
 DB 1501 CTTCAAGCAAACTAATGATGATCCCATGAAGACAGGAGGAAAGCCCTGAGCTCTTAAGATA 1560
 QY 1561 TCCATCTCTCTTGAACCAAAATCTTTCATCTTCAAGATGACCCCTCAATCCCATC 1620
 DB 1561 TCCATCTCTCTTGAACCAAAATCTTTCATCTTCAAGATGACCCCTCAATCCCATC 1620
 QY 1621 ATATAGGTGGTTCAGGAACCGGATAGCCCGTTTATGTGGTTCTTCAACAATAGAG 1680
 DB 1621 ATATAGGTGGTTCAGGAACCGGATAGCCCGTTTATGTGGTTCTTCAACAATAGAG 1680
 QY 1681 AAATCTCAAGAAACAACCCAGATGGAATTTTGAAGCAATGTGTTTGTGCTGC 1740
 DB 1681 AAATCTCAAGAAACAACCCAGATGGAATTTTGAAGCAATGTGTTTGTGCTGC 1740
 QY 1741 AGGCATTAAGATAGGATTAATCTATTCAAGAAAGAGCTCAGACATTTCTTAAGCATGG 1800
 DB 1741 AGGCATTAAGATAGGATTAATCTATTCAAGAAAGAGCTCAGACATTTCTTAAGCATGG 1800
 QY 1801 ATCTTAATCTATTAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGGAGAGGCC 1860
 DB 1801 ATCTTAATCTATTAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGGAGAGGCC 1860
 QY 1861 CGAGCAAGATATGATCAAGCAACATCCAGCTTCAAGGAGGAGGAGGAGGAGATCTC 1920
 DB 1861 CGAGCAAGATATGATCAAGCAACATCCAGCTTCAAGGAGGAGGAGGAGGAGATCTC 1920
 QY 1921 CTCAGAGAAACGGCCATATTTATGTGTGTGAGATGCAAGATATGCGCAAGATGTA 1980
 DB 1921 CTCAGAGAAACGGCCATATTTATGTGTGTGAGATGCAAGATATGCGCAAGATGTA 1980

QY 1981 CATGATGCGCTTGTGCAATTAATTAAGCAAGAGTTGAGTTGAAAACCTAGAGCAATG 2040
 DB 1981 CATGATGCGCTTGTGCAATTAATTAAGCAAGAGTTGAGTTGAAAACCTAGAGCAATG 2040
 QY 2041 AAAACCTGCGCACTTTAAAGAGAGAAACCGTACCTTCAGATATTTTGTCA 2094
 DB 2041 AAAACCTGCGCACTTTAAAGAGAGAAACCGTACCTTCAGATATTTTGTCA 2094

RESULT 6

AD087538
 ID AD087538 standard; cDNA; 3270 BP.

AC AD087538;
 DT 07-OCT-2004 (first entry)

XX Human tumour-associated antigenic target (TAT) cDNA sequence #4416.

XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
 XX cancer; cell proliferative disorder; gene; ss.

XX Homo sapiens.

XX WO2004060270-A2.

XX 22-JUL-2004.

XX 15-OCT-2003; 2003WO-US029126.

XX 18-OCT-2002; 2002US-0418988P.

XX (GENT) GENENTECH INC.

XX (WUTD/) WU T D.

XX (ZHOU/) ZHOU Y.

XX Wu TD, Zhou Y;

XX WPI; 2004-534300/51.

XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
 PT preventing or treating cell proliferative disorders such as cancer.

XX Claim 1; SEQ ID NO 4416; 5504bp; English.

XX The present invention describes an isolated tumour-associated antigenic
 CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
 CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
 CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
 CC sequence identity to (a)-(c); or (e) a sequence that hybridizes to (a)-
 CC (c). Also described: (1) an expression vector comprising the above
 CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
 CC a process for producing a polypeptide; (4) an isolated polypeptide
 CC comprising: (a) an amino acid sequence encoded by any of the above
 CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
 CC length coding region of the above nucleotide sequences; or (c) a sequence
 CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
 CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
 CC an isolated antibody that binds to the above polypeptide; (7) a process
 CC for producing the antibody; (8) an isolated oligopeptide that binds to
 CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
 CC binding organic molecule that binds to the above polypeptide; (10) a
 CC composition of matter comprising the above (chimeric) polypeptide,
 CC antibody, oligopeptide or TAT binding organic molecule, in combination
 CC with a carrier; (11) an article of manufacture comprising a container and
 CC the composition of matter contained within the container; (12) methods of
 CC inhibiting the growth of a cell that expresses the above protein, where
 CC the growth of the cell is at least in part dependent upon a growth
 CC potentiating effect of the above protein; (13) a method of
 CC therapeutically treating a mammal having a cancerous tumour comprising
 CC cells that express the above protein; (14) a method of determining the
 CC presence of a protein in a sample suspected of containing the protein
 CC described above; (15) methods of diagnosing the presence of a tumour in a

CC mammal; (16) a method for treating or preventing a cell proliferative
 CC disorder associated with increased expression or activity of the above
 CC protein; and (17) a method of binding an antibody, oligopeptide or
 CC organic molecule to a cell that expresses the protein described above.
 CC The TAT sequences have cytostatic activities, and can be used in gene
 CC therapy. The composition and methods are useful for diagnosing,
 CC preventing or treating cancer. The composition is also used for preparing
 CC a medicament for the therapeutic treatment or diagnostic detection of a
 CC cell proliferative disorder or cancer. The present sequence represents a
 CC human TAT cDNA sequence from the present invention.

XX Sequence 3270 BP; 934 A; 702 C; 680 G; 954 T; 0 U; 0 Other;

XX Query Match 95.1%; Score 1995; DB 13; Length 3270;
 XX Best Local Similarity 99.9%; Pred. No. 0;
 XX Matches 2095; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAGAGGTTTCTGTATATATGCTACACAGAGGACAGGCAAGCCATCGAGAA 60
 DB 112 ATGAGAGGTTTCTGTATATATGCTACACAGAGGACAGGCAAGCCATCGAGAA 171
 QY 61 GAAATATGAGACCAAGCTGTGTACATGATTTTCTGAGATCTTCACTATAGTGA 120
 DB 172 GAAATATGAGACCAAGCTGTGTACATGATTTTCTGAGATCTTCACTATAGTGA 231
 QY 121 TCCGATTAAGTATGACCTTAAACCGAAACAGCTCTCTGTGTGTGTGTTCTACAG 180
 DB 232 TCCGATTAAGTATGACCTTAAACCGAAACAGCTCTCTGTGTGTGTGTTCTACAG 291
 QY 181 GGCACCGAGAGACCAACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCA 240
 DB 292 GGCACCGAGAGACCAACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCA 351
 QY 241 CTCGGGTTGATTTCTTGTCTCACTGCGGTAATGGTTACTGGTCTCGGTATTCAGAA 300
 DB 352 CTCGGGTTGATTTCTTGTCTCACTGCGGTAATGGTTACTGGTCTCGGTATTCAGAA 411
 QY 301 TACACCTACTTTTGCAATGGGGGGAAGATTAATGATTAACGACTTCAAGAGCTGAGCC 360
 DB 412 TACACCTACTTTTGCAATGGGGGGAAGATTAATGATTAACGACTTCAAGAGCTGAGCC 471
 QY 361 CGGATTTCTATGACACTGACATGACATGACATGACATGACATGACATGACATGACAT 420
 DB 472 CGGATTTCTATGACACTGACATGACATGACATGACATGACATGACATGACATGACAT 531
 QY 421 CCGTGATTTCTGACACTGACACTGACACTGACACTGACACTGACACTGACACTGAC 480
 DB 532 CCGTGATTTCTGACACTGACACTGACACTGACACTGACACTGACACTGACACTGAC 591
 QY 481 GAGGAGATAGGGGGGCACTCCGGTGACATCCCTGAGAGAGAGAGAGAGAGAGAGAG 540
 DB 592 GAGGAGATAGGGGGGCACTCCGGTGACATCCCTGAGAGAGAGAGAGAGAGAGAGAG 651
 QY 541 AAGTCAGAGCTCTACATGATTAATCTCAAGTCAGACTTCTGAGATTCATGAGAA 600
 DB 652 AAGTCAGAGCTCTACATGATTAATCTCAAGTCAGACTTCTGAGATTCATGAGAA 711
 QY 601 AAAAAAGATTCGAGGTTTGAAGCAAAATGACAGTACAGCAACCAATCCATGTTGTA 660
 DB 712 AAAAAAGATTCGAGGTTTGAAGCAAAATGACAGTACAGCAACCAATCCATGTTGTA 771
 QY 661 ATTGAAGATTTGAGGCTTCACTTACCGTTGGTATCCCACTCTCAAGAGCTCTG 720
 DB 772 ATTGAAGATTTGAGGCTTCACTTACCGTTGGTATCCCACTCTCAAGAGCTCTG 831
 QY 721 AATATTCCTGTTTACCCCAAGATATTTACAGTATCTGACAGAGTCTTGGCCAG 780
 DB 832 AATATTCCTGTTTACCCCAAGATATTTACAGTATCTGACAGAGTCTTGGCCAG 891
 QY 781 GAGGAAAGCAAGTATCTGACTTCAAGATTCAGATTTTCAAGTGCATTTCAAG 840
 DB 892 GAGGAAAGCAAGTATCTGACTTCAAGATTCAGATTTTCAAGTGCATTTCAAG 951

Qy	841	GCAGTTCAACTTACTACGAAGAAGTGGCCATAAAACA	CTGCGTGGTAAATTTGGACATT	900
Db	952	GCAGTTCAACTTACTACGAAGAAGTGGCCATAAAACA	CTGCGTGGTAAATTTGGACATT	1011
Qy	901	TCAAAATACAGACTTTTCTCTATCAGCGTGGAGATCG	CTTCAGCGGATCTGCGCTTAAACAGT	960
Db	1012	TCAAATACAGACTTTTCTCTATCAGCGTGGAGATCG	CTTCAGCGGATCTGCGCTTAAACAGT	1071
Qy	961	GATTCTGAGGTACAAAGCTTACTCCAAAGACTGAGCT	TGAAGATPAAAGAGACACTGC	1020
Db	1072	GATTCTGAGGTACAAAGCTTACTCCAAAGACTGAGCT	TGAAGATPAAAGAGACACTGC	1131
Qy	1021	GTCCCTTTGAAAAATPAAAGCAGACACAAAGAAAGAA	AGGAGTACTCTTAACCCAGACATTA	1080
Db	1132	GTCCCTTTGAAAAATPAAAGCAGACACAAAGAAAGAA	AGGAGTACTCTTAACCCAGACATTA	1191
Qy	1081	CCTGCGGGAGATGTTCTCTCAGTTCAATTTTACTG	TGTCGTTCTTGAATCCGAGCAATTCCT	1140
Db	1192	CCTGCGGGAGATGTTCTCTCAGTTCAATTTTACTG	TGTCGTTCTTGAATCCGAGCAATTCCT	1251
Qy	1141	AAAAAGCATTTTTGGCGAGCCCTTGTGACTATAC	AGTGAACAGTGTCTGAAAACGCAAG	1200
Db	1252	AAAAAGCATTTTTGGCGAGCCCTTGTGACTATAC	AGTGAACAGTGTCTGAAAACGCAAG	1311
Qy	1201	CTACAGAGCTGTGCAAGTAAACAAGGGGACCCCAT	TATPACCGCTTTGTATCCAGATATCC	1260
Db	1312	CTACAGAGCTGTGCAAGTAAACAAGGGGACCCCAT	TATPACCGCTTTGTATCCAGATATCC	1371
Qy	1261	TGTGCTGCTCTTGTGGATCTCTCCTCGCTTCCCT	CTTGCACAGCCACACTCAGTCTC	1320
Db	1372	TGTGCTGCTCTTGTGGATCTCTCCTCGCTTCCCT	CTTGCACAGCCACACTCAGTCTC	1431
Qy	1321	CTGCTCGAACATCTTCTCTPAACTTCAACCCAGAC	ACCATATTCGTGTGCAAGTCAAGTTTA	1380
Db	1432	CTGCTCGAACATCTTCTCTPAACTTCAACCCAGAC	ACCATATTCGTGTGCAAGTCAAGTTTA	1491
Qy	1381	TTTTCACCCAGAAAGCTCATTTTGTCTTCAACAT	TGTGGAAATTTCTGTCTTACCTGCACA	1440
Db	1492	TTTTCACCCAGAAAGCTCATTTTGTCTTCAACAT	TGTGGAAATTTCTGTCTTACCTGCACA	1551
Qy	1441	AACAGAGTTCGCGGAGGAGATATGTAACAGGCTGG	CGCGGACTTGTTGGTGTGCTTCAGTT	1500
Db	1552	ACAGAGTTCGCGGAGGAGATATGTAACAGGCTGG	CGCGGACTTGTTGGTGTGCTTCAGTT	1611
Qy	1501	CTTCAGCCAAACATPACATGATCTCCCATGAAAG	CACGCGGAAAGCCCTGCTCTTAAGATA	1560
Db	1612	CTTCAGCCAAACATPACATGATCTCCCATGAAAG	CACGCGGAAAGCCCTGCTCTTAAGATA	1671
Qy	1561	TCCATCTCTCTCGAACAACAATTTCTTCCAATT	ACAGATATGACCTCTCAATCCCATC	1620
Db	1672	TCCATCTCTCTCGAACAACAATTTCTTCCAATT	ACAGATATGACCTCTCAATCCCATC	1731
Qy	1621	ATPAAATGTGGGTCCAGGAACCGGCATAGCCCG	TTTATTTGGTTCCTATCAACATAGAGAG	1680
Db	1732	ATPAAATGTGGGTCCAGGAACCGGCATAGCCCG	TTTATTTGGTTCCTATCAACATAGAGAG	1791
Qy	1681	AAACTCCAGAAACAACCCAGATGGAATTTTGGAG	CATATGTGTTGTTTTTGGCTGC	1740
Db	1792	AAACTCCAGAAACAACCCAGATGGAATTTTGGAG	CATATGTGTTGTTTTTGGCTGC	1851
Qy	1741	AGGCAATAGATAGGAGTTATCTATTCAGAAAAG	CTCAGACATTTCTTTAAGCATGAG	1800
Db	1852	AGGCAATAGATAGGAGTTATCTATTCAGAAAAG	CTCAGACATTTCTTTAAGCATGAG	1911
Qy	1801	ATCTTAACTCATATPAAAGTTTCTCTTCAAGAG	ATGCTCTTGTGGGAGAGAAAGCC	1860
Db	1912	ATCTTAACTCATATPAAAGTTTCTCTTCAAGAG	ATGCTCTTGTGGGAGAGAAAGCC	1971
Qy	1861	CCAGCAAAATATGTATCAAGAACAACTCAGACT	TCAATGCGCAGAGGTGGCAGATCTTC	1920
Db	1972	CCAGCAAAATATGTATCAAGAACAACTCAGACT	TCAATGCGCAGAGGTGGCAGATCTTC	2031
Qy	1921	CTCCAGAGAAACGGCATATTTATATGTGTGAGAT	TGCAAGATATGSCCAAGATGTA	1980

Db	2032	CTCAGAGAAACGGCCATATTTATGTGTGTGGAATGCAGAAATATGCGCAAGATGTA	2091
Qy	1981	CATGATGCCCCCTGTGTGCAAAATATATAGCAAGAGTTGGATTGAAAACTAGAAACAATG	2040
Db	2092	CATGATGCCCCCTGTGTGCAAAATATATAGCAAGAGTTGGATTGAAAACTAGAAACAATG	2151
Qy	2041	AAAAACCTGGCCACTTTTAAAAAGAAAGAAACGCTAACCTTCAGGATATTTGGTCATTA	2097
Db	2152	AAAAACCTGGCCACTTTTAAAAAGAAAGAAACGCTAACCTTCAGGATATTTGGTCATTA	2208
RESULT 7			
ADM43212	ID	ADM43212 standard; cDNA; 2094 BP.	
XX	AC	ADM43212;	
XX	DT	03-JUN-2004 (first entry)	
XX	DE	Human methionine synthase reductase CDS G110A variant.	
XX	KW	Human; ss; Methionine synthase reductase polypeptide; HsmTRR; cancer;	
KW	KM	cardiovascular disease; neural tube defect; hyperhomocysteinemia;	
XX	OS	chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.	
XX	OS	Homo sapiens.	
PH	XX	Location/Qualifiers	
FT	FT	1..2094	
FT	FT	/*tag= a	
FT	FT	/product= "hsmTRR"	
FT	FT	/partial	
FT	FT	/note= "No stop codon shown"	
FT	FT	replace(66,A)	
FT	FT	/*tag= b	
FT	FT	/standard_name= "Single_nucleotide_polymorphism"	
FT	FT	replace(110,G)	
FT	FT	/*tag= c	
XX	XX	/standard_name= "Single_nucleotide_polymorphism"	
PN	XX	US2003082676-A1.	
PD	XX	01-MAY-2003.	
XX	PF	10-AUG-1999; 99US-00371347.	
XX	PR	16-JAN-1998; 98US-0071623P.	
XX	PR	15-JAN-1999; 99US-00232028.	
XX	PA	(GRAV// GRAVEL R A.	
PA	PA	(ROZE// ROZEN R.	
PA	PA	(LECL// LECLE R D.	
PA	PA	(WILS// WILSON A.	
PA	PA	(ROSE// ROSENBLATT D.	
XX	PI	Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;	
XX	DR	WPI; 2003-576610/54.	
DR	XX	P-F8DB; ADM43213.	
XX	XX		
PT	XX	New substantially pure nucleic acid encoding a mammalian methionine	
PT	XX	synthase reductase polypeptide, useful for diagnosing, preventing or	
PT	XX	treating conditions associated with altered methionine synthase activity,	
PT	XX	e.g. cancer.	
PS	XX	Disclosure; SEQ ID NO 43; 26pp; English.	
XX	XX		
CC	XX	The invention relates to a substantially pure nucleic acid that encodes a	
CC	XX	mammalian methionine synthase reductase polypeptide, HsmTRR, or that	
CC	XX	hybridises at high stringency to a nucleic acid appearing as ADM43208 or	
CC	XX	ADM43209. Also included are a non-human animal where one or both genetic	
CC	XX	alleles encoding the methionine synthase reductase polypeptide are	

CC mutated, an antibody that specifically binds the above methionine
CC synthase reductase polypeptide, a method of detecting the presence of the
CC above polypeptide, a method for detecting sequence variants for
CC methionine synthase reductase in a mammal, methods of treating or
CC preventing cancer (or cardiovascular disease or neural tube defects) in a
CC subject, methods of screening for a compound that modulates methionine
CC synthase reductase biological activity and a method for detecting an
CC increased risk of developing a neural tube defect in a mammalian embryo
CC or fetus. The nucleic acid is useful in diagnosing, preventing or
CC treating conditions associated with altered methionine synthase activity,
CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are
CC also associated with hyperhomocysteinemia. The gene for HsmTR is
CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
CC sequence of a variant human hsmTR cDNA.

XX Sequence 2094 BP; 592 A; 489 C; 480 G; 533 T; 0 U; 0 Other;

Query Match 95.0%; Score 1992; DB 11; Length 2094;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 2; Indels 0; Gaps 0;

Matches 2092; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAGAGGTTTCTGTACTATATGCTACACAGCAGGAGGCAAGGCCATCGCAGAA 60
DB 1 ATGAGAGGTTTCTGTACTATATGCTACACAGCAGGAGGCAAGGCCATCGCAGAA 60
QY 61 GAAATATGTAGACACCTGTGTACATGATATTTCTGCAGATCTTCACTATATTAAGAA 120
DB 61 GAAATATGTAGACACCTGTGTACATGATATTTCTGCAGATCTTCACTATATTAAGAA 120
QY 121 TCCGAAATATGACCTTAAACCCGAAAGAGCTCTCTGTGTGTGTGTCTTACACAG 180
DB 121 TCCGAAATATGACCTTAAACCCGAAAGAGCTCTCTGTGTGTGTGTCTTACACAG 180
QY 181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
DB 181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
QY 241 CTGCGCGGTGATTTCTTTGCTCACTCGCGATGAGTTACTGCGTCTCGTATTCAGAA 300
DB 241 CTGCGCGGTGATTTCTTTGCTCACTCGCGATGAGTTACTGCGTCTCGTATTCAGAA 300
QY 301 TTACACCTACTTTTGGCAATGGGGGGAAGATTAATGAATTAACGACTTAAAGCTTGGAGCC 360
DB 301 TTACACCTACTTTTGGCAATGGGGGGAAGATTAATGAATTAACGACTTAAAGCTTGGAGCC 360
QY 361 CGGCAATTTCTATGACACTGGAACATGAGATGACTGTGTAGTTTAAACCTTGTGTTGAG 420
DB 361 CGGCAATTTCTATGACACTGGAACATGAGATGACTGTGTAGTTTAAACCTTGTGTTGAG 420
QY 421 CCGTGATGCTGTGACTGTGGCCAGCCCTCAGAAACATTTTAAAGTCAAGCAGAGACA 480
DB 421 CCGTGATGCTGTGACTGTGGCCAGCCCTCAGAAACATTTTAAAGTCAAGCAGAGACA 480
QY 481 GAGGAAATAGTGGCGCACTCCCGGTGGCATCCTGCACTCTTGAAGACAGACCTTGG 540
DB 481 GAGGAAATAGTGGCGCACTCCCGGTGGCATCCTGCACTCTTGAAGACAGACCTTGG 540
QY 541 AAGTCAGAGCTGTACACATTTGAATCTCAAGTCGAGCTTCTGAGATTCAGATTCAGGA 600
DB 541 AAGTCAGAGCTGTACACATTTGAATCTCAAGTCGAGCTTCTGAGATTCAGATTCAGGA 600
QY 601 AGAAGAGATTTCTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATTCATGTTGTA 660
DB 601 AGAAGAGATTTCTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATTCATGTTGTA 660
QY 661 ATGGAAGACTTAAAGCTTCACTTACCCGTTGGTAAACCCCACTTCAACAGGCTCTG 720
DB 661 ATGGAAGACTTAAAGCTTCACTTACCCGTTGGTAAACCCCACTTCAACAGGCTCTG 720
QY 721 AATATTCCTGTGTTACCCCAAGATATTTTACAGGTACATCTGAGAGATCTTGGCCAG 780
DB 721 AATATTCCTGTGTTACCCCAAGATATTTTACAGGTACATCTGAGAGATCTTGGCCAG 780

DB 721 AATATTCCTGTGTTACCCCAAGATATTTTACAGGTACATCTGAGAGATCTTGGCCAG 780
QY 781 GAGGAAGCCAGATATCTGTGACTTCAGAGATTCAGGTTTCAAGTGCATTTCAAG 840
DB 781 GAGGAAGCCAGATATCTGTGACTTCAGAGATTCAGGTTTCAAGTGCATTTCAAG 840
QY 841 GCAATTCACCTACTACGAAATGATCCATTAACCACTCTGCTGTAGATTTGACAT 900
DB 841 GCAATTCACCTACTACGAAATGATCCATTAACCACTCTGCTGTAGATTTGACAT 900
QY 901 TCAATACAGACTTTTCTATCAGCTTGAGATGCTTCAAGCTGATCTGCTTACAT 960
DB 901 TCAATACAGACTTTTCTATCAGCTTGAGATGCTTCAAGCTGATCTGCTTACAT 960
QY 961 GATTCGAGGTACAAAGCTTCTCAAGACCTGAGCTTGAAGATTAAGAGACCTGC 1020
DB 961 GATTCGAGGTACAAAGCTTCTCAAGACCTGAGCTTGAAGATTAAGAGACCTGC 1020
QY 1021 GTCTTTTGAATAATTAAGCAGACACAAAGAAAGAGCTACCTTACCCAGCATATA 1080
DB 1021 GTCTTTTGAATAATTAAGCAGACACAAAGAAAGAGCTACCTTACCCAGCATATA 1080
QY 1081 CCGCGGAGATGTTCTCTCAGTTCAATTTTACCTGTGTCTTGAATCCGACAAATTCCT 1140
DB 1081 CCGCGGAGATGTTCTCTCAGTTCAATTTTACCTGTGTCTTGAATCCGACAAATTCCT 1140
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DB 1141 AAAAAAGCAATTTTCCGAGCCCTTGTGACATTAACAGTACAGTCTGAAGAGCCAG 1200
QY 1201 CTACAGAGCTGTGACATTAACAGAGGAGCCGATTAATAGCCGCTTGTGACAGATGCC 1260
DB 1201 CTACAGAGCTGTGACATTAACAGAGGAGCCGATTAATAGCCGCTTGTGACAGATGCC 1260
QY 1261 TGTGCTGTGTGTGATCTCTCTCGCTTCCCTTCTTCCGACGACCACTCACTCTC 1320
DB 1261 TGTGCTGTGTGTGATCTCTCTCGCTTCCCTTCTTCCGACGACCACTCACTCTC 1320
QY 1321 CTGCTCGAATCTTCTTAAATTTTCAACCCAGACCAATTCGAGGCAAGCTCAAGTTA 1380
DB 1321 CTGCTCGAATCTTCTTAAATTTTCAACCCAGACCAATTCGAGGCAAGCTCAAGTTA 1380
QY 1381 TTTCAACCCAGAAAGCTCAATTTGTCTTCAATTTGGAATTTCTGTCTACGACACA 1440
DB 1381 TTTCAACCCAGAAAGCTCAATTTGTCTTCAATTTGGAATTTCTGTCTACGACACA 1440
QY 1441 ACAGAGTTCTGCGGAAGGAGATGTACAGGCTGAGCTGCTGTGTGCTTCAAGTT 1500
DB 1441 ACAGAGTTCTGCGGAAGGAGATGTACAGGCTGAGCTGCTGTGTGCTTCAAGTT 1500
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DB 1501 CTTACAGCCAAATATCATGATCCCATGAAACAGCGGGAAGCCCTGCTCTTAAGATA 1560
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DB 1561 TCCATCTCTCTGGAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
QY 1621 ATTAATGTGGTTCAGAAACCCGATAGCCCGGTTATTTGGTCTCTACATAGAGAG 1680
DB 1621 ATTAATGTGGTTCAGAAACCCGATAGCCCGGTTATTTGGTCTCTACATAGAGAG 1680
QY 1681 AAACTCCAAAGAACACACCAAGATGGAATTTTGAAGCAATGTGTTTGTGGCTGC 1740
DB 1681 AAACTCCAAAGAACACACCAAGATGGAATTTTGAAGCAATGTGTTTGTGGCTGC 1740
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DB 1741 AGGCAATTAAGGATTAATCTAATTCAGAAAGAGCTCAGACATTTCTTAAGCATGG 1800
QY 1801 ATCTTAATCTCATTAAGGTTTCTTCTCAAGAGATGCTCTGTGTGGGAGAGAGGCC 1860
DB 1801 ATCTTAATCTCATTAAGGTTTCTTCTCAAGAGATGCTCTGTGTGGGAGAGAGGCC 1860

Qy	1861	CCAGCAAGTAGTGTGAACAACAATCCAGCTTCATGGCCAGCGATGGGAGAACTCTC	1920
Db	1861	CCAGCAAGTAGTGTGAACAACAATCCAGCTTCATGGCCAGCGATGGGAGAACTCTC	1920
Qy	1921	CTCCAGGAGAACGGCCATATTTATGTGTGTGAGATGCAAGAAATATGTGGCAAGATGTA	1980
Db	1921	CTCCAGGAGAACGGCCATATTTATGTGTGTGAGATGCAAGAAATATGTGGCAAGATGTA	1980
Qy	1981	CATGATGCCCCCTTGTGCAATTAATAAGCAAAGGTTGAGATTGAAAACTTGAAAGCAATG	2040
Db	1981	CATGATGCCCCCTTGTGCAATTAATAAGCAAAGGTTGAGATTGAAAACTTGAAAGCAATG	2040
Qy	2041	AAAAACCCCTGGCCACTTTAAAGAGAAAAAGCTCACTTCACAGATATTGGTCA	2094
Db	2041	AAAAACCCCTGGCCACTTTAAAGAGAAAAAGCTCACTTCACAGATATTGGTCA	2094
RESULT 8			
AAAS8935			
AAAS8935		standard; DNA; 3259 BP.	
AAAS8935;			
07-NOV-2000		(first entry)	
DNA		encoding a human methionine synthase reductase polypeptide.	
Human; methionine synthase reductase; MTRR; cancer;			
cardiovascular disease; Down's Syndrome; neural tube defect;			
premature coronary artery disease; 88.			
Homo sapiens.			
Key		Location/Qualifiers	
CDS		80..2176	
FT		/*tag= a	
FT		/product= "methionine synthase reductase"	
MO200042196-A2.			
20-JUL-2000.			
14-JAN-2000; 2000MO-IB000209.			
15-JAN-1999; 99US-00232028.			
10-AUG-1999; 99US-00371347.			
(UVMC-) UNIV MCGILL.			
Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;			
WPI; 2000-466131/40.			
P-PSDB; AAB07591.			
Mammalian methionine synthase reductase nucleic acid used for detecting			
an increased risk of developing a neural tube defect, Down's Syndrome or			
cardiovascular disease in a mammalian embryo or fetus.			
Claim 3; Fig 3; 85pp; English.			
The present sequence encodes a human methionine synthase reductase (MTRR)			
polypeptide. Inhibitors of MTRR polypeptide and polynucleotide are used			
for treating or preventing cancer, cardiovascular disease, Down's			
Syndrome or neural tube defects in a subject. The cardiovascular disease			
is premature coronary artery disease. The compounds are detected by			
methods which screen for modulators of MTRR biological activity. MTRR			
polypeptide or nucleic acid is examined for the presence of a			
polymorphism in the parents or the embryo or foetus, and the information			
used for detecting an increased risk of an embryo or foetus developing			
cancer, cardiovascular disease, Down's Syndrome or neural tube defects			
Sequence 3259 BP; 944 A; 706 C; 663 G; 946 T; 0 U; 0 Other;			

Query	Match	Similarity	92.7%	Score	19.44	DB	3	Length	3259
Best Local	Similarity	99.9%	Prod.	No. 0					
Matches	2094	Conservative	0	Mismatches	3	Indels	0	Gaps	0
QY	1	ATGAGGAGTTTCTGTTACTATATGTCTACACAGCAGGAGACAGCCAAAGCCATCGCAGAA	60						
Db	80	ATGAGGAGGTTTCTGTTACTATATGTCTACACAGCAGGAGACAGCCAAAGCCATCGCAGAA	139						
QY	61	GAATATATGAGGACAGGTGAGTACATGATTTTCTGCAATCTTCACTGTATTTAGGAA	120						
Db	140	GAATATGTTGACAGGTGAGTACATGATTTTCTGCAATCTTCACTGTATTTAGGAA	139						
QY	121	TCCGATATAGTATGACCTTAAACCCGAAACAGCTCTTGTGTGTGTCTTACACAG	180						
Db	200	TCCGATATATGATATGACCTTAAACCCGAAACAGCTCTTGTGTGTGTGTCTTACACAG	259						
QY	181	GGCACCCGAGAACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA	240						
Db	260	GGCACCCGAGAACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA	319						
QY	241	CTGCGCGGTGATTTCTTGTGCTCACCTCGGTATGAGGTTACTGGGTCTCGGTGATTCAGAA	300						
Db	320	CTGCGCGGTGATTTCTTGTGCTCACCTCGGTATGAGGTTACTGGGTCTCGGTGATTCAGAA	379						
QY	301	TACACCTACTTTTTCGAAATGAGGAGGAGATTAATGATTAACGACTTCAAGCTTTGAGCC	360						
Db	380	TACACCTACTTTTTCGAAATGAGGAGGAGATTAATGATTAACGACTTCAAGCTTTGAGCC	439						
QY	361	CGGATTTCTATATGACATGACATGACATGACATGACATGACATGACATGACATGACATGAC	420						
Db	440	CGGATTTCTATATGACATGACATGACATGACATGACATGACATGACATGACATGACATGAC	499						
QY	421	CCGTGATTTCTGAGACTCTGCGCAGCCCTCAGAAAGCATTTTATGATCAAGCAGAGCAA	480						
Db	500	CCGTGATTTCTGAGACTCTGCGCAGCCCTCAGAAAGCATTTTATGATCAAGCAGAGCAA	559						
QY	481	GAGAGATTAAGTGGCGCACTCCCGGTGGCATCACTGTCATCTCTTGAAGACAGACCTTGTG	540						
Db	560	GAGAGATTAAGTGGCGCACTCCCGGTGGCATCACTGTCATCTCTTGAAGACAGACCTTGTG	619						
QY	541	AAGTCAGAGCTGACATCATTTGAATCTCAAGTCGAGCTTCTGAGATTCGATGATTCAGAA	600						
Db	620	AAGTCAGAGCTGACATCATTTGAATCTCAAGTCGAGCTTCTGAGATTCGATGATTCAGAA	679						
QY	601	AGAAAGATTTCTGAGTTTGAAGCAAAATGACGTGAACAGCAACCAATCCATGTTGTGA	660						
Db	680	AGAAAGATTTCTGAGTTTGAAGCAAAATGACGTGAACAGCAACCAATCCATGTTGTGA	739						
QY	661	ATTGAAGATTTGAGTCTCACTTACCCGTTCCGTTACCCCACTCTCAAGAGCCCTCTG	720						
Db	740	ATTGAAGATTTGAGTCTCACTTACCCGTTCCGTTACCCCACTCTCAAGAGCCCTCTG	799						
QY	721	AATATTCCTGTTTACCCCCAGAAATATTTACAGTACATCTGACAGAGTCTTTGGCAG	780						
Db	800	AATATTCCTGTTTACCCCCAGAAATATTTACAGTACATCTGACAGAGTCTTTGGCAG	859						
QY	781	GAGGAAAGCCAGATATCTGATCTTCAAGCATCTCAAGTTTCTTCAAGTCCCATTTCAAG	840						
Db	860	GAGGAAAGCCAGATATCTGATCTTCAAGCATCTCAAGTTTCTTCAAGTCCCATTTCAAG	919						
QY	841	GCAGTCAACTTATACAGATGATGACATTAACCACTCTGCTGTATGAAATTTGACATTT	900						
Db	920	GCAGTCAACTTATACAGATGATGACATTAACCACTCTGCTGTATGAAATTTGACATTT	979						
QY	901	TCAAATACAGCTTTTCTTATCAGCTGAGAGTCTTCAAGCTGATCTGCTTACACGT	960						
Db	980	TCAAATACAGCTTTTCTTATCAGCTGAGAGTCTTCAAGCTGATCTGCTTACACGT	1039						
QY	961	GATTTCTGAGTACAAAGCTTATCTCAAGATGACATGACATGACATGACATGACATGACATGAC	1020						
Db	1040	GATTTCTGAGTACAAAGCTTATCTCAAGATGACATGACATGACATGACATGACATGACATGAC	1099						

Qy	1021	GTCCCTTTGAAATTAAGGCGAGACAAGAAAGAAAGAGCTACCTTAACCCAGCATATA	1089
Db	1100	GTCCCTTTGAAATTAAGGCGAGACAAGAAAGAAAGAGCTACCTTAACCCAGCATATA	1159
Qy	1081	CCTCGGGATCTTCTCCAGTTCAATTTTATCCTGTGTCTTTGAATCCGAGCAATTCCT	1140
Db	1160	CCTCGGGATCTTCTCCAGTTCAATTTTATCCTGTGTCTTTGAATCCGAGCAATTCCT	1219
Qy	1141	AAAAAGGCAATTTTGGCGAGCCCTTGTGGACTATACAGTGCAGTGTGAAAAGCGCAGG	1200
Db	1220	AAAAAGGCAATTTTGGCGAGCCCTTGTGGACTATACAGTGCAGTGTGAAAAGCGCAGG	1279
Qy	1201	CTACGAGAGCTGTGAGATPAACAAGGGGCGAGCCGATTTATCCGCTTTGTACAGATATCC	1260
Db	1280	CTACGAGAGCTGTGAGATPAACAAGGGGCGAGCCGATTTATCCGCTTTGTACAGATATCC	1339
Qy	1261	TGTGCTGTCTGTTGGATCTCTCTCTCGCTTTCCTCTTCCAGCCACACTCAGTCTC	1320
Db	1340	TGTGCTGTCTGTTGGATCTCTCTCTCGCTTTCCTCTTCCAGCCACACTCAGTCTC	1399
Qy	1321	CTGCTCCGAACATCTTCTTAACTTCAACCCGACATATGTGTGTGGAAGGCTCAAGTTTA	1380
Db	1400	CTGCTCCGAACATCTTCTTAACTTCAACCCGACATATGTGTGTGGAAGGCTCAAGTTTA	1459
Qy	1381	TTTCAACCAGGAAAGCTCATTGTTGTCTTCAACATGTGGAATTTCTGTCTACTGCCACA	1440
Db	1460	TTTCAACCAGGAAAGCTCATTGTTGTCTTCAACATGTGGAATTTCTGTCTACTGCCACA	1519
Qy	1441	ACAGAGTTCTGCGGAGGGAGATGTACAGGCTGCGCTTGTGTGCTTCACTT	1500
Db	1520	ACAGAGTTCTGCGGAGGGAGATGTACAGGCTGCGCTTGTGTGCTTCACTT	1579
Qy	1501	CTTCAGCCAAACATACATGCAATCCCATAGAAGCAGCGGAAAGCCCTGACTCTTAAGATA	1560
Db	1580	CTTCAGCCAAACATACATGCAATCCCATAGAAGCAGCGGAAAGCCCTGACTCTTAAGATA	1639
Qy	1561	TCGATCTCTCGAGCAACAAATTCCTTCCACTTACAGATGACCCCTCAATCCCATC	1620
Db	1640	TCGATCTCTCGAGCAACAAATTCCTTCCACTTACAGATGACCCCTCAATCCCATC	1699
Qy	1621	ATTAATGTGGGTCCAGGAAACCGGCACTACCCCGCTTAATTTGGGTCTCTAACATPAAGAG	1688
Db	1700	ATTAATGTGGGTCCAGGAAACCGGCACTACCCCGCTTAATTTGGGTCTCTAACATPAAGAG	1759
Qy	1681	AAACTCCAAAGAACCAACCCAGATGGAATTTTGGAGCAATGTGGTGTGTTTTTGGCTGC	1740
Db	1760	AAACTCCAAAGAACCAACCCAGATGGAATTTTGGAGCAATGTGGTGTGTTTTTGGCTGC	1819
Qy	1741	AGGCATAAGATAGGGATTATCTATTCAGAAAAGCTCAGACATTTCTTATAGATGGG	1800
Db	1820	AGGCATAAGATAGGGATTATCTATTCAGAAAAGCTCAGACATTTCTTATAGATGGG	1879
Qy	1801	ATCTTAACTCATCTPAAGGTTTCCTCTCAAGAGATGTCCTGTGTGGGAGAGGAGAACCC	1866
Db	1880	ATCTTAACTCATCTPAAGGTTTCCTCTCAAGAGATGTCCTGTGTGGGAGAGGAGAACCC	1933
Qy	1861	CCAGCAAGTATGTACAAAGCAACATCCAGCTTCAATGCGCAGCAGAGTGGCGAATCTCTC	1920
Db	1940	CCAGCAAGTATGTACAAAGCAACATCCAGCTTCAATGCGCAGCAGAGTGGCGAATCTCTC	1999
Qy	1921	CTCCAGAGGAACGGCATATTTATGTGTGTGAGATGCAAGAATATATGGCCAGAGATTA	1988
Db	2000	CTCCAGAGGAACGGCATATTTATGTGTGTGAGATGCAAGAATATATGGCCAGAGATTA	2055
Qy	1981	CATGATGCCCTTGTGCAATATATAAGCAAAAGTGTGAAAGTTGAAAACCTAGAGCAATG	2040
Db	2060	CATGATGCCCTTGTGCAATATATAAGCAAAAGTGTGAAAGTTGAAAACCTAGAGCAATG	2119
Qy	2041	AAAAACCTGTGCACTTTTAAAGAAAGAAAACGCTACCTTCAGAGATATTTGTGCTATA	2097
Db	2120	AAAAACCTGTGCACTTTTAAAGAAAGAAAACGCTACCTTCAGAGATATTTGTGCTATA	2176

XX	RESULT 9
XX	ID ADM43216
XX	ADM43216 standard; cDNA; 2091 BP.
XX	ADM43216;
XX	03-JUN-2004 (first entry)
XX	Human methionine synthase reductase CDS del 1726-1728 variant.
XX	Human; sex: Methionine synthase reductase polypeptide; HAMTRR; cancer;
XX	cardiovascular disease; neural tube defect; hyperhomocysteinaemia;
XX	chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.
XX	Homo sapiens.
XX	Location/Qualifiers
XX	1. 2091
XX	/*tag= a
XX	/product= "hamTRRdel1559"
XX	/partial
XX	/note= "No stop codon shown"
XX	replace(66,A)
XX	/tag= b
XX	/standard_name= "single_nucleotide_polymorphism"
XX	replace(110,A)
XX	/*tag= c
XX	/standard_name= "single_nucleotide_polymorphism"
XX	replace(1726,TTGT)
XX	/*tag= d
XX	US2003082676-A1.
XX	01-MAY-2003.
XX	10-AUG-1999; 99US-00371347.
XX	16-JAN-1998; 98US-00716222.
XX	15-JAN-1999; 99US-00232028.
XX	(GRAV/) GRAVEL R. A.
XX	(ROZE/) ROZEN R.
XX	(LECL/) LECLERC D.
XX	(WILS/) WILSON A.
XX	(ROSE/) ROSENBLATT D.
XX	Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX	WPI; 2003-576610/54.
XX	P-PSDB; ADM43217.
XX	New substantially pure nucleic acid encoding a mammalian methionine
XX	synthase reductase polypeptide, useful for diagnosing, preventing or
XX	treating conditions associated with altered methionine synthase activity,
XX	e.g. cancer.
XX	Disclosure; SEQ ID NO 45; 26pp; English.
XX	The invention relates to a substantially pure nucleic acid that encodes a
XX	mammalian methionine synthase reductase polypeptide, HAMTRR, or that
XX	hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
XX	ADM43309. Also included are a non-human animal where one or both genetic
XX	alleles encoding the methionine synthase reductase polypeptide are
XX	mutated, an antibody that specifically binds the above methionine
XX	synthase reductase polypeptide, a method of detecting the presence of the
XX	above polypeptide, a method for detecting sequence variants for
XX	methionine synthase reductase in a mammal, methods of treating or
XX	preventing cancer (or cardiovascular disease or neural tube defects) in a
XX	subject, methods of screening for a compound that modulates methionine
XX	synthase reductase biological activity and a method for detecting an
XX	increased risk of developing a neural tube defect in a mammalian embryo
XX	or foetus. The nucleic acid is useful in diagnosing, preventing or
XX	treating conditions associated with altered methionine synthase activity.

CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are
CC also associated with hyperhomocysteinemia. The gene for Hmtrr is
CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
CC sequence of a variant human hmtrr cDNA.

XX Sequence 2091 BP; 591 A; 489 C; 480 G; 531 T; 0 U; 0 Other;

Query Match 85.8%; Score 1800; DB 11; Length 2091;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2090; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

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QY 1 ATGAGAGGTTTCTGTTACTATATGCTACACAGAGGAGCAAGCAAGCCATGCGAGAA 60
Db 1 ATGAGAGGTTTCTGTTACTATATGCTACACAGAGGAGCAAGCAAGCCATGCGAGAA 60
QY 61 GAAATATGTAGCAAGAGCTGTGTACATGTAGATTTCTGCAAGATCTTCACTGTATTATGAA 120
Db 61 GAAATGTGTAGCAAGAGCTGTGTACATGTAGATTTCTGCAAGATCTTCACTGTATTATGAA 120
QY 121 TCCGATATGATGACTTAAACCCGAAACAGCTCTTGTGTGTGTGTTTCTACACAG 180
Db 121 TCCGATATGATGACTTAAACCCGAAACAGCTCTTGTGTGTGTGTTTCTACACAG 180
QY 121 TCCGATATGATGACTTAAACCCGAAACAGCTCTTGTGTGTGTGTTTCTACACAG 180
Db 121 TCCGATATGATGACTTAAACCCGAAACAGCTCTTGTGTGTGTGTTTCTACACAG 180
QY 181 GGCACCGGAGACCCACCCGACACAGCCGCAAGTTTGTAAAGAAATACAAACAAACA 240
Db 181 GGCACCGGAGACCCACCCGACACAGCCGCAAGTTTGTAAAGAAATACAAACAAACA 240
QY 241 CTGCGCGGTATTTCTTGTCTGCTACCTGTGGATATGGGTTACTGGGTCTCGGTGATTCA 300
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QY 301 TACACTACTTTTGGCAATGGGGGGAATATATGATTAACGACTTCAAGAGCTTGAGCC 360
Db 301 TACACTACTTTTGGCAATGGGGGGAATATATGATTAACGACTTCAAGAGCTTGAGCC 360
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Db 361 CGGCAATTTCTATGACACTGTGACATGTAGATGCTGTAGAGTTTGAACCTTGTGTGAG 420
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Db 421 CCGGTGATTTGCTGTGACTGTGGCCAGCCCTTCAAGAAAGATTTTGAAGTACAGAGGACA 480
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QY 601 AGAAGAGATTTCTGAGTTTGAAGCAAAATGCAAGTGAAGCAAGCAATCCAAATGTTGA 660
Db 601 AGAAGAGATTTCTGAGTTTGAAGCAAAATGCAAGTGAAGCAAGCAATCCAAATGTTGA 660
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QY 781 GAGGAAAGCCCAAGATATCTGTGACTTTCAGCAAGATCCAGTTTTCAGGCAATTTCAAG 840
Db 781 GAGGAAAGCCCAAGATATCTGTGACTTTCAGCAAGATCCAGTTTTCAGGCAATTTCAAG 840
QY 841 GCAATTCACCTTACTAGCAATGATGCAATAAAACCACTGCTGTGTAGATTTGCAATT 900
Db 841 GCAATTCACCTTACTAGCAATGATGCAATAAAACCACTGCTGTGTAGATTTGCAATT 900
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QY 901 TCAATATACAGACTTTTCTATACAGCTTGAGATGCTTCAAGCTGATCTGCCCTAACAT 960
Db 901 TCAATATACAGACTTTTCTATACAGCTTGAGATGCTTCAAGCTGATCTGCCCTAACAT 960
QY 961 GATTCGAGGTCAAGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1020
Db 961 GATTCGAGGTCAAGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1020
QY 1021 GTTCCTTTTGAATAAAGGAGAGACACAAAGAAAGAGAGCTTACCTTACCCAGCATATA 1080
Db 1021 GTTCCTTTTGAATAAAGGAGAGACACAAAGAAAGAGAGCTTACCTTACCCAGCATATA 1080
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QY 1381 TTTCAACCAGAAAGCTTCAATTTTGTCTTCAACATTTGTGGAATTTGTCTACTGACACA 1440
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Db 1621 ATTAATGTGTGTCAAGAAACCGGCAATAGCCCGCTTATTTGGGTTCTTCAACAATAGAG 1680
QY 1681 AAATCTCAAGAAACAAACCAAGATGGAATTTTGGAGCAATGTGTGTTTGTGTGCTGC 1740
Db 1681 AAATCTCAAGAAACAAACCAAGATGGAATTTTGGAGCAATGTGTGTTTGTGTGCTGC 1740
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QY 1738 AGCATTAAGATTAAGATTAATCTTACAGAAAGAGCTCAGACATTTCTTAAAGATGGG 1797
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QY 1801 ATCTTAATCTATTAAGATTTTCTTCTCAAGAGATGCTCTGTGTGGAGAGAGAGGCC 1860
Db 1801 ATCTTAATCTATTAAGATTTTCTTCTCAAGAGATGCTCTGTGTGGAGAGAGAGGCC 1860
QY 1798 ATCTTAATCTATTAAGATTTTCTTCTCAAGAGATGCTCTGTGTGGAGAGAGAGGCC 1857
Db 1798 ATCTTAATCTATTAAGATTTTCTTCTCAAGAGATGCTCTGTGTGGAGAGAGAGGCC 1857
QY 1861 CAGCAAGATTAATTAAGACAAATCATCCAGCTTCAAGGACAGAGAGGAGAGATCTCTC 1920
Db 1861 CAGCAAGATTAATTAAGACAAATCATCCAGCTTCAAGGACAGAGAGGAGAGATCTCTC 1920
QY 1858 CAGCAAGATTAATTAAGACAAATCATCCAGCTTCAAGGACAGAGAGGAGAGATCTCTC 1917
Db 1858 CAGCAAGATTAATTAAGACAAATCATCCAGCTTCAAGGACAGAGAGGAGAGATCTCTC 1917
QY 1921 CTCACAGAGAGCGGCATATTTATGTGTGTGAGATGCAAGATATGCGCAAGATGTA 1980
Db 1921 CTCACAGAGAGCGGCATATTTATGTGTGTGAGATGCAAGATATGCGCAAGATGTA 1980
QY 1918 CTCACAGAGAGCGGCATATTTATGTGTGTGAGATGCAAGATATGCGCAAGATGTA 1977
Db 1918 CTCACAGAGAGCGGCATATTTATGTGTGTGAGATGCAAGATATGCGCAAGATGTA 1977
QY 1981 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGGTTGAGTTGAAAACTAAGAACATG 2040
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D6	1978	CATGATGCCCTTGTGCAGATATTATAGCAAGAAGTTGGATGTTGAATACTGAAACCATG	2037
Gy	2041	AAAACCCTGGCCACTTTAAAAGAGAAAAACGTAACCTTCAGATATTGGTCA	2094
D6	2038	AAAACCCTGGCCACTTTAAAAGAGAAAAACGTAACCTTCAGATATTGGTCA	2091
 RESULT 10			
XX	ID	ADM43214	
XX	ADW43214	standard; cDNA; 2091 BP.	
XX	AC	ADM43214;	
XX	DT	03-JUN-2004 (first entry)	
XX	DE	Human methionine synthase reductase CDS del 1675-1678 variant.	
XX	KM	Human; 86; Methionine synthase reductase polypeptide; HsmTRR; cancer;	
XX	KM	cardiovascular disease; neutral tube defect; hyperhomocysteinemia;	
XX	KM	chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.	
XX	OS	Homo sapiens.	
FH	Key	Location/Qualifiers	
FH	CDS	1..2091	
FT	/tag=	a	
FT	/product=	"hsMTRRdelR559"	
FT	/partial		
FT	/note=	"No stop codon shown"	
FT	variation	replace(66,A)	
FT	/tag=	b	
FT	/standard_name=	"Single_nucleotide_polymorphism"	
FT	variation	replace(110,A)	
FT	/tag=	c	
FT	/standard_name=	"Single_nucleotide_polymorphism"	
FT	variation	replace(1675,AGAG)	
FT	/tag=	d	
XX	PN	US2003082676-A1.	
XX	PD	01-MAY-2003.	
XX	PP	10-AUG-1999; 99US-00371347.	
XX	PR	16-JAN-1998; 98US-0071622P.	
XX	PR	15-JAN-1999; 99US-00232028.	
PA	(GRAV//)	GRAVEL R A.	
PA	(ROZE//)	ROZEN R.	
PA	(LECL//)	LEClerc D.	
PA	(WILS//)	WILSON A.	
PA	(ROSE//)	ROSENBLATT D.	
P1	Gravel RA,	Rozen R, Leclerc D, Wilson A, Rosenblatt D;	
DR	MP1; 2003-576610/54.		
DR	P-PSDB; ADM43215.		
XX	PT	New substantially pure nucleic acid encoding a mammalian methionine	
XX	PT	synthase reductase polypeptide, useful for diagnosing, preventing or	
XX	PT	treating conditions associated with altered methionine synthase activity,	
XX	PT	e.g. cancer.	
XX	PS	Disclosure; SEQ ID NO 47; 26pp; English.	
CC	CC	The invention relates to a substantially pure nucleic acid that encodes a	
CC	CC	mammalian methionine synthase reductase polypeptide, HsmTRR, or that	
CC	CC	hybridises at high stringency to a nucleic acid appearing as ADM43208 or	
CC	CC	ADM43209. Also included are a non-human animal where one or both genetic	
CC	CC	alleles encoding the methionine synthase reductase polypeptide are	
CC	CC	mutated, an antibody that specifically binds the above methionine	
CC	CC	synthase reductase polypeptide, a method of detecting the presence of the	

CC above polypeptide, a method for detecting sequence variants for
CC methionine synthase reductase in a mammal, methods of treating or
CC preventing cancer (or cardiovascular disease or neural tube defects) in a
CC subject, methods of screening for a compound that modulates methionine
CC synthase reductase biological activity and a method for detecting an
CC increased risk of developing a neural tube defect in a mammalian embryo
CC or foetus. The nucleic acid is useful in diagnosing, preventing or
CC treating conditions associated with altered methionine synthase activity,
CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are
CC also associated with hyperhomocysteinemia. The gene for HSMTR is
CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
CC sequence of a variant human HSMTR cDNA.

SQ Sequence 2091 BP; 589 A; 489 C; 480 G; 533 T; 0 U; 0 Other;

Query Match 85.8%; Score 1800; DB 11; Length 2091;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2090; Conservative 0; Mismatches 1; Indels 3; Gaps 1.

QY	1	TTGAGGAGG	TTCTGTTA	CTATATATG	CTACACAGGAGGGGACAGGGCAAGG	CCATGGCAGAA	60
Db	1	ATGAGGAGG	TTCTGTTA	CTATATATG	CTACACAGGAGGGGACAGGGCAAGG	CCATGGCAGAA	60
QY	61	GAAATATG	TGAGCAAGCTGTG	GTACATGATTTTCTG	CAGATCTTCACTGTATTTAGTAA	120	
Db	61	GAAATGTG	TGAGCAAGCTGTG	GTACATGATTTTCTG	CAGATCTTCACTGTATTTAGTAA	120	
QY	121	TCCGATAA	GTATGACTTA	AAAAACCGAAACAGCTCCTCTG	TTGTGTGTGTTTCTTACACG	180	
Db	121	TCCGATAA	GTATGACTTA	AAAAACCGAAACAGCTCCTCTG	TTGTGTGTGTTTCTTACACG	180	
QY	181	GGCACCCG	AGACCCACCCGACACACAGCCCG	CAGTTTGTATAGAAATTCAGAACCA	CAACAA	240	
Db	181	GGCACCCG	AGACCCACCCGACACACAGCCCG	CAGTTTGTATAGAAATTCAGAACCA	CAACAA	240	
QY	241	CTGGCCGG	TGATTTCTTTGGCTCACTGGCGGTATG	GGGTACTGGGTATTCAGAA	300		
Db	241	CTGGCCGG	TGATTTCTTTGGCTCACTGGCGGTATG	GGGTACTGGGTATTCAGAA	300		
QY	301	TACACCTA	CTTTTGCAATGGGGGGAGATTA	TTGATTAACGACTTCAAGACCTTGAGCC	360		
Db	301	TACACCTA	CTTTTGCAATGGGGGGAGATTA	TTGATTAACGACTTCAAGACCTTGAGCC	360		
QY	361	CGGCATTT	CTATGACACTGACATGACAGATG	ACTGTGTATGAGTTTGAACCTGTGTGTAG	420		
Db	361	CGGCATTT	CTATGACACTGACAGATGACAGATG	ACTGTGTATGAGTTTGAACCTGTGTGTAG	420		
QY	421	CGGTGAT	TGTCGACCTGGCCAGCCCTCAGAAAGCA	TTTTTAAAGTCAAGCAGAGACAA	480		
Db	421	CGGTGAT	TGTCGACCTGGCCAGCCCTCAGAAAGCA	TTTTTAAAGTCAAGCAGAGACAA	480		
QY	481	GAGGAGAT	TAGTGGCGCACTCCCGGTGACATCA	CCTGACCTTTAGAGACAGACCTTGTG	540		
Db	481	GAGGAGAT	TAGTGGCGCACTCCCGGTGACATCA	CCTGACCTTTAGAGACAGACCTTGTG	540		
QY	541	AAGTCA	GAGCTGTACATGGAATCTCAAGT	CGACTTCTGAGATTTGATGATTCAGGA	600		
Db	541	AAGTCA	GAGCTGTACATGGAATCTCAAGT	CGACTTCTGAGATTTGATGATTCAGGA	600		
QY	601	AGAAAGAT	TCTGAGGTTTGAAGCAAAATGACAGAA	CAGAACCAATCCCAATGTTGA	660		
Db	601	AGAAAGAT	TCTGAGGTTTGAAGCAAAATGACAGAA	CAGAACCAATCCCAATGTTGA	660		
QY	661	ATTGAA	GACTTGAAGTCTCTCACTTAACCCG	TGCGTATCCCGCACTTCAAGCCCTCTGTG	720		
Db	661	ATTGAA	GACTTGAAGTCTCTCACTTAACCCG	TGCGTATCCCGCACTTCAAGCCCTCTGTG	720		
QY	721	AATAT	TCTGTGTTTACCCCGCAATATTTA	CAGGTACATCTGCAGGAATCTTGTGGCAG	780		
Db	721	AATAT	TCTGTGTTTACCCCGCAATATTTA	CAGGTACATCTGCAGGAATCTTGTGGCAG	780		

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QY 781 GAGAAAGCCAGATATCTGTGACTTCAGCAGATCCAGTCTTTTCAAGTTCGAATTTCAAG 840
DB 781 GAGAAAGCCAGATATCTGTGACTTCAGCAGATCCAGTCTTTTCAAGTTCGAATTTCAAG 840
QY 841 GCAGTTCAACTTCTCTAGATGATGACATTAACCACTGCTGCTGGAATTTGAGCATT 900
DB 841 GCAGTTCAACTTCTCTAGATGATGACATTAACCACTGCTGCTGGAATTTGAGCATT 900
QY 901 TCAATTCAGACTTTTCTCTAGATGATGACATTAACCACTGCTGCTGGAATTTGAGCATT 960
DB 901 TCAATTCAGACTTTTCTCTAGATGATGACATTAACCACTGCTGCTGGAATTTGAGCATT 960
QY 961 GATTCTGAGGTACCAAGCCCTTACCAAGACTGACGCTTGAAGTAAAGAGCACTGC 1020
DB 961 GATTCTGAGGTACCAAGCCCTTACCAAGACTGACGCTTGAAGTAAAGAGCACTGC 1020
QY 1021 GTGCTTTGAAAATTAAGGAGACACAAAGAAAGAGACTCTTACCCCGACATATA 1080
DB 1021 GTGCTTTGAAAATTAAGGAGACACAAAGAAAGAGACTCTTACCCCGACATATA 1080
QY 1081 CTTGCGGAGATGTTCTCTCAGATTCATTTTACCTGCTGCTGGAATTCGAGCAATTCCT 1140
DB 1081 CTTGCGGAGATGTTCTCTCAGATTCATTTTACCTGCTGCTGGAATTCGAGCAATTCCT 1140
QY 1141 AAAAGGCAATTTTGGAGAGCCCTTGTGACTATACAGTGAAGTGTGAAAAGCGCAGG 1200
DB 1141 AAAAGGCAATTTTGGAGAGCCCTTGTGACTATACAGTGAAGTGTGAAAAGCGCAGG 1200
QY 1201 CTACAGAGCTGTGACATTAACCAAGGAGGAGCGGATTAATAGCGGCTTGTACGAGATGC 1260
DB 1201 CTACAGAGCTGTGACATTAACCAAGGAGGAGCGGATTAATAGCGGCTTGTACGAGATGC 1260
QY 1261 TGTGCTGCTGTTGATCTCTCTGCTTCCCTTCTTCCAGCCAGCACTCAGTCTC 1320
DB 1261 TGTGCTGCTGTTGATCTCTCTGCTTCCCTTCTTCCAGCCAGCACTCAGTCTC 1320
QY 1321 CTGCTGCAATCTTCTCTAACTTCAACCCAGACATATTCGTGTGCAAGTCAAGTTTA 1380
DB 1321 CTGCTGCAATCTTCTCTAACTTCAACCCAGACATATTCGTGTGCAAGTCAAGTTTA 1380
QY 1381 TTTTCCAGGAAAGCTCAATTTGTCTCAACATGTGGAATTCGTCTACGCGCACA 1440
DB 1381 TTTTCCAGGAAAGCTCAATTTGTCTCAACATGTGGAATTCGTCTACGCGCACA 1440
QY 1441 ACAAGGTTCTGCGAAGGAGATGTATGACAGCTGCTGCTGCTGTTGTTGCTTCAATT 1500
DB 1441 ACAAGGTTCTGCGAAGGAGATGTATGACAGCTGCTGCTGCTGTTGTTGCTTCAATT 1500
QY 1501 CTTGAGCCAAACATATGATGATCCATGAAAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
DB 1501 CTTGAGCCAAACATATGATGATCCATGAAAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
QY 1561 TCCATCTCTCTCTGAAACAAATTTCTTCCACTTACAGATGACCCCTCAATCCCATC 1620
DB 1561 TCCATCTCTCTCTGAAACAAATTTCTTCCACTTACAGATGACCCCTCAATCCCATC 1620
QY 1621 ATATATGTTGAGTCCAGAACCGGAGATGAGCCGCTTTATTTGAGTTCTTACAAATGAG 1680
DB 1621 ATATATGTTGAGTCCAGAACCGGAGATGAGCCGCTTTATTTGAGTTCTTACAAATGAG 1680
QY 1681 AAATTCGAAGAACCAACCCAGATGAAATTTTGAAGCAATGTGTTGTTTGGCTGC 1740
DB 1681 AAATTCGAAGAACCAACCCAGATGAAATTTTGAAGCAATGTGTTGTTTGGCTGC 1740
QY 1741 AGGATATAGGATAGGATATATCTATTCAGAAAAGAGCTCAGACATTTCTTAAGCATGG 1800
DB 1741 AGGATATAGGATAGGATATATCTATTCAGAAAAGAGCTCAGACATTTCTTAAGCATGG 1800
QY 1801 ATCTTAATCTATCTAAAGTTTCTTCTCAGAGATGCTCTGTTGGGAGAGAGAAAGCC 1860
DB 1801 ATCTTAATCTATCTAAAGTTTCTTCTCAGAGATGCTCTGTTGGGAGAGAGAAAGCC 1860
QY 1861 CCAGCAAAAGTATGTATCAAGACATCCAGCTTCAAGGCGAGAGTGGCGAAGATCTTC 1920
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DB 1858 CCAGCAAAAGTATGTATCAAGACATCCAGCTTCAAGGCGAGAGTGGCGAAGATCTTC 1917
QY 1921 CTCACAGAGAACGGCATTATTTATGTGTGAGATGACAAAGATTTGGCCAAAGATGTA 1980
DB 1918 CTCACAGAGAACGGCATTATTTATGTGTGAGATGACAAAGATTTGGCCAAAGATGTA 1977
QY 1981 CATGATGCCCTTGTGCAATTAATTAACCAAGAGTTGAGTTGAAAACTAGAACATG 2040
DB 1978 CATGATGCCCTTGTGCAATTAATTAACCAAGAGTTGAGTTGAAAACTAGAACATG 2037
QY 2041 AAAACCTTGCCACTTTTAAAGAAAGAAAGCGTACCTCAGGATTTTGTCTA 2094
DB 2038 AAAACCTTGCCACTTTTAAAGAAAGAAAGCGTACCTCAGGATTTTGTCTA 2091
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RESULT 11

AAAS8977 standard; DNA; 3256 BP.

ID AAAS8977;

AC AAAS8977;

DE 07-NOV-2000 (first entry)

A human methionine synthase reductase DNA sequence with polymorphism.

Human; methionine synthase reductase; MTRR; cancer;

cardiovascular disease; Down's Syndrome; neural tube defect;

premature coronary artery disease; ss.

Homo sapiens.

MO200042196-A2.

14-JUN-2000; 2000NC-IB000209.

15-JAN-1999; 99US-00232028.

10-AUG-1999; 99US-00371347.

(UYMC-) UNITV MCGILL.

Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;

MPI; 2000-46131/40.

Mammalian methionine synthase reductase nucleic acid used for detecting

an increased risk of developing a neural tube defect, Down's Syndrome or

cardiovascular disease in a mammalian embryo or fetus.

Claim 8; Page; 85pp; English.

The present sequence represents a human methionine synthase reductase

(MTRR) DNA sequence, with a polymorphism comprising of a deletion of

nucleotides 1726-1728. Inhibitors of MTRR polypeptide and polynucleotide

are used for treating or preventing cancer, cardiovascular disease,

Down's Syndrome or neural tube defects in a subject. The cardiovascular

disease is premature coronary artery disease. The compounds are detected

by methods which screen for modulators of MTRR biological activity. MTRR

polypeptide or nucleic acid is examined for the presence of a

polymorphism in the parents or the embryo or foetus, and the information

used for detecting an increased risk of an embryo or foetus developing

cancer, cardiovascular disease, Down's Syndrome or neural tube defects.

note: the present sequence does not appear in the specification; it was

created using information provided

Sequence 3256 BP; 943 A; 705 C; 662 G; 946 T; 0 U; 0 Other;

Query Match 81.1%; Score 1701; DB 3; Length 3256;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2091; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

Qy	1	ATGAGGAGGTTTCGTGTACTATATAGCTACACAGAGGGAGACAGGAAAGGCCATCGCAGAA	60
Db	80	ATGAGGAGGTTTCGTGTACTATATAGCTACACAGAGGGAGACAGGAAAGGCCATCGCAGAA	139
Qy	61	GAAATATGTGAGCAAGCTGTGTGATCATGSAATTTTCTGCAGATCTTCACTGTATATAGTAA	120
Db	140	GAAATGTGTGAGCAAGCTGTGTGATCATGSAATTTTCTGCAGATCTTCACTGTATATAGTAA	199
Qy	121	TCCGATATAGTATGACCTTAAAAACCGAAACAGCTCTCTGTGTGTGTGTTTCTACACG	180
Db	200	TCCGATATAGTATGACCTTAAAAACCGAAACAGCTCTCTGTGTGTGTGTTTCTACACG	259
Qy	181	GGCACCCGAGACCCACCCGACACAGCCCGCAGATTTGTATAGAAATATACGAACCAACA	240
Db	260	GGCACCCGAGACCCACCCGACACAGCCCGCAGATTTGTATAGAAATATACGAACCAACA	319
Qy	241	CTGCACGGTGAATTTCTTTGGCTCACCTGCGATATGGGTTTACTGGGCTCGGATTTCAAA	300
Db	320	CTGCACGGTGAATTTCTTTGGCTCACCTGCGATATGGGTTTACTGGGCTCGGATTTCAAA	379
Qy	301	TACACCTACTTTTGCATATGGGGGAGATTAATTGATTAACGACTTCAAGACTTGAAGCC	360
Db	380	TACACCTACTTTTGCATATGGGGGAGATTAATTGATTAACGACTTCAAGACTTGAAGCC	439
Qy	361	CGGCATTTCTATGACACTGACATGCAATGACATGATCTGTGTAGTTTGAACCTTGTGTGAG	420
Db	440	CGGCATTTCTATGACACTGACATGCAATGACATGATCTGTGTAGTTTGAACCTTGTGTGAG	499
Qy	421	CCGGGATATGTGTGACCTCTGGCCAGCCCTCGAANAAGCATTTTATAGTCAAGCAGAGACA	480
Db	500	CCGGGATATGTGTGACCTCTGGCCAGCCCTCGAANAAGCATTTTATAGTCAAGCAGAGACA	559
Qy	481	GAGAGATATATGGCGCACACTCCCGGTGGCATCACTGCATCTTGAAGACAGACTTGTG	540
Db	560	GAGAGATATATGGCGCACACTCCCGGTGGCATCACTGCATCTTGAAGACAGACTTGTG	619
Qy	541	AAGTCAGAGCTGTACACATTTGAATTTCAAGTCAGACTTCTGAGATTCGATGATTCAGGA	600
Db	620	AAGTCAGAGCTGTACACATTTGAATTTCAAGTCAGACTTCTGAGATTCGATGATTCAGGA	679
Qy	601	AGAAAGATTTCTGAGTTTTTGAAGCAAAATGCATGTGAACAGCAACCAATCCAAATGTTGTA	660
Db	680	AGAAAGATTTCTGAGTTTTTGAAGCAAAATGCATGTGAACAGCAACCAATCCAAATGTTGTA	739
Qy	661	ATTGAAGACTTTGAGTCTCACTTACACCGGTCCGGTACCCCACTCTCAAGAGCTCTCTG	720
Db	740	ATTGAAGACTTTGAGTCTCACTTACACCGGTCCGGTACCCCACTCTCAAGAGCTCTCTG	799
Qy	721	AATATTCCTGTTTAAACCCAGAAATTTTACAGGTACATCTGCAGAGACTCTTTGGCCAG	780
Db	800	AATATTCCTGTTTAAACCCAGAAATTTTACAGGTACATCTGCAGAGACTCTTTGGCCAG	859
Qy	781	GAGGAAAGCCAAAGTATCTGTGACTTCAGCAGATCCAGTTTTTCAAGTCCCAATTTCAAG	840
Db	860	GAGGAAAGCCAAAGTATCTGTGACTTCAGCAGATCCAGTTTTTCAAGTCCCAATTTCAAG	919
Qy	841	GCAGTTCAACTTACAGATGATGCGCATTAATAAACCATCTGCTGTGTGAATTTGGAACAT	900
Db	920	GCAGTTCAACTTACAGATGATGCGCATTAATAAACCATCTGCTGTGTGAATTTGGAACAT	979
Qy	901	TCAATATCAGACTTTTCTATCAGCTTGAGATGTGCTTCAAGCTGATCTGCCCCTAACAG	960
Db	980	TCAATATCAGACTTTTCTATCAGCTTGAGATGTGCTTCAAGCTGATCTGCCCCTAACAG	1039
Qy	961	GATTCTGAGGTACAAAGCTTACTCAAAAGCTGCAGCTTGAAGATTAAGAAGACATGCG	1020
Db	1040	GATTCTGAGGTACAAAGCTTACTCAAAAGCTGCAGCTTGAAGATTAAGAAGACATGCG	1099
Qy	1021	GTCTCTTTGAAAAATAAGCAGACACAAAGAAGAAAGAGCTACTTACCACAGCATATA	1080
Db	1100	GTCTCTTTGAAAAATAAGCAGACACAAAGAAGAAAGAGCTACTTACCACAGCATATA	1159
Qy	1081	CTGCGGAGATGTTCTCTCAGGTCATTTTATCTGAGTCTTGAATTCGAGCAATTCCT	1140

Db	1160	CTCGCGGGATGTTCTCTCCAGTTCACTTTTAACTGGTGTCTTGAAATCCGAGCAATTCCT	1219
Qy	1141	AAAAAGCATTTTTCGAGGCCCTTGATGACTATACCAATGACAGTGCCTGAAAGCCGACG	1200
Db	1220	AAAAAGCATTTTTCGAGGCCCTTGATGACTATACCAATGACAGTGCCTGAAAGCCGACG	1279
Qy	1201	CTACAGGAGCTGTGCAGTAAGCAAGGGGACGCCATTAATAGCCGCTTTGTACAGATATCC	1266
Db	1280	CTACAGAGCTGTGCAGTAAGCAAGGGGACGCCATTAATAGCCGCTTTGTACAGATATCC	1339
Qy	1261	TGTGCTGCTGTTGGATCTTCCTGCTTCGCTTCCCTTCCTGCAAGCACTCAGTCTC	1320
Db	1340	TGTGCTGCTGTTGGATCTTCCTGCTTCGCTTCCCTTCCTGCAAGCACTCAGTCTC	1399
Qy	1321	CTGCTCCGAACATCTTCCCTTAACTTCACACCGACACATATTCGTGTGCAAGCTCAAGTTA	1380
Db	1400	CTGCTCCGAACATCTTCCCTTAACTTCACACCGACACATATTCGTGTGCAAGCTCAAGTTA	1459
Qy	1381	TTTCACCCAGGAAAGCTCCATTTTGTCTTCACAATTGTGGAATTTCTGTCTACTGCCACA	1440
Db	1460	TTTCACCCAGGAAAGCTCCATTTTGTCTTCACAATTGTGGAATTTCTGTCTACTGCCACA	1519
Qy	1441	ACAGAGTCTTCGCGAAGGAGATGTACAGGCTGCGCTGCTGTGTGTTGCTTCACTT	1500
Db	1520	ACAGAGTCTTCGCGAAGGAGATGTACAGGCTGCGCTGCTGTGTGTTGCTTCACTT	1579
Qy	1501	CTTCAGGCCAACATATACATGATGCCATCCATGAAACACAGCCGGAAAGCCCTGGCTCTTAAGTA	1566
Db	1580	CTTCAGGCCAACATATACATGATGCCATCCATGAAACACAGCCGGAAAGCCCTGGCTCTTAAGTA	1639
Qy	1561	TCCATCTCTCCTCGAACACAAATTCCTTCCACTTACCAAGATGACCCCTCAATCCCATC	1620
Db	1640	TCCATCTCTCCTCGAACACAAATTCCTTCCACTTACCAAGATGACCCCTCAATCCCATC	1699
Qy	1621	ATTAATGTGGGTCCAGGAACCGGCATAGCCCCCTTATATGGGTTCTTACACATATAGAG	1688
Db	1700	ATTAATGTGGGTCCAGGAACCGGCATAGCCCCCTTATATGGGTTCTTACACATATAGAG	1756
Qy	1681	AAACTCCAAAGAACACACCCAGATGGAATTTTGGAGCAATGTGGTGTCTTTTGGCTGC	1740
Db	1757	AAACTCCAAAGAACACACCCAGATGGAATTTTGGAGCAATGTGGTGTCTTTTGGCTGC	1816
Qy	1741	AGGCATTAAGATAGGATTAATCTAATCCAGAAAGACTCAGACATTTCTTAAGCATGG	1800
Db	1817	AGGCATTAAGATAGGATTAATCTAATCCAGAAAGACTCAGACATTTCTTAAGCATGG	1876
Qy	1801	ATCTTAATCTCATTAAGCTTCTCTCCAGAGATGCTCCTGTATGGGAGAGAGCAACCC	1866
Db	1877	ATCTTAATCTCATTAAGCTTCTCTCCAGAGATGCTCCTGTATGGGAGAGAGCAACCC	1933
Qy	1861	CCAGCAAAAGTATGTACAGACACATCCAGCTTCATGCGCAGCAGTGTGCGAGATCTTC	1920
Db	1937	CCAGCAAAAGTATGTACAGACACATCCAGCTTCATGCGCAGCAGTGTGCGAGATCTTC	1996
Qy	1921	CTCCAGAGAAACGGCATATTTATGTGTGTGAGATGCAAAAGATATGGCCAAAGATTA	1988
Db	1997	CTCCAGAGAAACGGCATATTTATGTGTGTGAGATGCAAAAGATATGGCCAAAGATTA	2056
Qy	1981	CATGATGCCCTTGTGCAAAATATAGCAAAAGGTGTGAGTTTGAAAACCTAGAAAGCATG	2040
Db	2057	CATGATGCCCTTGTGCAAAATATAGCAAAAGGTGTGAGTTTGAAAACCTAGAAAGCATG	2116
Qy	2041	AAACCCCTGGCCACTTTAAAGAGAAAAGCTTACCTTCAGAGATATTTGCTATTA	2097
Db	2117	AAACCCCTGGCCACTTTAAAGAGAAAAGCTTACCTTCAGAGATATTTGCTATTA	2173

RESULT 12
AAA58976
ID AAA58976 standard; DNA; 3255 BP
XX
AC AAA58976;

XX 07-NOV-2000 (first entry)
XX A human methionine synthase reductase DNA sequence with polymorphism.
DE Human; methionine synthase reductase; MTRR; cancer;
XX cardiovascular disease; Down's Syndrome; neural tube defect;
KW premature coronary artery disease; ss.
XX Homo sapiens.
XX NC0200042196-A2.
XX 20-JUL-2000.
XX 14-JAN-2000; 2000MO-IB000209.
XX 15-JAN-1999; 99US-00232028.
XX 10-AUG-1999; 99US-00371347.
XX (UYMC-) UNIV MCGILL.
XX Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX WPI; 2000-466131/40.
XX Mammalian methionine synthase reductase nucleic acid used for detecting
XX an increased risk of developing a neural tube defect. Down's Syndrome or
XX cardiovascular disease in a mammalian embryo or fetus.
XX Claim 7; Page; 85pp; English.
XX The present sequence represents a human methionine synthase reductase
XX (MTRR) DNA sequence, with a polymorphism comprising of a deletion of
XX nucleotides 1675-1678. Inhibitors of MTRR polypeptide and polynucleotide
XX are used for treating or preventing cancer, cardiovascular disease,
XX Down's Syndrome or neural tube defects in a subject. The cardiovascular
XX disease is premature coronary artery disease. The compounds are detected
XX by methods which screen for modulators of MTRR biological activity. MTRR
XX polypeptide or nucleic acid is examined for the presence of a
XX polymorphism in the parents or the embryo or foetus, and the information
XX used for detecting an increased risk of an embryo or foetus developing
XX cancer, cardiovascular disease, Down's Syndrome or neural tube defects.
XX note: the present sequence does not appear in the specification; it was
XX created using information provided
XX Sequence 3255 BP; 942 A; 704 C; 663 G; 946 T; 0 U; 0 Other;
XX
XX Query Match 78.2%; Score 1640; DB 3; Length 3255;
XX Best Local Similarity 99.7%; Pred. No. 0;
XX Matches 2090; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
QY 1 ATGAGAGAGTTCTGTTACTATATGCTACACAGAGGAGACGAAAGGCATGCGAA 60
DB 80 ATGAGAGAGTTCTGTTACTATATGCTACACAGAGGAGACGAAAGGCATGCGAA 139
QY 61 GAAATATGTGACAGAGCTGTGTATCATGATTTTCTGCAGATCTTCACTGTATTGAA 120
DB 140 GAAATGTGTGACAGAGCTGTGTATCATGATTTTCTGCAGATCTTCACTGTATTGAA 199
QY 121 TCCGATTAAGTATGACCTTAAAAACCGAAACAGCTCTCTTGTGTGTGTGTTTCAACAG 180
DB 200 TCCGATTAAGTATGACCTTAAAAACCGAAACAGCTCTCTTGTGTGTGTGTTTCAACAG 259
QY 181 GGCACCGGAGACCAACCGACACAGCCCGCAAGTTTGTAAAGAAATACGAACCAACA 240
DB 260 GGCACCGGAGACCAACCGACACAGCCCGCAAGTTTGTAAAGAAATACGAACCAACA 319
QY 241 CTGCGGTTGATTTCTTGTCTACACTGCGGTATGGTTACTGGGTCTCGGTATTGAAA 300
DB 320 CTGCGGTTGATTTCTTGTCTACACTGCGGTATGGTTACTGGGTCTCGGTATTGAAA 379
QY 301 TACACCTACTTTGCAATGGGGGGAAGATTAATTGATAAAGCACTTCAAGAGCTTGAAGCC 360

DB 380 TACACCTACTTTGCAATGGGGGGAAGATTAATTGATAAAGCACTTCAAGAGCTTGAAGCC 439
QY 361 CGGATTTTCTATGACACTGACATGACAGATGACTGTGTAGTTTAAAGCTTGTGTAG 420
DB 440 CGGATTTTCTATGACACTGACATGACAGATGACTGTGTAGTTTAAAGCTTGTGTAG 439
QY 421 CCGTGATTTGCTGACTGTGCGCAGCTTCAAGACATTTTAAAGTCAAGAGAGACAA 480
DB 500 CCGTGATTTGCTGACTGTGCGCAGCTTCAAGACATTTTAAAGTCAAGAGAGACAA 559
QY 481 GAGAGATTAAGTGGCCGACCTCCCGGTGGATGACCTGACCTTGTGAGACAGACCTTGTG 540
DB 560 GAGAGATTAAGTGGCCGACCTCCCGGTGGATGACCTGACCTTGTGAGAGACAGACCTTGTG 619
QY 541 AAGTCAGAGCTGTACACATTTGAATCTCAAGTCGACCTTGTGATTCGATTTGAGA 600
DB 620 AAGTCAGAGCTGTACACATTTGAATCTCAAGTCGACCTTGTGATTCGATTTGAGA 679
QY 601 AGAAGGATTTGAGGTTTAAAGCAAAATGACGTGAACAGAACCAATCCAAATGTTGTA 660
DB 680 AGAAGGATTTGAGGTTTAAAGCAAAATGACGTGAACAGAACCAATCCAAATGTTGTA 739
QY 661 ATTGAAGATTTGAGTCTTCACTTACCCGTTGGTACCCCACTTCAAGAGCTTCTGTG 720
DB 740 ATTGAAGATTTGAGTCTTCACTTACCCGTTGGTACCCCACTTCAAGAGCTTCTGTG 739
QY 721 AATATTCCTGTTTACCCCAAGATTTTAAAGTATCATGTGACAGAGTCTTGTGCGCAG 780
DB 800 AATATTCCTGTTTACCCCAAGATTTTAAAGTATCATGTGACAGAGTCTTGTGCGCAG 859
QY 781 GAGAAAGCCCAAGATCTGTGACTTCAAGCATGACATGCTTTTCAAGTCCAAATTTCAAG 840
DB 860 GAGAAAGCCCAAGATCTGTGACTTCAAGCATGACATGCTTTTCAAGTCCAAATTTCAAG 919
QY 841 GCAATTCATTTCTGACAGATGATGCAATTAACCACTGCTGTGATGAAATGGAATTT 900
DB 920 GCAATTCATTTCTGACAGATGATGCAATTAACCACTGCTGTGATGAAATGGAATTT 979
QY 901 TCAATATCAAGATCTTCTGACAGCTGTGAGATGCTTCAAGCTGTGATCTTCAAGT 960
DB 980 TCAATATCAAGATCTTCTGACAGCTGTGAGATGCTTCAAGCTGTGATCTTCAAGT 1039
QY 961 GATTTGAGGTACAAAGCTTCTCAAGACCTGACCTTGAAGATTAAGAGAGCACTGC 1020
DB 1040 GATTTGAGGTACAAAGCTTCTCAAGACCTGACCTTGAAGATTAAGAGAGCACTGC 1099
QY 1021 GTCTTTTGAATTAAGGACAGACCAAGAAAGAGAGCTTACCTTCAAGCATATA 1080
DB 1100 GTCTTTTGAATTAAGGACAGACCAAGAAAGAGAGCTTACCTTCAAGCATATA 1159
QY 1081 CCGCGGAGATGTTCTCTCCAGTTCATTTTAACTGCTGTGAAATCCGAGCAATTTCT 1140
DB 1160 CCGCGGAGATGTTCTCTCCAGTTCATTTTAACTGCTGTGAAATCCGAGCAATTTCT 1219
QY 1141 AAAAAGCATTTTGTGCGAGCCCTTGTGACTATACAGTACAGTGTGAAAAAGCGCAGG 1200
DB 1220 AAAAAGCATTTTGTGCGAGCCCTTGTGACTATACAGTACAGTGTGAAAAAGCGCAGG 1279
QY 1201 CTACAGAGCTGTGCAAGTAAACAAGGGGCGCCGATTAATAGCCGTTTGTACAGAGATGCC 1260
DB 1280 CTACAGAGCTGTGCAAGTAAACAAGGGGCGCCGATTAATAGCCGTTTGTACAGAGATGCC 1339
QY 1261 TGTGCTGCTGTTGTGATCTCTCTGCTTCCCTTCTTGCAGCAGCAGCACTCACTCTC 1320
DB 1340 TGTGCTGCTGTTGTGATCTCTCTGCTTCCCTTCTTGCAGCAGCAGCACTCACTCTC 1399
QY 1321 CTGCTGAACATCTTCTTAACTTCAACCCGACCAATATTTGTGTGCAAGCTCAAGTTTA 1380
DB 1400 CTGCTGAACATCTTCTTAACTTCAACCCGACCAATATTTGTGTGCAAGCTCAAGTTTA 1459
QY 1381 TTTCACCCAGGAAGCTTCAATTTTGTCTTCAATTTGTGAATTTTGTCTTACTGCGACA 1440

Db	1466	TTTCAACCCAGGAAAGCTCCATTTTGTCTTCAACATGTGGAAATTTCTGTCTACTGCCACA	15129
Qy	1441	ACAGAGGTTCTGCGAAGGGAGTATGTACAGGCTGGCTGGCTTGTGGTTCCTCAAGTT	15000
Db	1520	ACAGAGGTTCTGCGAAGGGAGTATGTACAGGCTGGCTGGCTTGTGGTTCCTCAAGTT	15799
Qy	1501	CTTGAGGCCAAACATACATGATGATCCCATGAAACAGCCGGGAAAGGCCCTGGGCTCTTAAGTA	15660
Db	1580	CTTGAGGCCAAACATACATGATGATCCCATGAAACAGCCGGGAAAGGCCCTGGGCTCTTAAGTA	16399
Qy	1561	TCCATCTCTCTCTGGAACAACAATTCCTTCCACTTACAGATGACCCCTCAATCCCATC	16200
Db	1640	TCCATCTCTCTCTGGAACAACAATTCCTTCCACTTACAGATGACCCCTCAATCCCATC	16959
Qy	1621	ATATATGGTGGTCCAGGAACCCGGCATAGCCCCCGTTTATTTGGGTTCTTACACATATAGAG	16800
Db	1696	ATATATGGTGGTCCAGGAACCCGGCATAGCCCCCGTTTATTTGGGTTCTTACACATATAGAG	17559
Qy	1681	AAACTCCAGAAACAACACCCAGATGGAATTTTGGAGCAATGTGTGTTTTTTGGCTGC	17400
Db	1756	AAACTCCAGAAACAACACCCAGATGGAATTTTGGAGCAATGTGTGTTTTTTGGCTGC	18159
Qy	1741	AGGCATTAAGATAGGATTAATCTATTCAAAAAGAGCTCAGACATTTCTTAAAGATGG	18000
Db	1816	AGGCATTAAGATAGGATTAATCTATTCAAAAAGAGCTCAGACATTTCTTAAAGATGG	18759
Qy	1801	ATCTTAACTCATCTAAAGGTTTCCCTTCAAGAGATGTCTCTGTGGGGAGAGGAAGCC	18660
Db	1876	ATCTTAACTCATCTTAAAGGTTTCCCTTCAAGAGATGTCTCTGTGGGGAGAGGAAGCC	19359
Qy	1861	CCAGCAAAAGTATGTACAAACAACATCCAGTTCATGGCCAGAGGTGGCAGAAATCCTC	19200
Db	1936	CCAGCAAAAGTATGTACAAACAACATCCAGTTCATGGCCAGAGGTGGCAGAAATCCTC	19959
Qy	1921	CTCAGAGGAACGGGCATATTATGTGTGTGGAGATGCAAGAATATATGGCCAAAGATGA	19800
Db	1996	CTCAGAGGAACGGGCATATTATGTGTGTGGAGATGCAAGAATATATGGCCAAAGATGA	20559
Qy	1981	CATGATGCCCTTGTGCAAAATATATAGCAAAAGGTTGAGTTGAAAACTGAAGCATG	20400
Db	2056	CATGATGCCCTTGTGCAAAATATATAGCAAAAGGTTGAGTTGAAAACTGAAGCATG	21159
Qy	2041	AAAAACCTGGCCACTTTTAAAAAGAAAAACGCTACTCTTCAGATATTTGGTCTATA	2097
Db	2116	AAAAACCTGGCCACTTTTAAAAAGAAAAACGCTACTCTTCAGATATTTGGTCTATA	2172

PA (APPL-) APPLERA CORP.
XX
XX Cargill M, Devlin JT, Iakubova O;
PI
XX WPI; 2004-533949/51.
DR P-FSDB; ADO39857.
XX
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PI the individual's nucleic acids.
PS Claim 7, SEQ ID NO 692; 145bp; English.

Seq	Sequence	3256 BP	927 A	691 C	669 G	940 T	0 U	29 Other
Query	Match	50.6%	Score	1062	DB	13	Length	3256
Beat	Local Similarity	99.1%	Pred.	No.	0			
Matches	2012	Conservative	0	Mismatches	19	Indels	0	Gaps 0
QY	67	TTGTGAGCAAGCTGTGTGATCATGATATTTCTGCAGATCTTCACTGTATTAAGTAATCCGAT	126					
Db	160	TGTGAGCAAGCTGTGTGATCATGATATTTCTGCAGATCTTCACTGTATTAAGTAATCCGAT	219					
QY	127	AAGTATGACCTTAAAAACCGAAACAGCTCTCTTGTGTGTGTGTTTCTTACACCGGACACC	186					
Db	220	AAGTATGACCTTAAAAACCGAAACAGCTCTCTTGTGTGTGTGTTTCTTACACCGGACACC	279					
QY	187	GGAGACCCACCCGACACAGCCCGGAAGTTTGTAAAGAAATACAGAACCAAACTGCGC	246					
Db	280	GGAGACCCACCCGACACAGCCCGGAAGTTTGTAAAGAAATACAGAACCAAACTGCGC	339					
QY	247	GTTGATTTCTTTGCTCACTCCGCGTATGAGGTTACTGGGTCCTCGGTGATTCGAATACAC	306					
Db	340	GTTGATTTCTTTGCTCACTCCGCGTATGAGGTTACTGGGTCCTCGGTGATTCGAATACAC	399					
QY	307	TACTTTTGCAATGGGGGGAGATTAATGATTAACGACTTCAAGACTTGGAGCCCGGACAT	366					
Db	400	TACTTTTGCAATGGGGGGAGATTAATGATTAACGACTTCAAGACTTGGAGCCCGGACAT	459					
QY	367	TTCTATGACACTGACACATGACAGATGACCTGTGTAGGTTTAGAATTGTGGTGTGAGCCGTGG	426					
Db	460	TTCTATGACACTGACACATGACAGATGACCTGTGTAGGTTTAGAATTGTGGTGTGAGCCGTGG	519					
QY	427	ATTGTGAGACTCTGGCCAGCCCTCAGAAAGCAATTTAGTCAACGACAGACAAAGAGAG	486					

Db 520 ATTGCTGGACTCTGGCCAGCCCTCAGAAAGCATTTTGGTCAAGCAGAGCAAGAGAG 579
Qy 487 ATAAAGGCGCACTCCGGTGGCACTGCACTCTTGAGAGACAGACCTTGGAACTCA 546
Db 580 ATAAAGTGGCCACTCCGGTGGCACTGCACTCTTGAGAGACAGACCTTGGAACTCA 639
Qy 547 GAGCTGTACACATTTGAATCTCAAGTGGAGCTTGGAGTTCCATGATTTCAAGAGAAAG 606
Db 640 GAGCTGTACACATTTGAATCTCAAGTGGAGCTTGGAGTTCCATGATTTCAAGAGAAAG 639
Qy 607 GATTTGAGGTTTGAAGCAAAATGCAGTGACAGCAACCAATCCATGTTGTAATTGAA 666
Db 700 GATTTGAGGTTTGAAGCAAAATGCAGTGACAGCAACCAATCCATGTTGTAATTGAA 759
Qy 667 GACTTGAATCTCACTTACCCGTTGGGTACCCCACTCTCAAGCCTCTGTAATATT 726
Db 760 GACTTGAATCTCACTTACCCGTTGGGTACCCCACTCTCAAGCCTCTGTAATATT 819
Qy 727 CTTGGTTTACCCCGAATTTTACAGTACATCTGAGAGAGTCTTTGGCCAGAGGAA 786
Db 820 CTTGGTTTACCCCGAATTTTACAGTACATCTGAGAGAGTCTTTGGCCAGAGGAA 879
Qy 787 AGCCAAATATCTGTGACTTCAAGCAGATCCAGTTTTCAGTGCCAAATTTCAAAAGCAGT 846
Db 880 AGCCAAATATCTGTGACTTCAAGCAGATCCAGTTTTCAGTGCCAAATTTCAAAAGCAGT 939
Qy 847 CAATTACTACGAATGATGCAATTAACAACACTCTGCTGGTAGAATTGACATTTCAAT 906
Db 940 CAATTACTACGAATGATGCAATTAACAACACTCTGCTGGTAGAATTGACATTTCAAT 999
Qy 907 ACAGACTTTTCTATCAGCTTGAGAGTCTTCAAGCTGATCTGCTTAAACATGATTTCT 966
Db 1000 ACAGACTTTTCTATCAGCTTGAGAGTCTTCAAGCTGATCTGCTTAAACATGATTTCT 1059
Qy 967 GAGGTACAAAGCCTACTCCAAAGACTGAGCTTGAAGTAAAGAGAGACCTGAGTCTT 1026
Db 1060 GAGGTACAAAGCCTACTCCAAAGACTGAGCTTGAAGTAAAGAGAGACCTGAGTCTT 1119
Qy 1027 TTGAAATTAAGGAGACACAAAGAAAGAGACTTACCTTACCAGCATATACCTGGC 1086
Db 1120 TTGAAATTAAGGAGACACAAAGAAAGAGACTTACCTTACCAGCATATACCTGGC 1179
Qy 1087 GGATGTTCTCTCCAGTCAATTTTACCTGAGTCTTGAATCCAGAGAAATTCCTAAAG 1146
Db 1180 GGATGTTCTCTCCAGTCAATTTTACCTGAGTCTTGAATCCAGAGAAATTCCTAAAG 1239
Qy 1147 GCATTTTGGAGGCTTGTGGAATATACAGTGAAGTGTGAAAGCCGAGGCTACAG 1206
Db 1240 GCATTTTGGAGGCTTGTGGAATATACAGTGAAGTGTGAAAGCCGAGGCTACAG 1299
Qy 1207 GAGCTGTGAGTAAACAAGGGGAGCCGATTAATAGCCGTTTGTACAGATGCTGTGCC 1266
Db 1300 GAGCTGTGAGTAAACAAGGGGAGCCGATTAATAGCTTGTACAGATGCTGTGCC 1359
Qy 1267 TGCCTTGTGATCTCTCTCTGCTTTCCTTCTTCCAGCAGCAGCAGTCTCTGCTC 1326
Db 1360 TGCCTTGTGATCTCTCTCTGCTTTCCTTCTTCCAGCAGCAGCAGTCTCTGCTC 1419
Qy 1327 GAAATCTCTCTAACTTCAACCCAGACATATTCGTGTGAGAGCTCAAGTTTATTTTAC 1386
Db 1420 GAAATCTCTCTAACTTCAACCCAGACATATTCGTGTGAGAGCTCAAGTTTATTTTAC 1479
Qy 1387 CCAGGAAGCTCAATTTTGTCTTCAACATTTGTGGAATTTTGTCTACTGCGCAACAGAG 1446
Db 1480 CCAGGAAGCTCAATTTTGTCTTCAACATTTGTGGAATTTTGTCTACTGCGCAACAGAG 1539
Qy 1447 GTTCTGGGGAAGGAGATGTAAGGCTGAGTCTGCTTGTGTTGCTTCAATTTCTTACAG 1506
Db 1540 GTTCTGGGGAAGGAGATGTAAGGCTGAGTCTGCTTGTGTTGCTTCAATTTCTTACAG 1599
Qy 1507 CCAGAACTATCATGATCCCATGAAAGACAGTGGGAAAGCCCTGCTCTTAAGATATTCATC 1566
Db 1600 CCAGAACTATCATGATCCCATGAAAGACAGTGGGAAAGCCCTGCTCTTAAGATATTCATC 1659

Qy 1567 TCTCTCGAACAACAATTTCTTTCATCTTACAGATGACCCCTCAATCCCATCATATG 1626
Db 1660 TCTCTCGAACAACAATTTCTTTCATCTTACAGATGACCCCTCAATCCCATCATATG 1719
Qy 1627 GTGGGTCCAGGAACCGGCAATGCGGCTTATTTGGGTCTTCAACATGAGAGAACTC 1686
Db 1720 GTGGGTCCAGGAACCGGCAATGCGGCTTATTTGGGTCTTCAACATGAGAGAACTC 1779
Qy 1687 CAGAACCAACCCAGATGGAATTTTGGAGCAATGTGTTGTTTTTGGCTGACAGCAT 1746
Db 1780 CAGAACCAACCCAGATGGAATTTTGGAGCAATGTGTTGTTTTTGGCTGACAGCAT 1839
Qy 1747 AAGGATAGGATATCTTATTCAGAAAAAGCTCAGCATTTTCTTAAAGCATGGGATCTTA 1806
Db 1840 AAGGATAGGATATCTTATTCAGAAAAAGCTCAGCATTTTCTTAAAGCATGGGATCTTA 1899
Qy 1807 ACTCATCTAAAGGTTCTCTTCAAGAGATGCTCTGTTGGGGAGAGAGAGCCCAAGCA 1866
Db 1900 ACTCATCTAAAGGTTCTCTTCAAGAGATGCTCTGTTGGGGAGAGAGAGCCCAAGCA 1959
Qy 1867 AAGTATGTACAAGACAATCCAGCTTCAATGGCCAGAGAGTGGCAAGATCCTCTCAG 1926
Db 1960 AAGTATGTACAAGACAATCCAGCTTCAATGGCCAGAGAGTGGCAAGATCCTCTCAG 2019
Qy 1927 GAGAACGCCATATTTATGTGTGAGATGCAAGAAATATGGCCAAAGATGTACATGAT 1986
Db 2020 GAGAACGCCATATTTATGTGTGAGATGCAAGAAATATGGCCAAAGATGTACATGAT 2079
Qy 1987 GCCCTGTGCAATTAATAGCAAGAGTTGGAGTTGAAAACTAAGCAATGAAAAAC 2046
Db 2080 GCCCTGTGCAATTAATAGCAAGAGTTGGAGTTGAAAACTAAGCAATGAAAAAC 2139
Qy 2047 CTGGCCACTTTAAAGAGAAAAAGCTACCTTCAAGATATTTGGTCATTA 2097
Db 2140 CTGGCCACTTTAAAGAGAAAAAGCTACCTTCAAGATATTTGGTCATTA 2190

RESULT 14
ADQ39030
ID ADQ39030 standard; DNA; 3274 BP.
XX
AC ADQ39030;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 693.
XX
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
KW cardiac; gene therapy; human; gene; db.
XX
OS Homo sapiens.
XX
PN W02004058052-A2.
XX
PD 15-JUL-2004.
XX
PF 22-DEC-2003; 2003MO-US040978.
XX
PR 20-DEC-2002; 2002US-0434778P.
PR 10-MAR-2003; 2003US-0453135P.
PR 30-APR-2003; 2003US-0466412P.
PR 23-SEP-2003; 2003US-0504955P.
XX
PA (APPL-) APPLERA CORP.
XX
PI Cargill M, Devlin JI, Iakubova O;
XX
XX
DR WPI; 2004-533949/51.
DR P-PSDB; ADQ39858.
XX
PT Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in

Pr the individual's nucleic acids.

XX Claim 7; SEQ ID NO 693; 145pp; English.

XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a human myocardial infarction-
CC associated gene containing one or more SNP's of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 3274 BP; 932 A; 694 C; 672 G; 946 T; 0 U; 30 Other;

Query Match 50.6%; Score 1062; DB 13; Length 3274;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2012; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 67 TGTGAGCAAGCTGTGTGATCATGATTTTTCGACGATCTTCACTGTAATTGATGATCCGAT 126
DB 178 TGTGAGCAAGCTGTGTGATCATGATTTTTCGACGATCTTCACTGTAATTGATGATCCGAT 237
QY 127 AAGTATGACCTAAACCCGAAACAGCTCTTGTGTGTGTGTTCTTCAACGGGACAC 186
DB 238 AAGTATGACCTAAACCCGAAACAGCTCTTGTGTGTGTGTTCTTCAACGGGACAC 297
QY 187 GGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACACTGCGG 246
DB 298 GGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACACTGCGG 357
QY 247 GTTGAATTTCTTGTCTCACTGCGGTATGGGTATCTGGGTCTCGGTATTCAGAAATACAC 306
DB 358 GTTGAATTTCTTGTCTCACTGCGGTATGGGTATCTGGGTCTCGGTATTCAGAAATACAC 417
QY 307 TACTTTTGAATGGGGGGAATATGATTAACGACTTCAAGAGCTTGGAGCCCGGACAT 366
DB 418 TACTTTTGAATGGGGGGAATATGATTAACGACTTCAAGAGCTTGGAGCCCGGACAT 477
QY 367 TTCTATGACACTGACATGACATGACTGTGTAGTTAGAACTTGTGTGAGCCGTGG 426
DB 478 TTCTATGACACTGACATGACATGACTGTGTAGTTAGAACTTGTGTGAGCCGTGG 537
QY 427 ATTGCTGACACTGCGCAGCCCTCAGAAAGCATTTTAAGTCAAGCAGAGACAAAGAG 486
DB 538 ATTGCTGACACTGCGCAGCCCTCAGAAAGCATTTTAAGTCAAGCAGAGACAAAGAG 597
QY 487 ATTAAGTGGGCACTCCCGGTGGCATCACTGATCTTGAAGACAGACCTTGAAGTCA 546
DB 598 ATTAAGTGGGCACTCCCGGTGGCATCACTGATCTTGAAGACAGACCTTGAAGTCA 657
QY 547 GAGCTGCTACACATTTGATCTCAAGTCAAGCTTCTGAGATTTCAGATTCAGAGAAAG 606
DB 658 GAGCTGCTACACATTTGATCTCAAGTCAAGCTTCTGAGATTTCAGATTCAGAGAAAG 717

QY 607 GATTCGAGGTTTTTGAAGCAAAATGACAGTAACAGCAACCAATCCAAATGTTAATTGA 666
DB 718 GATTCGAGGTTTTTGAAGCAAAATGACAGTAACAGCAACCAATCCAAATGTTAATTGA 777
QY 667 GACTTTCAGTCTCACTTACCCGTTGCGTACCCCACTCTCAAGCTCTCTGAATAT 726
DB 778 GACTTTCAGTCTCACTTACCCGTTGCGTACCCCACTCTCTGAATAT 837
QY 727 CTTGTTTACCCCGCAATATTTTACAGGTATCTTCAGAGATCTTCTGGCCAGAGGAA 786
DB 838 CTTGTTTACCCCGCAATATTTTACAGGTATCTTCAGAGATCTTCTGGCCAGAGGAA 897
QY 787 AGCCAAATCTGATGACTTCAGCAGATCCAGTTTTCAGTSCCAATTTCAAGGAGTT 846
DB 898 AGCCAAATCTGATGACTTCAGCAGATCCAGTTTTCAGTSCCAATTTCAAGGAGTT 957
QY 847 CAATTTACTACGATGATGCTCAATAAAACCACTGCTGTGTGAATTTGACATTTCAAT 906
DB 958 CAATTTACTACGATGATGCTCAATAAAACCACTGCTGTGTGAATTTGACATTTCAAT 1017
QY 907 ACAGACTTTTCTATCAGCTTGAAGTGCCTTCAAGCTATCTGCTTCAAGTATCT 966
DB 1018 ACAGACTTTTCTATCAGCTTGAAGTGCCTTCAAGCTATCTGCTTCAAGTATCT 1077
QY 967 GAGGTAAAGGCTTCCCAAGACGCTTGAAGATTAAGAGAGCACTGCGCTT 1026
DB 1078 GAGGTAAAGGCTTCCCAAGACGCTTGAAGATTAAGAGAGCACTGCGCTT 1137
QY 1027 TTGAATAATTAAGCAGACACAAAGAAAGAGAGCTTACCCAGCATATACCTGCG 1086
DB 1138 TTGAATAATTAAGCAGACACAAAGAAAGAGAGCTTACCCAGCATATACCTGCG 1197
QY 1087 GATGTTCTCTCAGTTCAATTTTACCTGTGTCTTGAATTCAGACATTTCTTAAAG 1146
DB 1198 GATGTTCTCTCAGTTCAATTTTACCTGTGTCTTGAATTCAGACATTTCTTAAAG 1257
QY 1147 GATTTTTCGAGCCCTTGTGACATTAACAGTGAACAGTCTGAAGAGGCGAGCTACAG 1206
DB 1258 GATTTTTCGAGCCCTTGTGACATTAACAGTGAACAGTCTGAAGAGGCGAGCTACAG 1317
QY 1207 GAGCTGTGACATTAACAGAGGCGAGCCGATTAAGCCGCTTGTGAAGATGCTGTGCG 1266
DB 1318 GAGCTGTGACATTAACAGAGGCGAGCCGATTAAGCCGCTTGTGAAGATGCTGTGCG 1377
QY 1267 TGTGTTGATCTCTCTCTGCTTCTCTTCTTTCAGCCACACTCACTGCTCTGCTC 1326
DB 1378 TGTGTTGATCTCTCTCTGCTTCTCTTCTTTCAGCCACACTCACTGCTCTGCTC 1437
QY 1327 GAAATCTCTCTTAACTTCAACCCAGACCAATATGCTGTGCAAGCTCAAGTTAATTTCAC 1386
DB 1438 GAAATCTCTCTTAACTTCAACCCAGACCAATATGCTGTGCAAGCTCAAGTTAATTTCAC 1497
QY 1387 CAGAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTCTGTACTGCTCAACAGAG 1446
DB 1498 CAGAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTCTGTACTGCTCAACAGAG 1557
QY 1447 GTTCTGCGAAGGAGATATGACAGCTGCTGCGCTTGTGTGTTCTTCAAGTTCTTCAG 1506
DB 1558 GTTCTGCGAAGGAGATATGACAGCTGCTGCGCTTGTGTGTTCTTCAAGTTCTTCAG 1617
QY 1507 CCAAAATATCATGATCCCATGAAGACAGCGGAAAGCCCTGAGCTCTTAAGATATCATC 1566
DB 1618 CCAAAATATCATGATCCCATGAAGACAGCGGAAAGCCCTGAGCTCTTAAGATATCATC 1677
QY 1567 TCTCTCTGAACAACAATCTTTCATCACTTACAGATGACCCCTCATATCCCATATATG 1626
DB 1678 TCTCTCTGAACAACAATCTTTCATCACTTACAGATGACCCCTCATATCCCATATATG 1737
QY 1627 GTGGGTCAAGAAACCGGATAGCCCGCTTATTTGGTTCTTCAACATATGAGAAATCTC 1686
DB 1738 GTGGGTCAAGAAACCGGATAGCCCGCTTATTTGGTTCTTCAACATATGAGAAATCTC 1797

QY 1687 CAAGAAACACCCAGATGGAATTTTGGAGCAATGCTGTTTGGCTGAGGCAT 1746
DB 1798 CAAGAAACACCCAGATGGAATTTTGGAGCAATGCTGTTTGGCTGAGGCAT 1857
QY 1747 AAGGATGAGGATTTATTCATTCAGAAAAGAGCTGAGCATTTCTTAAAGATGGATCTTA 1806
DB 1858 AAGGATGAGGATTTATTCATTCAGAAAAGAGCTGAGCATTTCTTAAAGATGGATCTTA 1917
QY 1807 ACTCATCTAAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGAGAAAGCCCGACA 1866
DB 1918 ACTCATCTAAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGAGAAAGCCCGACA 1977
QY 1867 AAGATGTACAGACACATCCAGCTTCATGCGACAGAGAGTGGGAGAAATCTCTCCAG 1926
DB 1978 AAGATGTACAGACACATCCAGCTTCATGCGACAGAGAGTGGGAGAAATCTCTCCAG 2037
QY 1927 GAGAACGGCCATATTTATGTGTGTGAGATGCAAGATATGCGCAAGATGATCATGAT 1986
DB 2038 GAGAACGGCCATATTTATGTGTGTGAGATGCAAGATATGCGCAAGATGATCATGAT 2097
QY 1987 GCCCTGTGCAATATATATGCAAGAGAGTGGAGTTGAAATACTGAGCAATGAAACC 2046
DB 2098 GCCCTGTGCAATATATATGCAAGAGAGTGGAGTTGAAATACTGAGCAATGAAACC 2157
QY 2047 CTGGCCCACTTAAAGAAAGAAAACGCTACCTTCAGATATTTGGTCTATAA 2097
DB 2158 CTGGCCCACTTAAAGAAAGAAAACGCTACCTTCAGATATTTGGTCTATAA 2208

RESULT 15
ID ACN42470 standard; cDNA; 3189 BP.
XX ACN42470;
XX ACN42470;
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1345.
XX
KM as; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
OS dltbp.
XX Homo sapiens.
XX
PN MO2004023973-A2.
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Henthorn TA, Suchorolski MT, Altus CM, Plets SD, Elder LV;
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spino PA, Stewart EA, Wingrove J, Viltz UA, Kitron ES;
PI Xu Y, Khong M, Policky JW, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX
DR WPI; 2004-329368/30.
DR P-PSDB; ABM83818.
XX
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 1; Page; 190pp; English.

XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dltbp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorder,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dltbp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dltbp polynucleotide of
CC the invention. Note: The sequence data for this patent is not represented
CC in the printed specification, but was obtained in electronic format
CC directly from WIPO at www.wipo.int/pct/en/sequences/lifting.htm
XX
SQ Sequence 3189 BP; 916 A; 679 C; 665 G; 929 T; 0 U; 0 Other;
Query Match 48.0%; Score 1007; DB 13; Length 3189;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1057; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ANAGAGAGTTTCTGTTTATCTATATGCTTACACAGACAGGACAGGCAATCCAGAA 60
DB 112 ATAGAGAGTTTCTGTTTATCTATATGCTTACACAGACAGGACAGGCAATCCAGAA 171
QY 61 GAAATATGTGAGCAAGCTGTGTACATGATGATTTTCTGAGATCTTCACTATATAGTAA 120
DB 172 GAAATATGTGAGCAAGCTGTGTACATGATGATTTTCTGAGATCTTCACTATATAGTAA 231
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DB 292 GGCACCGGAGACCCACCCGACACAGCCCGCAATTTGTTAAGAAATACAGAACCA 351
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Job time : 738.49 secs

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Title: US-09-371-347A-41

Perfect score: 2097
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

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Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2046	97.6	3259	3 US-09-318-448-23	Sequence 23, Appl
2	1995	95.1	3242	4 US-09-949-016-4215	Sequence 4215, Ap
3	386	18.4	390	3 US-08-905-223-71	Sequence 71, Appl
4	330	15.7	601	4 US-09-949-016-150019	Sequence 150019, A
5	330	15.7	35916	4 US-09-949-016-15957	Sequence 15957, A
6	279	13.3	601	4 US-09-949-016-150020	Sequence 150020, A
7	189	9.0	601	4 US-09-949-016-150037	Sequence 150037, A
8	158	7.5	2475	4 US-09-566-921-88	Sequence 88, Appl
9	155	7.4	601	4 US-09-949-016-150030	Sequence 150030, A
10	145	6.9	601	4 US-09-949-016-150031	Sequence 150031, A
11	137	6.5	601	4 US-09-949-016-150046	Sequence 150046, A
12	137	6.5	601	4 US-09-949-016-150047	Sequence 150047, A
13	125	6.0	601	4 US-09-949-016-150029	Sequence 150029, A
14	121	5.8	601	4 US-09-949-016-150041	Sequence 150041, A
15	121	5.8	601	4 US-09-949-016-150042	Sequence 150042, A
16	119	5.7	601	4 US-09-949-016-150008	Sequence 150008, A
17	119	5.7	601	4 US-09-949-016-150055	Sequence 150055, A
18	110	5.2	601	4 US-09-949-016-150048	Sequence 150048, A
19	94	4.5	601	4 US-09-949-016-150032	Sequence 150032, A
20	78	3.7	601	4 US-09-949-016-150007	Sequence 150007, A
21	75	3.6	601	4 US-09-949-016-150018	Sequence 150018, A
22	65	3.1	244	4 US-09-471-276-495	Sequence 495, App
23	30	1.4	1681	4 US-09-023-655-453	Sequence 453, App
24	20	1.0	273	4 US-09-513-999C-14761	Sequence 14761, A
25	20	1.0	440	3 US-09-397-787-305	Sequence 305, App
26	20	1.0	444	4 US-09-621-976-14139	Sequence 14139, A
27	20	1.0	445	3 US-09-397-787-274	Sequence 274, App

C	28	20	1.0	174259	4 US-09-949-016-11968	Sequence 11968, A
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C	30	19	0.9	169	1 US-08-166-346A-8	Sequence 8, Appl
C	31	19	0.9	459	4 US-09-621-976-8324	Sequence 8324, Ap
C	32	19	0.9	3969	3 US-09-518-386B-4	Sequence 4, Appl
C	33	19	0.9	4396	3 US-09-821-736-1	Sequence 13507, A
C	34	19	0.9	14721	4 US-09-949-016-13507	Sequence 13507, A
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C	41	19	0.9	203093	4 US-09-949-016-14445	Sequence 14445, A
C	42	18	0.9	78	2 US-08-749-852-56	Sequence 56, Appl
C	43	18	0.9	78	2 US-08-749-852-58	Sequence 58, Appl
C	44	18	0.9	511	4 US-09-902-540-1374	Sequence 1374, Ap
C	45	18	0.9	531	4 US-09-252-991A-2223	Sequence 2223, Ap

ALIGNMENTS

RESULT 1	US-09-318-448-23	US-09-318-448-23
Sequence 23, Application US/09318448		
Patent No. 6210950		
GENERAL INFORMATION:		
APPLICANT: Johnson, William G.		
APPLICANT: Stenroos, Edward S.		
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING		
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS		
FILE REFERENCE: 601-1-057		
CURRENT APPLICATION NUMBER: US/09/318,448		
CURRENT FILING DATE: 1999-05-25		
NUMBER OF SEQ ID NOS: 46		
SOFTWARE: PatentIn Ver. 2.0		
SEQ ID NO 23		
LENGTH: 3259		
TYPE: DNA		
ORGANISM: Homo sapiens		
US-09-318-448-23		
Query Match	97.6%	Score 2046; DB 3; Length 3259;
Best Local Similarity	100.0%	Pred. No. 0;
Matches 2096; Conservative	0;	Mismatches 1; Indels 0; Gaps 0;
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DB	140	GAATGTGTGAGCAAGCTGTGTACATGATTTTCTGCAAGATCTTCACTGTATTGTA 159
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DB	200	TCCGATTAAGTATACCTTAACAAACCGAAGCTCTTGTGTGTGTTTTCACAG 259
QY	181	GGCAGCGAGACCCACCCGACAGCAGCCGAGTTTGAAGAAATACAGAACAAACA 240
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DB	320	CTCCGCGTGAATTTCTTGTCTACCTCGGTATGAGTTACTGGCTCTCGGTATTCAG 379
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DB	380	TAAACTACTTTTGCATGGGCGGAGATTAATGAATTAACGACTTGAAGGCTGAGCC 439
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QY 601 AGAAAGATTCGAGGTTTGAAGCAAAATGCACTGAGCAAGCAACCAATCCATGTTGA 660
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QY 1501 CTTTACCCAAACATACATGATCCCATGAAAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
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QY 1741 AGGCATTAAGGATGGAATTAATTAATTCAGAAAGACCTCAGACATTTCTTAAGCATGGG 1800
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Db 2000 CTCACAGAGAGCGGCATATTTATGTGTGAGATGCAAAAGATTAATGCGCAAGATGTA 2059
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Db 2120 AAAACCTGCGCATTAAAGAAAGAAACGCTACCTTCAGATATTTGCTCATTA 2176

RESULT 2
US-09-949-016-4215
; Sequence 4215, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4215
; LENGTH: 3242
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4215

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Matches 2095; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 2000 CTCACAGAGAACGCGCATATTTATGTGTGTGAGATGCAAGAAATATGCGCAAGATGTA 2059
QY 1981 CATGATGCCCTTGTGCAATTAATAGCAAAAGAGTTGAGTTGAAAACTAGAACATG 2040
Db 2060 CATGATGCCCTTGTGCAATTAATAGCAAAAGAGTTGAGTTGAAAACTAGAACATG 2119
QY 2041 AAAAAGCTGCGCACTTTAAAGAAAGAAAGCTACCTCAGGATTTTGTGATATA 2097
Db 2120 AAAAAGCTGCGCACTTTAAAGAAAGAAAGCTACCTCAGGATTTTGTGATATA 2176

RESULT 3
US-08-905-223-71
; Sequence 71, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclercq, Aymeric

APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
TISSUE TYPE: Brain
FEATURE:
NAME/KEY: s1g_peptide
LOCATION: 289..357
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 6.9
OTHER INFORMATION: seq SLSLASHSVSC/SN
US-08-905-223-71

Query Match 18.4%; Score 386; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 4.9e-188;
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 970 GTACAAAGCTTACCTCCAAAGACTGCACTTGAAGATAAAAGAGCACTGCGCTTTTG 1029
DB 3 GTACAAAGCTTACCTCCAAAGACTGCACTTGAAGATAAAAGAGCACTGCGCTTTTG 62
QY 1030 AAAATAAAGGAGAGACAAAGAAAGAGCTACTTACCCCGCATATACCTGCGGGA 1089
DB 63 AAAATAAAGGAGAGACAAAGAAAGAGCTACTTACCCCGCATATACCTGCGGGA 122
QY 1090 TGTTCCTCAGTTCATTTTACCTGCTGTTGAAATCCGAGCAATTCCTAAAAAGCA 1149
DB 123 TGTTCCTCAGTTCATTTTACCTGCTGTTGAAATCCGAGCAATTCCTAAAAAGCA 182
QY 1150 TTTTGGAGAGCCCTTGGAGCTATACAGTGAAGAGAGAGAGAGAGAGAGAGAG 1209
DB 183 TTTTGGAGAGCCCTTGGAGCTATACAGTGAAGAGAGAGAGAGAGAGAGAGAG 242
QY 1210 CTGTCAGTAAACAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1269
DB 243 CTGTCAGTAAACAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 302
QY 1270 TTGTTGATCTGAA 1329
DB 303 TTGTTGATCTGAA 362
QY 1330 CATCTTCTAACTTCAACCCAGACC 1355

DB 363 CATCTTCTAACTTCAACCCAGACC 388

RESULT 4
US-09-949-016-150019
Sequence 150019, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 150019
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-150019

Query Match 15.7%; Score 330; DB 4; Length 601;
Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 GTTAGAATCTTGGTGGAGCCGTGATGCTGCACTTGCGCCAGCCCTCAGAAACATT 460
DB 178 GTTAGAATCTTGGTGGAGCCGTGATGCTGCACTTGCGCCAGCCCTCAGAAACATT 237
QY 461 TTAGGTCAAGCAGAGAGACAAAGAGATAGTGGCCACTCCGGTGATCCTTGAT 520
DB 238 TTAGGTCAAGCAGAGAGACAAAGAGATAGTGGCCACTCCGGTGATCCTTGAT 297
QY 521 CCTTGAGAGACAGCCTTGGAGAGTCAAGTCACTTCAATCAATCAAGTCAAGTTC 580
DB 298 CCTTGAGAGACAGCCTTGGAGAGTCAAGTCACTTCAATCAATCAAGTCAAGTTC 357
QY 581 TGAGATTCAGATTCAGAGAAAGAAAGATTCGAGTTTGAAGCAAAATGACGTGACA 640
DB 358 TGAGATTCAGATTCAGAGAAAGAAAGATTCGAGTTTGAAGCAAAATGACGTGACA 417
QY 641 GCAACCAATCAATGTTGTAATTAAGATTTGAGTCTCACTTACCCGTTGGTACCC 700
DB 418 GCAACCAATCAATGTTGTAATTAAGATTTGAGTCTCACTTACCCGTTGGTACCC 477
QY 701 CACTTCACAGAGCTCTGGAATATTCGAGTTTACCCCGAATTTTACAGGTACATC 760
DB 478 CACTTCACAGAGCTCTGGAATATTCGAGTTTACCCCGAATTTTACAGGTACATC 537
QY 761 TGCAGAGTCTCTTGCCAGG 781
DB 538 TGCAGAGTCTCTTGCCAGG 558

RESULT 5
US-09-949-016-15957
Sequence 15957, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 15957
LENGTH: 35916
TYPE: DNA
ORGANISM: Human
US-09-949-016-15957

Query Match 15.7%; Score 330; DB 4; Length 35916;

Best Local Similarity 99.7%; Pred. No. 4.2e-159;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGTTGAGCCGTGATGTTGCTGCACTGCGCCAGCCCTCAGAAAGCATT 460
DB 10781 GTTTAGAACTTGTGTTGAGCCGTGATGTTGCTGCACTGCGCCAGCCCTCAGAAAGCATT 10840
QY 461 TTAGGTCAAGCAGAGGACAAGAGAGATTAAGTGGCCACTCCCGGTGGATCACTGCAT 520
DB 10841 TTAGGTCAAGCAGAGGACAAGAGAGATTAAGTGGCCACTCCCGGTGGATCACTGCAT 10900
QY 521 CCTTGAGCAGACCTTGTGAACTCAGAGCTGCTACACATTGAATTCAGATCGAGCTTC 580
DB 10901 CCTTGAGCAGACCTTGTGAACTCAGAGCTGCTACACATTGAATTCAGATCGAGCTTC 10960
QY 581 TGAAGTTCATGATTCAGAGGAGAAAGATTCGAGGTTTGAAGCAAAATGACGTAACA 640
DB 10961 TGAAGTTCATGATTCAGAGGAGAAAGATTCGAGGTTTGAAGCAAAATGACGTAACA 11020
QY 641 GCAACCAATCCAAATGTTGTAATTAAGACTTTGAGTCTCTACCTTACCCGTTGGTACCC 700
DB 11021 GCAACCAATCCAAATGTTGTAATTAAGACTTTGAGTCTCTACCTTACCCGTTGGTACCC 11080
QY 701 CACTCTCAAGCCTCTCTGAATATTCCTGTTTACCCCAAAATTTTACAGGTACATC 760
DB 11081 CACTCTCAAGCCTCTCTGAATATTCCTGTTTACCCCAAAATTTTACAGGTACATC 11140
QY 761 TGCAGAGTCTCTGGCCAGG 781
DB 11141 TGCAGAGTCTCTGGCCAGG 11161

RESULT 6

US-09-949-016-150020
Sequence 150020, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 150020
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-150020

Query Match 13.3%; Score 279; DB 4; Length 601;

Best Local Similarity 99.5%; Pred. No. 5.9e-133;
Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGTTGAGCCGTGATGTTGCTGCACTGCGCCAGCCCTCAGAAAGCATT 460
DB 165 GTTTAGAACTTGTGTTGAGCCGTGATGTTGCTGCACTGCGCCAGCCCTCAGAAAGCATT 224
QY 461 TTAGGTCAAGCAGAGGACAAGAGAGATTAAGTGGCCACTCCCGGTGGATCACTGCAT 520
DB 225 TTAGGTCAAGCAGAGGACAAGAGAGATTAAGTGGCCACTCCCGGTGGATCACTGCAT 284
QY 521 CCTTGAGCAGACCTTGTGAACTCAGAGCTGCTACACATTGAATTCAGATCGAGCTTC 580
DB 285 CCTTGAGCAGACCTTGTGAACTCAGAGCTGCTACACATTGAATTCAGATCGAGCTTC 344
QY 581 TGAAGTTCATGATTCAGAGGAGAAAGATTCGAGGTTTGAAGCAAAATGACGTAACA 640
DB 345 TGAAGTTCATGATTCAGAGGAGAAAGATTCGAGGTTTGAAGCAAAATGACGTAACA 404
QY 641 GCAACCAATCCAAATGTTGTAATTAAGACTTTGAGTCTCTACCTTACCCGTTGGTACCC 700
DB 405 GCAACCAATCCAAATGTTGTAATTAAGACTTTGAGTCTCTACCTTACCCGTTGGTACCC 464
QY 701 CACTCTCAAGCCTCTCTGAATATTCCTGTTTACCCCAAAATTTTACAGGTACATC 760
DB 465 CACTCTCAAGCCTCTCTGAATATTCCTGTTTACCCCAAAATTTTACAGGTACATC 524
QY 761 TGCAGAGTCTCTGGCCAGG 781
DB 525 TGCAGAGTCTCTGGCCAGG 545

RESULT 7

US-09-949-016-150037
Sequence 150037, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 150037
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-150037

Query Match 9.0%; Score 189; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.2e-86;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1369 AGCTCAAGTTTATTTCCACCAGAAAGCTCTTTGCTTCAACATTTGGAATTTCTG 1428
DB 18 AGCTCAAGTTTATTTCCACCAGAAAGCTCTTTGCTTCAACATTTGGAATTTCTG 77
QY 1429 TCTACTGCCACAAGAGGTTCTGCGAAGGAGATATGTACAGGCTGCTGCTGTTG 1488
DB 78 TCTACTGCCACAAGAGGTTCTGCGAAGGAGATATGTACAGGCTGCTGCTGTTG 137
QY 1489 GTTGCTTCAGTTCTTCAAGCAAAATCATCATGATCCATGAAGACAGCGGAAAGCCCTG 1548
DB 138 GTTGCTTCAGTTCTTCAAGCAAAATCATCATGATCCATGAAGACAGCGGAAAGCCCTG 197

QY	1549	GCTCCTAAG	1557
Db	198	GCTCCTAAG	206

RESULT 8
US-09-566-921-88
; Sequence 88, Application US/09566921

Oy 525 GAGGACAGACCCTTGGAAGTCAGAGCTGCACA CATTGAATCTCAAGTCAGCTTGTGAG 584
| | | | |
D6 16 GAGGACAGACCCTTGGAAGTCAGAGCTGCACA CATTGAATCTCAAGTCAGCTTGTGAG 75
| | | | |

DY 585 ATTCGATGATT CAGGAAGAAGGATTCTGAGTTTGAAGCAAAATGCAGTGAAACAGCAA 644

Db 76 ATTCGATGATT CAGGAAGAAGGATTCTGAGTTTGAAGCAAAATGCAGTGAAACAGCAA 1359

Qy 645 CCATCCATGTTGTAATTGAAGACTTTGAGTCTTAC 682
|||
Db 136 CCAATCCATGTTGTAATTGAAGACTTTGAGTCTTAC 173

```

RESULT 9
US-09-949-016-150030
; Sequence 150030, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01107
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150030
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-150030

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Query Match	7.4%	Score 155;	DB 4;	Length 601;
Best Local Similarity	100.0%;	Pred. No. 3.8e-69;		
Matches 155; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	Db	Qy	Db
904	320	964	379
AAATAGACATTTTCCATCTCAGCCCTGGAGAGATCCCTTACCGGATCTGCGCTTAACAGTGAT	AAATACAGATCTTTTCTATCAGCCCTGGAGATGCTCTTACCGGATCTGCGCTTAACAGTGAT	TCTGAGGTACAAAGCCCTACTCCAAAGACTGACGCTTGAAGATAAAGAAGACACTGCGCTC	TCTGAGGTACAAAGCCCTACTCCAAAGACTGAGCTTGAAGATAAAGAAGACACTGCGCTC
963	379	439	474
CTTTTGAATAATAAAGCGACACAAAGAAGAAAGG	CTTTTGAATAATAAAGCGACACAAAGAAGAAAGG		

```

RESULT 10
US-09-949-016-150031
; Sequence 150031. Application US/094949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150031
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150031

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Query Match	6.9%	Score 145;	DB 4;	Length 601;
Best Local Similarity	100.0%	Pred. No. 5.4e-64;		
Matches 145;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	904	AAACAGACCTTTCTCTATCAGCCGCGAGATCCTTCAGCGGATCTGCGCTTAACAGTGAT	963
QY <td>156 <td>AAATACAGCTTTTCTCTATCAGCCGCGAGATCCTTCAGCGGATCTGCGCTTAACAGTGAT <td>215</td> </td></td>	156 <td>AAATACAGCTTTTCTCTATCAGCCGCGAGATCCTTCAGCGGATCTGCGCTTAACAGTGAT <td>215</td> </td>	AAATACAGCTTTTCTCTATCAGCCGCGAGATCCTTCAGCGGATCTGCGCTTAACAGTGAT <td>215</td>	215
Db <td>964 <td>TCTGAGGTACAAAGCCTACTCCAAAGACTGAGCTTGAAGATTAAGAGAGACATCGCTC <td>1022</td> </td></td>	964 <td>TCTGAGGTACAAAGCCTACTCCAAAGACTGAGCTTGAAGATTAAGAGAGACATCGCTC <td>1022</td> </td>	TCTGAGGTACAAAGCCTACTCCAAAGACTGAGCTTGAAGATTAAGAGAGACATCGCTC <td>1022</td>	1022
QY <td>216 <td>TCTGAGGTACAAAGCCTACTCCAAAGACTGAGCTTGAAGATTAAGAGAGACATCGCTC <td>275</td> </td></td>	216 <td>TCTGAGGTACAAAGCCTACTCCAAAGACTGAGCTTGAAGATTAAGAGAGACATCGCTC <td>275</td> </td>	TCTGAGGTACAAAGCCTACTCCAAAGACTGAGCTTGAAGATTAAGAGAGACATCGCTC <td>275</td>	275
Db <td>1024 <td>CTTTTGAATAATTAAGCGAGACACA <td>1048</td> </td></td>	1024 <td>CTTTTGAATAATTAAGCGAGACACA <td>1048</td> </td>	CTTTTGAATAATTAAGCGAGACACA <td>1048</td>	1048
QY <td>276 <td>CTTTTGAATAATTAAGCGAGACACA <td>300</td> </td></td>	276 <td>CTTTTGAATAATTAAGCGAGACACA <td>300</td> </td>	CTTTTGAATAATTAAGCGAGACACA <td>300</td>	300

```

RESULT 11
US-09-949-016-150046
; Sequence 150046; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

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[illegible]

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RESULT 14
US-09-949-016-150041
; Sequence 150041, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150041
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150041

```

Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1556 AGATATCATCTCTCTCGAACAACAATCTTTCACCTTACGAGATGACCCCTCAATCC 1615
|||
DB 124 AGATATCATCTCTCTCGAACAACAATCTTTCACCTTACGAGATGACCCCTCAATCC 183

QY 1616 CCATCATTAATGTTGGGTCCAGGAACCGGCATAGCCCGTTTATTTGGTTCTTACACATA 1675
|||
DB 184 CCATCATTAATGTTGGGTCCAGGAACCGGCATAGCCCGTTTATTTGGTTCTTACACATA 243

QY 1676 G 1676
244 G 244

RESULT 15

US-09-949-016-150042
; Sequence 150042, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150042
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150042

Query Match 5.8%; Score 121; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.2e-51;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1556 AGATATCATCTCTCTCGAACAACAATCTTTCACCTTACGAGATGACCCCTCAATCC 1615
|||
DB 95 AGATATCATCTCTCTCGAACAACAATCTTTCACCTTACGAGATGACCCCTCAATCC 154

QY 1616 CCATCATTAATGTTGGGTCCAGGAACCGGCATAGCCCGTTTATTTGGTTCTTACACATA 1675
|||
DB 155 CCATCATTAATGTTGGGTCCAGGAACCGGCATAGCCCGTTTATTTGGTTCTTACACATA 214

QY 1676 G 1676
215 G 215

Search completed: August 27, 2005, 16:18:16
Job time : 237.757 secs

Query Match	100.0%	Score 2097	DB 10	Length 2097
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2097	0	Mismatches	0	Indels
				Gaps

1 ATGAGAGCTTTCGTTACTATATATGCTACACAGAGGACACGAAAAGGCATGCGAGAA 60
 |||||||

Db 1 ATGAGAGGTTTCTGTACTATATGCTACACAGCAGGAGACAGCAAAAGCCATCGCAGAA 60
Qy 61 GAATATGTAGCAGAGCTGTGTGATCATGATGATTTCTGCAGATCTTCACTGTATATGAA 120
Db 61 GAATATGTAGCAGAGCTGTGTGATCATGATGATTTCTGCAGATCTTCACTGTATATGAA 120
Qy 121 TCCGATTAAGTATGACCTTAAAAACCGAAACAGCTCTCTTGTGTGTGTGTTTCTACACG 180
Db 121 TCCGATTAAGTATGACCTTAAAAACCGAAACAGCTCTCTTGTGTGTGTGTTTCTACACG 180
Qy 181 GGACCGGAGAGCCACCGCAGACAGCCGCAAGTTTGTAAAGAAATACGAACCAACA 240
Db 181 GGACCGGAGAGCCACCGCAGACAGCCGCAAGTTTGTAAAGAAATACGAACCAACA 240
Qy 241 CTGCGGTTGATTTCTTGTCTCAGCTGCGGTATGGTTACTGCGTCTCGGTATTCAGAA 300
Db 241 CTGCGGTTGATTTCTTGTCTCAGCTGCGGTATGGTTACTGCGTCTCGGTATTCAGAA 300
Qy 301 TACACCTACTTTTGCATTTGGGGGAGATATTTGATTAAGACTTCAAGCTTGGAGCC 360
Db 301 TACACCTACTTTTGCATTTGGGGGAGATATTTGATTAAGACTTCAAGCTTGGAGCC 360
Qy 361 CGGCAATTTCTATGACATGACATGACATGACTGTGAGGTTTGAACCTTGTGTGAG 420
Db 361 CGGCAATTTCTATGACATGACATGACATGACTGTGAGGTTTGAACCTTGTGTGAG 420
Qy 421 CCGTGAATGCTGAGACTCTGCGCAGCCCTCAGAAAGATTTTATGATCAGCAGAGCA 480
Db 421 CCGTGAATGCTGAGACTCTGCGCAGCCCTCAGAAAGATTTTATGATCAGCAGAGCA 480
Qy 481 GAGGAGTAAAGTGGCGCATCTCCGGTGGCATCACTGCTGCTTGAAGACAGACTTGTG 540
Db 481 GAGGAGTAAAGTGGCGCATCTCCGGTGGCATCACTGCTGCTTGAAGACAGACTTGTG 540
Qy 541 AAGTCAGAGCTGTACACATTTGATGATGATGAGCTTGCAGATTCAGATTTGAGGA 600
Db 541 AAGTCAGAGCTGTACACATTTGATGATGATGAGCTTGCAGATTCAGATTTGAGGA 600
Qy 601 AGAAGAGATTTCTGAGGTTTGTGAACAAATGCAAGTGAACAGCAACCAATCAATGTTGA 660
Db 601 AGAAGAGATTTCTGAGGTTTGTGAACAAATGCAAGTGAACAGCAACCAATCAATGTTGA 660
Qy 661 ATTGAAGATTTGAGTCTCACTTACCCGTTCCGTTACCCCACTCTCAAGACTCTCTG 720
Db 661 ATTGAAGATTTGAGTCTCACTTACCCGTTCCGTTACCCCACTCTCTCAAGACTCTCTG 720
Qy 721 AATATTCCTGTTTACCCCGAGATATTTTACAGGTATCTGACAGAGTCTCTTGGCCAG 780
Db 721 AATATTCCTGTTTACCCCGAGATATTTTACAGGTATCTGACAGAGTCTCTTGGCCAG 780
Qy 781 GAGGAAAGCCAAAGTATCTGTGACTTCAGCAGATCAGTTTTCAGTGCATTTCAAG 840
Db 781 GAGGAAAGCCAAAGTATCTGTGACTTCAGCAGATCAGTTTTCAGTGCATTTCAAG 840
Qy 841 GCAATTTCACTTACTAAGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 900
Db 841 GCAATTTCACTTACTAAGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 900
Qy 901 TCAATATCAGACTTTTCTATCAGCTGAGAGATGCTTCAAGCTGATCTGCGCTTAAAGT 960
Db 901 TCAATATCAGACTTTTCTATCAGCTGAGAGATGCTTCAAGCTGATCTGCGCTTAAAGT 960
Qy 961 GATTTCTGAGGTACAAAGCTTCTCMAAGACTGAGCTTGAAGATTAAGAGAGACTGTC 1020
Db 961 GATTTCTGAGGTACAAAGCTTCTCMAAGACTGAGCTTGAAGATTAAGAGAGACTGTC 1020
Qy 1021 GTCTTTTGAATAATTAAGGAGACACAAAGAAAGAGAGTACCTTACCCAGACATATA 1080
Db 1021 GTCTTTTGAATAATTAAGGAGAGACACAAAGAAAGAGAGTACCTTACCCAGACATATA 1080
Qy 1081 CTTGCGGAGATGTTCTCTCAGATTTTATCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 1140
Db 1081 CTTGCGGAGATGTTCTCTCAGATTTTATCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 1140

Qy 1141 AAAAAGCATTTTTCGAGCCCTTGTGACTATACAGTGAACAGTCTGAAAAAGCCAGG 1200
Db 1141 AAAAAGCATTTTTCGAGCCCTTGTGACTATACAGTGAACAGTCTGAAAAAGCCAGG 1200
Qy 1201 CTACAGAGCTGTGACGTAAACAAAGGAGCAGCCGATTAATAGCCGTTTGTACAGATGCC 1260
Db 1201 CTACAGAGCTGTGACGTAAACAAAGGAGCAGCCGATTAATAGCCGTTTGTACAGATGCC 1260
Qy 1261 TGTGCTGCTGTGTGATCTCTCTCTGCTTCTCTTCTTCCCTTCCAGCAGCAGTCTC 1320
Db 1261 TGTGCTGCTGTGTGATCTCTCTCTGCTTCTCTTCTTCCCTTCCAGCAGCAGTCTC 1320
Qy 1321 CTGCTGAAATCTTCTTAACTTCAACCCAGACATATTCGTGACAGTCAAGTTTA 1380
Db 1321 CTGCTGAAATCTTCTTAACTTCAACCCAGACATATTCGTGACAGTCAAGTTTA 1380
Qy 1381 TTTACCCAGAAAGCTCCATTTTGTCTTCAACATTTGTGGAATTTCTGCTACTGACACA 1440
Db 1381 TTTACCCAGAAAGCTCCATTTTGTCTTCAACATTTGTGGAATTTCTGCTACTGACACA 1440
Qy 1441 ACAGAGTTCTGCGAAGGAGATATGATACAGCTGAGCTGCTGTTGTGTGCTGAGTT 1500
Db 1441 ACAGAGTTCTGCGAAGGAGATATGATATGATACAGCTGAGCTGCTGTTGTGTGCTGAGTT 1500
Qy 1501 CTTGAGCCAAACATACATGATCCATGAAAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
Db 1501 CTTGAGCCAAACATACATGATCCATGAAAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
Qy 1561 TCCATCTCTCTGGAACAAATTTCTTCCATTAACAGATGACCCCTCAATCCCATTC 1620
Db 1561 TCCATCTCTCTGGAACAAATTTCTTCCATTAACAGATGACCCCTCAATCCCATTC 1620
Qy 1621 ATATAGTGGGTCCAGAAACCGGATAGCCCTTATTTGGGTTCTTACAACTAGAGAG 1680
Db 1621 ATATAGTGGGTCCAGAAACCGGATAGCCCTTATTTGGGTTCTTACAACTAGAGAG 1680
Qy 1681 AAATCTCAAGAACCAACCCAGATGAAATTTTGAAGCAATGTGTGTTTGTGCTGC 1740
Db 1681 AAATCTCAAGAACCAACCCAGATGAAATTTTGAAGCAATGTGTGTTTGTGCTGC 1740
Qy 1741 AGGCAATTAAGATGGAATTAATCTATTCAGAAAGAGCTCAGATTTCTTAAGCATGGG 1800
Db 1741 AGGCAATTAAGATGGAATTAATCTATTCAGAAAGAGCTCAGATTTCTTAAGCATGGG 1800
Qy 1801 ATCTTAATCATTAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGAGAGAGGCC 1860
Db 1801 ATCTTAATCATTAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGAGAGAGGCC 1860
Qy 1861 CCAAGAAAGTATGTAACAAGCAATCCAGCTTCAATGAGCAGAGTGGCGAATCTTC 1920
Db 1861 CCAAGAAAGTATGTAACAAGCAATCCAGCTTCAATGAGCAGAGTGGCGAATCTTC 1920
Qy 1921 CTCAGAGAAAGGCGCATTTATTTATGTGTGAGATGCAAGAAATATGGCCAGAGATGA 1980
Db 1921 CTCAGAGAAAGGCGCATTTATTTATGTGTGAGATGCAAGAAATATGGCCAGAGATGA 1980
Qy 1981 CATGATGCCCTTGTGCAATATATAGCAAGAGTGTGAGTTGAAAACTAGAAAGCATG 2040
Db 1981 CATGATGCCCTTGTGCAATATATAGCAAGAGTGTGAGTTGAAAACTAGAAAGCATG 2040
Qy 2041 AAAACCTGGCCACTTTAAAAAGAAAGAAAGCGTACCTTCAAGATATTTGTCATTA 2097
Db 2041 AAAACCTGGCCACTTTAAAAAGAAAGAAAGCGTACCTTCAAGATATTTGTCATTA 2097

RESULT 2

US-09-371-347-1

; Sequence 1, Application US/09371347

; Publication No. US20030082676A1

; GENERAL INFORMATION:

; APPLICANT: Roy A. Gravel et al.

; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE;

TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
FILE OF INVENTION: DEFECTS CARDIOVASCULAR DISEASE, AND CANCER
FILE REFERENCE: 50004/003003
CURRENT APPLICATION NUMBER: US/09/371,347
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/071,622
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 09/232,028
PRIOR FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 1
LENGTH: 2097
TYPE: DNA
ORGANISM: Homo sapiens
US-09-371-347-1

Query Match 97.6%; Score 2046; DB 10; Length 2097;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGAGAGGTTCTGTACTATATGCTACACAGCAGGAGGACAGGCAAGGCCATCGCAGAA 60
DB 1 ATGAGAGAGGTTCTGTACTATATGCTACACAGCAGGAGGACAGGCAAGGCCATCGCAGAA 60
QY 61 GAAATATGAGCAGAGCTGTGTACATGATTTCTGCGAGATCTTCACTGTATTAAGAA 120
DB 61 GAAATATGAGCAGAGCTGTGTACATGATTTCTGCGAGATCTTCACTGTATTAAGAA 120
QY 121 TCCGATATGATGACCTTAATAACCGAAAGAGCTCTCTGTGTGTGTGTGTGTCTACAG 180
DB 121 TCCGATATGATGACCTTAATAACCGAAAGAGCTCTCTGTGTGTGTGTGTGTCTACAG 180
QY 181 GGCACCGGAGACCCACCGCAGACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
DB 181 GGCACCGGAGACCCACCGCAGACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
QY 241 CTGCGGTTGATTTCTTGTCTCAGCTGCGGTATGAGGTACTGAGTCTCGGTATTCAGAA 300
DB 241 CTGCGGTTGATTTCTTGTCTCAGCTGCGGTATGAGGTACTGAGTCTCGGTATTCAGAA 300
QY 301 TACACCTACTTTTGAATGAGGAGGAGATTAATGATTAACAGCTTCAAGAGCTTGAAGCC 360
DB 301 TACACCTACTTTTGAATGAGGAGGAGATTAATGATTAACAGCTTCAAGAGCTTGAAGCC 360
QY 361 CGGCAATTTCTATGACACTGACATGCAATGATGATGATGATGATGATGATGATGATGAT 420
DB 361 CGGCAATTTCTATGACACTGACATGCAATGATGATGATGATGATGATGATGATGATGAT 420
QY 421 CCGTGAATGCTGAGACTGTGCGCAGCCCTCAGAAAGCAATTTTGTGTCAGAGAGAGCA 480
DB 421 CCGTGAATGCTGAGACTGTGCGCAGCCCTCAGAAAGCAATTTTGTGTCAGAGAGAGCA 480
QY 481 GAGGAGATAGTGGGCACTCCGCGTGGGATCACTGCACTTCTTGAAGAGCAGAGCTTGTG 540
DB 481 GAGGAGATAGTGGGCACTCCGCGTGGGATCACTGCACTTCTTGAAGAGCAGAGCTTGTG 540
QY 541 AAGTCAGAGCTGTACACATTTGAATCTCAAGTCAAGCTTCTGAGATTCAGATTCAGAA 600
DB 541 AAGTCAGAGCTGTACACATTTGAATCTCAAGTCAAGCTTCTGAGATTCAGATTCAGAA 600
QY 601 AGAAGAGATTTGAGGTTTGAAGCAAAATGCAAGTCAAGCAAGCAATTCAGATTCAGAA 660
DB 601 AGAAGAGATTTGAGGTTTGAAGCAAAATGCAAGTCAAGCAAGCAATTCAGATTCAGAA 660
QY 661 ATGAGAGATTTGAGGTTTGAAGCAAAATGCAAGTCAAGCAAGCAATTCAGATTCAGAA 720
DB 661 ATGAGAGATTTGAGGTTTGAAGCAAAATGCAAGTCAAGCAAGCAATTCAGATTCAGAA 720
QY 721 AATATTCCTGTTTACCCCAAGATATTTTACAGATCATCTGACAGAGTCTTGTGCGCAG 780
DB 721 AATATTCCTGTTTACCCCAAGATATTTTACAGATCATCTGACAGAGTCTTGTGCGCAG 780

QY 781 GAGGAGAGCAGATATCTGTGACTTCAAGAGATTCAGATTCAGATTCAGATTCAGAA 840
DB 781 GAGGAGAGCAGATATCTGTGACTTCAAGAGATTCAGATTCAGATTCAGATTCAGAA 840
QY 841 GAGGTTCAACTTACTACAGATATGATCCATTAAGCACTCTGCTGTGATTAAGTGA 900
DB 841 GAGGTTCAACTTACTACAGATATGATCCATTAAGCACTCTGCTGTGATTAAGTGA 900
QY 901 TCAATATCAAGATTTTCTTCAAGCTGAGATGCTTCAAGGATATTCAGATTCAGAA 960
DB 901 TCAATATCAAGATTTTCTTCAAGCTGAGATGCTTCAAGGATATTCAGATTCAGAA 960
QY 961 GATTCAGAGTCAAGAGCTTCAAGAGCTGAGATTCAGATTCAGATTCAGATTCAGAA 1020
DB 961 GATTCAGAGTCAAGAGCTTCAAGAGCTGAGATTCAGATTCAGATTCAGATTCAGAA 1020
QY 1021 GTCTTTTGAATTAAGGAGCAGACCAAGAGAGAGGAGTACCTTACCCAGCATATA 1080
DB 1021 GTCTTTTGAATTAAGGAGCAGACCAAGAGAGAGGAGTACCTTACCCAGCATATA 1080
QY 1081 CCGTGGGATATCTTCAAGTTCATTTTACCTGAGTCTGAAATCCAGCAATTCCT 1140
DB 1081 CCGTGGGATATCTTCAAGTTCATTTTACCTGAGTCTGAAATCCAGCAATTCCT 1140
QY 1141 AAAAGGCAATTTTGGAGCCCTTGTGACATATACAGATGAGTGTGAAAGGCGCAG 1200
DB 1141 AAAAGGCAATTTTGGAGCCCTTGTGACATATACAGATGAGTGTGAAAGGCGCAG 1200
QY 1201 CTACAGAGCTGTGAGTAAACAGAGGAGGAGGATTAATAGCCGCTTGTGAGATG 1260
DB 1201 CTACAGAGCTGTGAGTAAACAGAGGAGGAGGATTAATAGCCGCTTGTGAGATG 1260
QY 1261 TGTGCTGCTGTGTGATCTCTCTGCTGCTTCCCTCTTGTGCAAGCAGCAGCTG 1320
DB 1261 TGTGCTGCTGTGTGATCTCTCTGCTGCTTCCCTCTTGTGCAAGCAGCAGCTG 1320
QY 1321 CTGCTGAGACATCTTCTTAACTTCAACCCAGACATATTCGTGCAAGCTCAAGTTA 1380
DB 1321 CTGCTGAGACATCTTCTTAACTTCAACCCAGACATATTCGTGCAAGCTCAAGTTA 1380
QY 1381 TTTCAACCCAGAGAGCTTCAATTTTGTCTTCAATTTGTGATGATTCATCTG 1440
DB 1381 TTTCAACCCAGAGAGCTTCAATTTTGTCTTCAATTTGTGATGATTCATCTG 1440
QY 1441 ACAAGGTTCTGCGAGAGGAGATATGATGAGCTGCTGCTGCTGCTGCTGCTGCTG 1500
DB 1441 ACAAGGTTCTGCGAGAGGAGATATGATGAGCTGCTGCTGCTGCTGCTGCTGCTG 1500
QY 1501 CTTCAAGCCAAATACATGATCCCATGAGAGCAGGAGGAGAGCCCTGAGCTCTAAGATA 1560
DB 1501 CTTCAAGCCAAATACATGATCCCATGAGAGCAGGAGGAGAGCCCTGAGCTCTAAGATA 1560
QY 1561 TCCATCTCTCTGAGCAACAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
DB 1561 TCCATCTCTCTGAGCAACAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
QY 1621 ATATATGAGGTTCTGAGAGCCGATAGCCGCTTATTTGAGTTCTTCAACAATAGAG 1680
DB 1621 ATATATGAGGTTCTGAGAGCCGATAGCCGCTTATTTGAGTTCTTCAACAATAGAG 1680
QY 1681 AATATCCAGAGCAACACAGATGAGAAATTTTGGAGCAATGATGATTTTGTGCTG 1740
DB 1681 AATATCCAGAGCAACACAGATGAGAAATTTTGGAGCAATGATGATTTTGTGCTG 1740
QY 1741 AGGCAATTAAGGATTAATCTATTTCAAGAAAGAGCTCAGATTTCTTAAAGATGAG 1800
DB 1741 AGGCAATTAAGGATTAATCTATTTCAAGAAAGAGCTCAGATTTCTTAAAGATGAG 1800
QY 1801 ATCTTAATCTATTAAGGATTTCTTCTCAAGATGCTCTGTTGAGGAGAGAGAGCC 1860
DB 1801 ATCTTAATCTATTAAGGATTTCTTCTCAAGATGCTCTGTTGAGGAGAGAGAGCC 1860
QY 1861 CCAGCAAGATATGATCAAGCAACATCAGCTTCAATGCGCAGAGAGTGTGCAATCTCT 1920

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Db      1861  CGAGCAAGATGATGACAAAGCAACATCAGCTTCATGCGACAGAGGGGAGAAATCTC 1920
Qy      1921  CTCACAGAGAACGGCCATATTTATGTGTGAGAGATCAAAAGATATGCGCAAGATGTA 1980
Db      1921  CTCACAGAGAACGGCCATATTTATGTGTGAGAGATCAAAAGATATGCGCAAGATGTA 1980
Qy      1981  CATGATCCCTTGTGTGCAATATATATAGCAAAAGAGTTGAGTTGAAAACTAGAAGCATG 2040
Db      1981  CATGATCCCTTGTGTGCAAAATATATAGCAAAAGAGTTGAGTTGAAAACTAGAAGCATG 2040
Qy      2041  AAAACCTGGCCACTTTAAAAAGAAAGAAACGCTACCTTCAAGATATTTGCTATTA 2097
Db      2041  AAAACCTGGCCACTTTAAAAAGAAAGAAACGCTACCTTCAAGATATTTGCTATTA 2097

RESULT 3
US-09-371-347-24
; Sequence 24, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 3259
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-371-347-24

Query March      97.6%; Score 2046; DB 10; Length 3259;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  ATGAGAGGTTCTGTTACTATATATGCTACACAGCAGGAGACAGCAAGCCATGACAGAA 60
Db      80  ATGAGAGGTTCTGTTACTATATATGCTACACAGCAGGAGACAGCAAGCCATGACAGAA 139
Qy      61  GAAATATGTAGAGCAAGCTGTGTGATCATGAGATTTTCTGCAATCTTCACTGATTAAGTAA 120
Db      140  GAAATGTGTAGAGCAAGCTGTGTGATCATGAGATTTTCTGCAATCTTCACTGATTAAGTAA 199
Qy      121  TCCGATATGATGACTTAAAAACCGAAACAGCTCCTGTGTGTGTGTGTTTCTACCAAG 180
Db      200  TCCGATATGATGACTTAAAAACCGAAACAGCTCCTGTGTGTGTGTGTTTCTACCAAG 259
Qy      181  GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
Db      260  GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 319
Qy      241  CTGCGCGGTGATTTCTTTGTCTCACTGCGGTGATAGGTTTCTGCGTCTCGGATTTCAAG 300
Db      320  CTGCGCGGTGATTTCTTTGTCTCACTGCGGTGATAGGTTTCTGCGTCTCGGATTTCAAG 379
Qy      301  TACACCTACTTTTCAATGGGGGAGATATTAATTAACAAGACTTCAAGAGCTTGAGCC 360
Db      380  TACACCTACTTTTCAATGGGGGAGATATTAATTAACAAGACTTCAAGAGCTTGAGCC 439
Qy      361  CGGCAATTTCTATGACATGACATGACAGATGCTGTAGGTTTGAACCTTGTGTTGAG 420
Db      440  CGGCAATTTCTATGACATGACATGACAGATGCTGTAGGTTTGAACCTTGTGTTGAG 499
Qy      421  CCGTGATGTGCTGAGACTCTGGCAGCCCTCAGAAAGCATTTTAGGTCAAGACAGAGCAA 480
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Db      500  CCGTGATGTGCTGAGACTCTGGCAGCCCTCAGAAAGCATTTTAGGTCAAGACAGAGCAA 559
Qy      481  GAGAGATATAGTGGCCGACATCCCGGTGGATCACTGCAATCTTTGAGGACAGACTTGTG 540
Db      560  GAGAGATATAGTGGCCGACATCCCGGTGGATCACTGCAATCTTTGAGGACAGACTTGTG 619
Qy      541  AAGTCAGACTGTGACACATTTGATATCTCAAGTCAGACTTCTGAGATTCGATGATTCAGGA 600
Db      620  AAGTCAGACTGTGACACATTTGATATCTCAAGTCAGACTTCTGAGATTCGATGATTCAGGA 679
Qy      601  AGAAGAGATTCGAGGTTTGAAGCAAAATGCAAGTAACAGCAACCAATCCAAATGTTGTA 660
Db      680  AGAAGAGATTCGAGGTTTGAAGCAAAATGCAAGTAACAGCAACCAATCCAAATGTTGTA 739
Qy      661  ATTGAAGCTTTGAGTCTCACTTACCCGTGGGTACCCCACTCTCACAGGCTCTGTG 720
Db      740  ATTGAAGCTTTGAGTCTCACTTACCCGTGGGTACCCCACTCTCACAGGCTCTGTG 799
Qy      721  AATATTCCTGTGTTACCCCAAGATATTTTACAGGTACATCTGACAGAGATCTTTGGCCAG 780
Db      800  AATATTCCTGTGTTACCCCAAGATATTTTACAGGTACATCTGACAGAGATCTTTGGCCAG 859
Qy      781  GAGAAAGCCAGATCTGTAAGTCAAGAGATCCAGTTTTCAGAGGCCAATTTCAAG 840
Db      860  GAGAAAGCCAGATCTGTAAGTCAAGAGATCCAGTTTTCAGAGGCCAATTTCAAG 919
Qy      841  GCAGTTCAACTTACTACGATGATGCAATTAACCACTCTGTGTGATGATTTGACATT 900
Db      920  GCAGTTCAACTTACTACGATGATGCAATTAACCACTCTGTGTGATGATTTGACATT 979
Qy      901  TCAATATCAGACTTTTCTATCAGCTCGAGATGCTTCAAGCTGATTCGCCCTTAACAT 960
Db      980  TCAATATCAGACTTTTCTATCAGCTCGAGATGCTTCAAGCTGATTCGCCCTTAACAT 1039
Qy      961  GATTCGAGGTAAAGCCATCTCAAGCTGAGCTTGAAGATTAAGAGAGCACTGC 1020
Db      1040  GATTCGAGGTAAAGCCATCTCAAGCTGAGCTTGAAGATTAAGAGAGCACTGC 1099
Qy      1021  GTCCCTTTGAAATTAAGGACAGACACAAAGAAAGAGAGCTACTTACCACGACATATA 1080
Db      1100  GTCCCTTTGAAATTAAGGACAGACACAAAGAAAGAGAGCTACTTACCACGACATATA 1159
Qy      1081  CTGCGGAGATGTTCTCTCCAGTCAATTTTCTGCTGTCTTGAATTCGAGCAATTTCT 1140
Db      1160  CTGCGGAGATGTTCTCTCCAGTCAATTTTCTGCTGTCTTGAATTCGAGCAATTTCT 1219
Qy      1141  AAAAAGGCAATTTTGGAGGCCCTGTGGACTATACAGAGTACAGTGTGTAAGAGCGCAG 1200
Db      1220  AAAAAGGCAATTTTGGAGGCCCTGTGGACTATACAGAGTACAGTGTGTAAGAGCGCAG 1279
Qy      1201  CTACAGAGCTGTGCAGTAAACAAAGGGGACGCCGATTAAGCCGTTTGTACAGATGCC 1260
Db      1280  CTACAGAGCTGTGCAGTAAACAAAGGGGACGCCGATTAAGCCGTTTGTACAGATGCC 1339
Qy      1261  TGTGCTGTGTTGTGATCTCTCTCTGCTGCTTCCCTTTCTTGCAAGCACTCAAGTCTC 1320
Db      1340  TGTGCTGTGTTGTGATCTCTCTCTGCTGCTTCCCTTTCTTGCAAGCACTCAAGTCTC 1399
Qy      1321  CTGCTGGAACATCTTCTTAACCTTCAACCCGACCAATATTGATGAGCTCAAGTTTA 1380
Db      1400  CTGCTGGAACATCTTCTTAACCTTCAACCCGACCAATATTGATGAGCTCAAGTTTA 1459
Qy      1381  TTTCACCAGGAAGCTCAATTTTGTCTTCAACATTTGTGGAATTTGTCTACTGCCACA 1440
Db      1460  TTTCACCAGGAAGCTCAATTTTGTCTTCAACATTTGTGGAATTTGTCTACTGCCACA 1519
Qy      1441  ACAAGAGTTTCTGCGAAGGAGATATGACAGCTGCTGCTGCTTGTGTTGCTTCAAGTT 1500
Db      1520  ACAAGAGTTTCTGCGAAGGAGATATGACAGCTGCTGCTGCTTGTGTTGCTTCAAGTT 1579
Qy      1501  CTTCAAGCAAACTATACATGATCCCATGAAGACAGGGGGAAGCCCTGAGCTCTCAAGATA 1560
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Db 1580 CTTGACCCAAACATACATGATCCCATGAAAGACGCGGAAAGCCCTGCTCTTAAGATA 1639
Qy 1561 TCCATCTCTCTGAGCAACAAATCTTTCCACTTACAGATGACCCCTCAATCCCATC 1620
Db 1640 TCCATCTCTCTGAGCAACAAATCTTTCCACTTACAGATGACCCCTCAATCCCATC 1699
Qy 1621 ATAATGTTGGTTCAGAAACCGGATAGCCCGTTTATTTGGTTCTTACAACTAGAGAG 1680
Db 1700 ATATATGTTGGTTCAGAAACCGGATAGCCCGTTTATTTGGTTCTTACAACTAGAGAG 1759
Qy 1681 AAATCTCAAGAACACACCCAGATGGAATTTTGGAGCAATGTGTTGTTTTTGGCTGC 1740
Db 1760 AAATCTCAAGAACACACCCAGATGGAATTTTGGAGCAATGTGTTGTTTTTGGCTGC 1819
Qy 1741 AGGCATAGGATGAGATTAATCTATTCAGAAAGAGCTCAGACATTTCTTAAAGATGG 1800
Db 1820 AGGCATAGGATGAGATTAATCTATTCAGAAAGAGCTCAGACATTTCTTAAAGATGG 1879
Qy 1801 ATCTTAATCATTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1860
Db 1880 ATCTTAATCATTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1939
Qy 1861 CCAGCAAGATATGACAAAGCAATCCAGCTTCATGCGCAGAGGTGGGAGATCTTC 1920
Db 1940 CCAGCAAGATATGACAAAGCAATCCAGCTTCATGCGCAGAGGTGGGAGATCTTC 1999
Qy 1921 CTCACAGAAACCGGCATATTTATGTTGTTGAGATGCAAAAGATATGCGCAAGATTA 1980
Db 2000 CTCACAGAAACCGGCATATTTATGTTGTTGAGATGCAAAAGATATGCGCAAGATTA 2059
Qy 1981 CATGATGCTTGTGCAAAATATATAGCAAAAGGTTGAGTTGAAAACTAGAAAGATG 2040
Db 2060 CATGATGCTTGTGCAAAATATATAGCAAAAGGTTGAGTTGAAAACTAGAAAGATG 2119
Qy 2041 AAAACCTGGCCACTTTAAAAAGAAAGAAACGCTACCTTCAGAGATTTTGGTCATTA 2097
Db 2120 AAAACCTGGCCACTTTAAAAAGAAAGAAACGCTACCTTCAGAGATTTTGGTCATTA 2176

RESULT 4
US-09-371-347-43
; Sequence 43, Application US/09371347
; Publication No. US2003082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-43

Query Match 95.1%; Score 1995; DB 10; Length 2097;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2095; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATAGAGAGGTTTCTGTAATATGCTACACAGAGGAGACAGAAAGGCATGCGAGAA 60
Db 1 ATAGAGAGGTTTCTGTAATATGCTACACAGAGGAGACAGAAAGGCATGCGAGAA 60
Qy 61 GAAATATGAGCAAGCTGTGTAATGATGATTTTCTGCAATCTTCACTATTAATGAA 120
Db 61 GAAATATGAGCAAGCTGTGTAATGATGATTTTCTGCAATCTTCACTATTAATGAA 120

Db 61 GAAATATGAGCAAGCTGTGTAATGATGATTTTCTGCAATCTTCACTATTAATGAA 120
Qy 121 TCCGATTAAGTATGACCTTAAAAACGAAACAGCTCTCTGTTGTTGTTTCTACAG 180
Db 121 TCCGATTAAGTATGACCTTAAAAACGAAACAGCTCTCTGTTGTTGTTTCTACAG 180
Qy 181 GGCACCGAGAACCCAGCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCA 240
Db 181 GGCACCGAGAACCCAGCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCA 240
Qy 241 CTGCGGATGATTTCTTTGCTCACTGCGGTATGAGTTATCTGGTCTCGGTATTCAG 300
Db 241 CTGCGGATGATTTCTTTGCTCACTGCGGTATGAGTTATCTGGTCTCGGTATTCAG 300
Qy 301 TACACCTACTTTTGCAATGAGGAGAAAGATTAATGATTAACGACTTCAAGAGCTTGA 360
Db 301 TACACCTACTTTTGCAATGAGGAGAAAGATTAATGATTAACGACTTCAAGAGCTTGA 360
Qy 361 CGGCAATTTCTATGACACTGGAATGACAGATGAATGATAGTTTGAATCTGTGTTAG 420
Db 361 CGGCAATTTCTATGACACTGGAATGACAGATGAATGATAGTTTGAATCTGTGTTAG 420
Qy 421 CCGTGATGCTGGAATCTGCGCAAGCTCTCAAGAACATTTTAAAGTCAAGAGACAA 480
Db 421 CCGTGATGCTGGAATCTGCGCAAGCTCTCAAGAACATTTTAAAGTCAAGAGACAA 480
Qy 481 GAGGAGATAGTGGGCACTCCCGGATGATACCTGATCCCTTGAAGACAGACCTGTG 540
Db 481 GAGGAGATAGTGGGCACTCCCGGATGATACCTGATCCCTTGAAGACAGACCTGTG 540
Qy 541 AAGTCAGACCTCTACACATTAATCTCAAGTCAAGCTTCTGAGATTCAGATTCAGAG 600
Db 541 AAGTCAGACCTCTACACATTAATCTCAAGTCAAGCTTCTGAGATTCAGATTCAGAG 600
Qy 601 AGAAGAGATTCGAGGTTTGAAGCAAAATGCAATGCAAGCAACCAATTCATGTTGA 660
Db 601 AGAAGAGATTCGAGGTTTGAAGCAAAATGCAATGCAAGCAACCAATTCATGTTGA 660
Qy 661 ATTGAAGATTTGAGTCTCACTTACCCGTTGGATACCCCACTGCAAGCTCTCTG 720
Db 661 ATTGAAGATTTGAGTCTCACTTACCCGTTGGATACCCCACTGCAAGCTCTCTG 720
Qy 721 AATATTCCTGTTTACCCCAAGATTTTAAAGATTCAGATTCAGAGATCTCTGCGCAG 780
Db 721 AATATTCCTGTTTACCCCAAGATTTTAAAGATTCAGATTCAGAGATCTCTGCGCAG 780
Qy 781 GAGGAAAGCCAGATATCTGTGACTTCAGAGATTCAGATTTTCAAGTCCCAATTCAG 840
Db 781 GAGGAAAGCCAGATATCTGTGACTTCAGAGATTCAGATTTTCAAGTCCCAATTCAG 840
Qy 841 GCAGTTCACTTACATGCAATGATGCAATTAACCACTCTGTGTGAATTTGACATT 900
Db 841 GCAGTTCACTTACATGCAATGATGCAATTAACCACTCTGTGTGAATTTGACATT 900
Qy 901 TCAATATGAGACTTTCTATCAGCTGAGAGATCTTCAAGGATTCAGGATTCAGCTCA 960
Db 901 TCAATATGAGACTTTCTATCAGCTGAGAGATCTTCAAGGATTCAGGATTCAGCTCA 960
Qy 961 GATTTGAGGTAACAAAGCTTACCAAGACTGCAAGCTTGAAGATTAAGAGAGACTGC 1020
Db 961 GATTTGAGGTAACAAAGCTTACCAAGACTGCAAGCTTGAAGATTAAGAGAGACTGC 1020
Qy 1021 GTCTTTTGAATTAAGGACACACAAAGAAAGAGAGATCTTACCCAGCATTA 1080
Db 1021 GTCTTTTGAATTAAGGACACACAAAGAAAGAGAGATCTTACCCAGCATTA 1080
Qy 1081 CCGCGGAGATTTCTCTCAGATTCATTTTACCTGATCTTGAATTCGAGCAATTCCT 1140
Db 1081 CCGCGGAGATTTCTCTCAGATTCATTTTACCTGATCTTGAATTCGAGCAATTCCT 1140
Qy 1141 AAAAGGCAATTTTGGAGCCCTTGTGACTATACAGTGAAGATTCAGAGAGAGAG 1200
Db 1141 AAAAGGCAATTTTGGAGCCCTTGTGACTATACAGTGAAGATTCAGAGAGAGAG 1200

QY 1201 CTACAGAGCTGTGACGATTAACAAAGGGGACGCCGATTAATAGCCGCTTTGTAACGATGCC 1260
DB 1201 CTACAGAGCTGTGACGATTAACAAAGGGGACGCCGATTAATAGCCGCTTTGTAACGATGCC 1260
QY 1261 TGTGACCTGCTGTGATGATCTCTCTGCTTTCCCTTTGCGACGACCACTGATCTC 1320
DB 1261 TGTGACCTGCTGTGATGATCTCTCTGCTTTCCCTTTGCGACGACCACTGATCTC 1320
QY 1321 CTGCTGACACATCTTCTTAACTTCAACCCAGACATATTCGTGTGACGCTCAAGTTTA 1380
DB 1321 CTGCTGACACATCTTCTTAACTTCAACCCAGACATATTCGTGTGACGCTCAAGTTTA 1380
QY 1381 TTTTACCCAGAGAAAGCTTCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACTGCCACA 1440
DB 1381 TTTTACCCAGAGAAAGCTTCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACTGCCACA 1440
QY 1441 ACAGAGGTTCTGCGAAGGGAGTATGTAACGGCTGCGCTTGTGTGCTTCAGTT 1500
DB 1441 ACAGAGGTTCTGCGAAGGGAGTATGTAACGGCTGCGCTTGTGTGCTTCAGTT 1500
QY 1501 CTTCAGCCAAACATACATGATGCCATGAAAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
DB 1501 CTTCAGCCAAACATACATGATGCCATGAAAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
QY 1561 TCCATCTCTCTGGAACAACAATTTCTTCACTTACCAAGATGACCCCTGATCCCATC 1620
DB 1561 TCCATCTCTCTGGAACAACAATTTCTTCACTTACCAAGATGACCCCTGATCCCATC 1620
QY 1621 ATATATGAGGTTCCAGAGAACCGGCAATGCCCCGTTTATTTGGGTTCTTCAACATAGAG 1680
DB 1621 ATATATGAGGTTCCAGAGAACCGGCAATGCCCCGTTTATTTGGGTTCTTCAACATAGAG 1680
QY 1681 AAATCCAGAAACAACACCCAGATGAAATTTTGGACAAATGTGTGTTTTTGGCTGC 1740
DB 1681 AAATCCAGAAACAACACCCAGATGAAATTTTGGACAAATGTGTGTTTTTGGCTGC 1740
QY 1741 AGGCATTAAGATGAGATTAATCTATTCAGAAAAGAGCTCAGACATTTCTTAAAGATGG 1800
DB 1741 AGGCATTAAGATGAGATTAATCTATTCAGAAAAGAGCTCAGACATTTCTTAAAGATGG 1800
QY 1801 ATCTTAATCTATTCAAAGGTTTTCTTCTCAAGAGATCTCTGTGTGGGAGAGAGAGCC 1860
DB 1801 ATCTTAATCTATTCAAAGGTTTTCTTCTCAAGAGATCTCTGTGTGGGAGAGAGAGCC 1860
QY 1861 CCAGCAAGATATGTAACAAGACATCATGAGCTTATGCGCAGCAGGTGGCGAATCTTC 1920
DB 1861 CCAGCAAGATATGTAACAAGACATCATGAGCTTATGCGCAGCAGGTGGCGAATCTTC 1920
QY 1921 CTCCAGAGAAAGGCAATTTATGTGTGTGAGATGCAAAAGATATGCGCAAGATGTA 1980
DB 1921 CTCCAGAGAAAGGCAATTTATGTGTGTGAGATGCAAAAGATATGCGCAAGATGTA 1980
QY 1981 CATATATCCCTTTGCAATTAATAAGCAAAAGAGTTGAGTGAATAAATCTAAGAGCATG 2040
DB 1981 CATATATCCCTTTGCAATTAATAAGCAAAAGAGTTGAGTGAATAAATCTAAGAGCATG 2040
QY 2041 AAAACCTGGCCATTTTAAAGAGAAAAAGCTACCTTCAGATTTTGGTCAATA 2097
DB 2041 AAAACCTGGCCATTTTAAAGAGAAAAAGCTACCTTCAGATTTTGGTCAATA 2097

RESULT 5

US-09-371-347-45
; Sequence 45, Application US/09371347
; Publication No. US2003082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHYLONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371.347

; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-45

Query Match 86.0%; Score 1803; DB 10; Length 2094;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 ATGAGAGGTTCTGTACTATATGCTATACAGCAGGAGCAGGCAAGGCAATCGCAGAA 60
DB 1 ATGAGAGGTTCTGTACTATATGCTATACAGCAGGAGCAGGCAAGGCAATCGCAGAA 60
QY 61 GAATATGTGAGCAAGCTGTGTACATGATTTTCTGCAATCTTCACTGTATTAGTGA 120
DB 61 GAATATGTGAGCAAGCTGTGTACATGATTTTCTGCAATCTTCACTGTATTAGTGA 120
QY 121 TCCGATTAAGTATGACTTAAACCCGAACAGCTCTCTTGTGTGTGTTTCTTACAG 180
DB 121 TCCGATTAAGTATGACTTAAACCCGAACAGCTCTCTTGTGTGTGTTTCTTACAG 180
QY 181 GGCACGGAGAGCCACCCGACACAGCCCGAAGTTGTTAAGAAATACAGAACAAACA 240
DB 181 GGCACGGAGAGCCACCCGACACAGCCCGAAGTTGTTAAGAAATACAGAACAAACA 240
QY 241 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGAGTTACTGGGTCTCGGTATTCAGAA 300
DB 241 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGAGTTACTGGGTCTCGGTATTCAGAA 300
QY 301 TACACCTACTTTTGGCAATGGGGGAAAGATTAATGATTAACGACTTCAAGAGCTTGA 360
DB 301 TACACCTACTTTTGGCAATGGGGGAAAGATTAATGATTAACGACTTCAAGAGCTTGA 360
QY 361 CGGCATTTCTATGACACTGACATGACATGACATGATGATGATGATGATGATGATGAT 420
DB 361 CGGCATTTCTATGACACTGACATGACATGACATGATGATGATGATGATGATGATGAT 420
QY 421 CCGTGAATGCTGGAATCTGCGCAGCCCTCAGAAACATTTTGAAGTCAAGCAGAGCA 480
DB 421 CCGTGAATGCTGGAATCTGCGCAGCCCTCAGAAACATTTTGAAGTCAAGCAGAGCA 480
QY 481 GAGGAGTAAAGTGGGCACTCCCGGTGGCATCACTGCACTCTTGAAGACAGACTTGTG 540
DB 481 GAGGAGTAAAGTGGGCACTCCCGGTGGCATCACTGCACTCTTGAAGACAGACTTGTG 540
QY 541 AATTCAGAGCTGTACACATGAAATCTCAAGTGAAGCTTCTGAGATTCAGATTCAGAG 600
DB 541 AATTCAGAGCTGTACACATGAAATCTCAAGTGAAGCTTCTGAGATTCAGATTCAGAG 600
QY 601 AGAAGGATTTCTAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCATGTTGTA 660
DB 601 AGAAGGATTTCTAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCATGTTGTA 660
QY 661 ATTGAAGCTTTGAGTCTCTCACTTACCCGTTGGTACCCCACTCTCAAGCCTCTCTG 720
DB 661 ATTGAAGCTTTGAGTCTCTCACTTACCCGTTGGTACCCCACTCTCAAGCCTCTCTG 720
QY 721 AATATTCCTGTTTACCCCAAGAAATTTTACAGTATCATTCGAGAGAGTCTTTGGCAG 780
DB 721 AATATTCCTGTTTACCCCAAGAAATTTTACAGTATCATTCGAGAGAGTCTTTGGCAG 780
QY 781 GAGGAAAGCAAGTATCTGTGACTTCAGAGATCCAGATTTTCAAGTGCATTTCAAG 840
DB 781 GAGGAAAGCAAGTATCTGTGACTTCAGAGATCCAGATTTTCAAGTGCATTTCAAG 840

QY	841	GCAGTTCACCTTACGACGAATGATGCCATAAAACA	CTGCGTGGTATGAAATTTGACATT	900
Db	841	GCAGTTCACCTTACTACGAATGATGCCATAAAACA	CTGCGTGGTATGAAATTTGACATT	900
QY	901	TCAATAACAGACTTTTCCCTATCAGCCTTGAGATG	CCCTTCAGCGGATCTGCGCTTAACAGT	960
Db	901	TCAATAACAGACTTTTCCCTATCAGCGTGGATATG	CCCTTCAGCGGATCTGCGCTTAACAGT	960
QY	961	GATTCCTGAGGTACAAAGCTTACCTCCAAAGACTG	CACTTGAAAGATTAAGAAGACACTGC	1020
Db	961	GATTCCTGAGGTACAAAGCTCTACAAAGACTGCA	AGCTTGAAAGATTAAGAAGACACTGC	1020
QY	1021	GTCCCTTTGAAATAATTAAGGCGACACAAAGAA	GAAGACTTACCTTACCCACAGATTA	1080
Db	1021	GTCCCTTTGAAATAATTAAGGCGAGACAAAGAA	GAAGAGCTTACCTTACCCACAGATTA	1080
QY	1081	CCTGCGGGAGTGTCTCTCAGTTCATTTTACCTG	TGTCTTGAAATCCGAGCAATTCCT	1140
Db	1081	CCTGCGGGAGTGTCTCTCAGTTCATTTTACCTG	TGTCTTGAAATCCGAGCAATTCCT	1140
QY	1141	AAAAAGGCATTTTTGCAGACCCCTTGATGACTTA	ACAGTGAACAGTGTGAAAGAAGCGCAGG	1200
Db	1141	AAAAAGGCATTTTTGCAGACCCCTTGATGACTTA	ACAGTGAACAGTGTGAAAGAAGCGCAGG	1200
QY	1201	CTACAGGAGCTGTGCAATTAACAGGGGACGCCG	ATTATACCGCTTTGTATCGAGATGCC	1260
Db	1201	CTACAGGAGCTGTGCAATTAACAGGGGACGCCG	ATTATATACCGCTTTGTATCGAGATGCC	1260
QY	1261	TGTGCGTGTCTGTTGGATCTCTCTCTGCTTCC	CTTGTTCGAGGCCACACTAGTCTC	1320
Db	1261	TGTGCGTGTCTGTTGGATCTCTCTCTGCTTCC	CTTGTTCGAGGCCACACTAGTCTC	1320
QY	1321	CTGCTCGAACACTCTTCTTAACTTCAACCCAG	ACCATATTCGTGTGCAAGCTCAAGTTTA	1380
Db	1321	CTGCTCGAACACTCTTCTTAACTTCAACCCAG	ACCATATTCGTGTGCAAGCTCAAGTTTA	1380
QY	1381	TTTCAACCCAGAAAGCTCAATTTTGTCTTCA	CAATGTGGAATTTCTGTCTATCGCCACA	1440
Db	1381	TTTCAACCCAGAAAGCTCAATTTTGTCTTCA	CAATGTGGAATTTCTGTCTATCGCCACA	1440
QY	1441	ACAGAGTTCGCGGAAGGAGATATGTA	CAGGCTGGCTGGCTTGTGGTTCCTCAGTT	1500
Db	1441	ACAGAGTTCGCGGAAGGAGATATGTA	CAGGCTGGCTGGCTTGTGGTTCCTCAGTT	1500
QY	1501	CTTCAGCCAAACATATCATGTATCCCATTA	GAACAGCGGAAAGCCCTGAGCTCTTAAGATA	1560
Db	1501	CTTCAGCCAAACATATCATGTATCCCATTA	GAACAGCGGAAAGCCCTGAGCTCTTAAGATA	1560
QY	1561	TCCATCTCTCTCGAACAACAATTCCTTCA	CTTACAGATGACCCCTCAATCCCATC	1620
Db	1561	TCCATCTCTCTCGAACAACAATTCCTTCA	CTTACAGATGACCCCTCAATCCCATC	1620
QY	1621	ATAATGTGTGGTCCGAGAACCGGCAATAC	CCCCGTTATTTGGGTTCTTACACATTAAGAG	1680
Db	1621	ATAATGTGTGGTCCGAGAACCGGCAATAC	CCCCGTTATTTGGGTTCTTACACATTAAGAG	1680
QY	1681	AAACTCCAAAGAACCAACCCAGATGGAATTTT	GGAGCATGTGGTTGTTTTTTGGCTGC	1740
Db	1681	AAACTCCAAAGAACCAACCCAGATGGAATTTT	GGAGCATGTGGTTGTTTTTTGGCTGC	1740
QY	1741	AGGCATAAGATAGGATATCTATTCGAAAAG	ACTCAGACATTTCTTAAGCATGGG	1800
Db	1741	AGGCATAAGATAGGATATCTATTCGAAAAG	ACTCAGACATTTCTTAAGCATGGG	1800
QY	1801	ATCTTAATCTCATTAAGGTTTCTTCTCA	AGATGTCTCTGTGTGGGAGAGAGAACCC	1860
Db	1798	ATCTTAATCTCATTAAGGTTTCTTCTCA	AGATGTCTCTGTGTGGGAGAGAGAACCC	1857
QY	1861	CCAGCAAAAGTATGTACAGAACACATCCAG	CTTCAATGSCCAGAGGTGGCGAGATCTCTC	1920
Db	1858	CCAGCAAAAGTATGTACAGAACACATCCAG	CTTCAATGSCCAGAGGTGGCGAGATCTCTC	1917
QY	1921	CTCCAGAGAAACGCGCATATTTATGTGTG	GAAGTGAACAAAGATATATGSCCAAGATGTA	1980

Db	1918	CTCAGAGAAAGGCCCATTTTATGTGTGAGATGCAAAGATATGCGCAAGATCTA	1977
Qy	1981	CATGATGCCCTTGTGCAATTAATTAAGCAAAAGGTTGAGTTGAAAACTAGAGCAATG	2040
Db	1978	CATGATGCCCTTGTGCAATTAATTAAGCAAAAGGTTGAGTTGAAAACTAGAGCAATG	2037
Qy	2041	AAAACCTGCGCACTTTAAAAAGAAAGAAAAACGCTACCTTCAGATATTTGGTCTAA	2097
Db	2038	AAAACCTGCGCACTTTAAAAAGAAAGAAAAACGCTACCTTCAGATATTTGGTCTAA	2094

RESULT 6

US-09-371-347-47

; Sequence 47, Application US/09371347

; Publication No. US20030082676A1

; GENERAL INFORMATION:

; APPLICANT: Roy A. Gravel et al.

; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:

; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBER

; FILE REFERENCE: 50004/003003

; CURRENT APPLICATION NUMBER: US/09/371,347

; PRIOR FILING DATE: 1999-08-10

; PRIOR APPLICATION NUMBER: 60/071,622

; PRIOR FILING DATE: 1998-01-16

; PRIOR APPLICATION NUMBER: 09/232,028

; PRIOR FILING DATE: 1999-01-15

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: PaSeq for Windows Version 4.0

; SEQ ID NO 47

; LENGTH: 2093

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-371-347-47

Query Match 83.1%; Score 1742; DB 10; Length 2093;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2092; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

Qy	1	ATGAGGAGGTTCTGTTACTATATGCTACACAGAGGGAACAGAAAGCCCATGCGAA	60
Db	1	ATGAGGAGGTTCTGTTACTATATGCTACACAGAGGGAACAGAAAGCCCATGCGAA	60
Qy	61	GAAATATGTGAGCAAGCTGTGTGATCATGSAATTTCTGCAAGTCTTCACTGTATTAGTAA	120
Db	61	GAAATGTGTGAGCAAGCTGTGTGATCATGSAATTTCTGCAAGTCTTCACTGTATTAGTAA	120
Qy	121	TCCGATTAAGTATGACCTTAAAAACGAAACAGCTCCTCTGTTGTGTGTGTTCTACACG	180
Db	121	TCCGATTAAGTATGACCTTAAAAACGAAACAGCTCCTCTGTTGTGTGTGTTCTACACG	180
Qy	181	GGCACCAGGAGCCACCCAGACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA	240
Db	181	GGCACCAGGAGCCACCCAGACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA	240
Qy	241	CTGCGCGTTGATTTCTTTGCTCACTCGCGGTATGGGTTACTGGGTCTCGGTATTCAGAA	300
Db	241	CTGCGCGTTGATTTCTTTGCTCACTCGCGGTATGGGTTACTGGGTCTCGGTATTCAGAA	300
Qy	301	TACACCTTACTTTTGCATATGAGGGGGAAGTAATTGATTAACGACTTCAAGAGCTTGAGCC	360
Db	301	TACACCTTACTTTTGCATATGAGGGGGAAGTAATTGATTAACGACTTCAAGAGCTTGAGCC	360
Qy	361	CGGCAATTTCTATGACATCTGACATGACAGATGACGTGTGATTAAGACTTGTGTGAG	420
Db	361	CGGCAATTTCTATGACATCTGACATGACAGATGACGTGTGATTAAGACTTGTGTGAG	420
Qy	421	CGGTGATATGTGACACTCTGGCCAGCCCTCAGAAAGCAATTTAGTCAAGCAGAGCAAA	480
Db	421	CGGTGATATGTGACACTCTGGCCAGCCCTCAGAAAGCAATTTAGTCAAGCAGAGCAAA	480
Qy	481	GAGGAGATTAAGTGGCGCACTCCCGGTGGCATCACTGATCCTTGAAGACAGACTTGTG	540

Db 481 GAGAGGTAAGTGGCGGACCTCCGGTGGCATCACCTGCATCTTGGAGGACAGACCTTGTG 540
Qy 541 AAGCAGAGGCTGCTACATCACTTGAATCTCAAGTGCAGGCTTCTGAGATTGCATGATTCAGGA 600
Db 541 AAGTCAGAGGCTGCTACATCACTTGAATCTCAAGTGCAGGCTTCTGAGATTGCATGATTCAGGA 600
Qy 601 AGAAGAGATTCTGAGGTTTGAAGCAAAATGCACTGAGCAACCAATCCAAATGTTGTA 660
Db 601 AGAAGAGATTCTGAGGTTTGAAGCAAAATGCACTGAGCAACCAATCCAAATGTTGTA 660
Qy 661 ATGGAAGACTTTAGTCTCACTTACCCGTTCCGTTACCCCACTCTTCAAGGCTCTCTG 720
Db 661 ATGGAAGACTTTAGTCTCACTTACCCGTTCCGTTACCCCACTCTTCAAGGCTCTCTG 720
Qy 721 AATATTCCTGTTTACCCCGAGATATTTACAGGTACATCTGACAGAGTCTTCTGGCCAG 780
Db 721 AATATTCCTGTTTACCCCGAGATATTTACAGGTACATCTGACAGAGTCTTCTGGCCAG 780
Qy 781 GAGGAAAGCCAAAGTATCTGTGACTTCAGCAGATCCAGTTTTCAGTGCATTTCAAG 840
Db 781 GAGGAAAGCCAAAGTATCTGTGACTTCAGCAGATCCAGTTTTCAGTGCATTTCAAG 840
Qy 841 GCAGTTCACTTACTAGAAATGATGCAATAAACCACTGCTGGTGGAAATGGACAT 900
Db 841 GCAGTTCACTTACTAGAAATGATGCAATAAACCACTGCTGGTGGAAATGGACAT 900
Qy 901 TCAATATCAGACTTTTCTCTACAGCTGAGAGTCCCTTCAAGGCTGATCTCCCTAACAT 960
Db 901 TCAATATCAGACTTTTCTCTACAGCTGAGAGTCCCTTCAAGGCTGATCTCCCTAACAT 960
Qy 961 GATTCTGAGGTACAAAGCCTTACCTCAAAAGACTGCAAGTTTGAAGTAAAGAGCACTGC 1020
Db 961 GATTCTGAGGTACAAAGCCTTACCTCAAAAGACTGCAAGTTTGAAGTAAAGAGCACTGC 1020
Qy 1021 GTCCCTTTGAAATTAAGGAGACACAAAGAAAGAGACTCTTACCCCGACATATA 1080
Db 1021 GTCCCTTTGAAATTAAGGAGACACAAAGAAAGAGACTCTTACCCCGACATATA 1080
Qy 1081 CCTGCGGAGATGTTCTCTCAAGTTCATTTTACCTGCTGCTTGAATCCGAGCAATTCCT 1140
Db 1081 CCTGCGGAGATGTTCTCTCAAGTTCATTTTACCTGCTGCTTGAATCCGAGCAATTCCT 1140
Qy 1141 AAAAAGGCAATTTTGGCAGCCCTTGTGACTATACAGTACAGTGTGAAAAGCCGAG 1200
Db 1141 AAAAAGGCAATTTTGGCAGCCCTTGTGACTATACAGTACAGTGTGAAAAGCCGAG 1200
Qy 1201 CTACAGGAGCTGTGCACTTAAACAAAGGGGCAAGCGATATATAGCCGCTTGTACAGATGCC 1260
Db 1201 CTACAGGAGCTGTGCACTTAAACAAAGGGGCAAGCGATATATAGCCGCTTGTACAGATGCC 1260
Qy 1261 TGTGCTGCTTGTGATCTCTCTGCTTCCCTTCTTCCAGCCAGCCACTCACTCTC 1320
Db 1261 TGTGCTGCTTGTGATCTCTCTGCTTCCCTTCTTCCAGCCAGCCACTCACTCTC 1320
Qy 1321 CTGCTCGAATCTTCTCTAACTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTA 1380
Db 1321 CTGCTCGAATCTTCTCTAACTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTA 1380
Qy 1381 TTTCACCCAGAAAGCTCAATTTTGTCTCAACATTTGGAATTTCTGTCTACCTGACCA 1440
Db 1381 TTTCACCCAGAAAGCTCAATTTTGTCTCAACATTTGGAATTTCTGTCTACCTGACCA 1440
Qy 1441 ACAGAGGTTCTGCGAAGGAGATATGACAGCTGAGCTGAGCTTGTGTTGCTTCAATT 1500
Db 1441 ACAGAGGTTCTGCGAAGGAGATATGACAGCTGAGCTGAGCTTGTGTTGCTTCAATT 1500
Qy 1501 CTTCAGGCAAAATCATCATCTCCATGAGACAGCGGAAAGCCCTGAGCTCTCAAGATA 1560
Db 1501 CTTCAGGCAAAATCATCATCTCCATGAGACAGCGGAAAGCCCTGAGCTCTCAAGATA 1560
Qy 1561 TCATCTCTCTCTGAAACAAAGAAATTTCTTCACTTACAGATGAGCCCTCAATCCCATC 1620
Db 1561 TCATCTCTCTCTGAAACAAAGAAATTTCTTCACTTACAGATGAGCCCTCAATCCCATC 1620

Db 1561 TCATCTCTCTCTGAAACAAAGAAATTTCTTCACTTACAGATGAGCCCTCAATCCCATC 1620
Qy 1621 ATATAGTGGGTCCAGAAACCGGCATAGCCCGCTTATTGGTTCCTACAAATAGAG 1680
Db 1621 ATATAGTGGGTCCAGAAACCGGCATAGCCCGCTTATTGGTTCCTACAAATAGAG 1680
Qy 1681 AAATCTCAAGAACCAACCCAGATGAAATTTTGAAGCAATGTGTTTGTGCTGC 1740
Db 1681 AAATCTCAAGAACCAACCCAGATGAAATTTTGAAGCAATGTGTTTGTGCTGC 1740
Qy 1741 AGGCATTAAGATGAGATTAATCTATTCAGAAAGAGCTCAGATTTCTTAAGCATGG 1800
Db 1741 AGGCATTAAGATGAGATTAATCTATTCAGAAAGAGCTCAGATTTCTTAAGCATGG 1800
Qy 1797 ATCTTAATCATCTTAAGGTTTCTCTCAAGAGATGCTCTTGTGGGAGAGGAAGCC 1856
Db 1797 ATCTTAATCATCTTAAGGTTTCTCTCAAGAGATGCTCTTGTGGGAGAGGAAGCC 1856
Qy 1861 CCAGCAAAAGTATGACAAACATCCAGCTTCATGCGCAGAGGTCGAGAAATCTTC 1920
Db 1861 CCAGCAAAAGTATGACAAACATCCAGCTTCATGCGCAGAGGTCGAGAAATCTTC 1920
Qy 1921 CTCAGAGAGAGGCGCATTTTATGTGTGAGATGCAAAAGATTTGCGCAAGATGTA 1980
Db 1921 CTCAGAGAGAGGCGCATTTTATGTGTGAGATGCAAAAGATTTGCGCAAGATGTA 1980
Qy 1981 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGTGTGAAGTTGAAATCTAGAGCATG 2040
Db 1981 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGTGTGAAGTTGAAATCTAGAGCATG 2040
Qy 1977 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGTGTGAAGTTGAAATCTAGAGCATG 2036
Db 1977 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGTGTGAAGTTGAAATCTAGAGCATG 2036
Qy 2041 AAAACCTGGCCACTTTTAAAGAAAGAAACGCTTACCTTCAAGATTTTGTCTATA 2097
Db 2041 AAAACCTGGCCACTTTTAAAGAAAGAAACGCTTACCTTCAAGATTTTGTCTATA 2097
RESULT 7
US-10-741-600-692
; Sequence 692, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: PASTESQ for Windows Version 4.0
; SEQ ID NO 692
; LENGTH: 3256
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-692
Query Match 50.6%; Score 1062; DB 21; Length 3256;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2012; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Qy 67 TGTGAGCAAGCTGTGTAACATGATTTTCTGAGATCTTCACTGATATTAAGTAATCCGAT 126
Db 160 TGTGAGCAAGCTGTGTAACATGATTTTCTGAGATCTTCACTGATATTAAGTAATCCGAT 219
Qy 127 AAGTATGACTTAAACCGAAACAGCTCCTTGTGTGTGTGTTTCTACAGGGGACC 186
Db 220 AAGTATGACTTAAACCGAAACAGCTCCTTGTGTGTGTGTTTCTACAGGGGACC 279
Qy 187 GAGACCCACCGGACAGCCGCGCAAGTTTGTAAAGAAATACAGAACCAACCTGCGG 246
Db 280 GAGACCCACCGGACAGCCGCGCAAGTTTGTAAAGAAATACAGAACCAACCTGCGG 339
Qy 247 GTTATTTCTTGTGCTACCGGTGATGAGTTTCTGAGTCTCGGTGTTTCAAGATTCACC 306
Db 340 GTTATTTCTTGTGCTACCGGTGATGAGTTTCTGAGTCTCGGTGTTTCAAGATTCACC 399

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QY 307 TACTTTGCAATGAGGGAAGATTAATTGATTAACGACTTCAAGAGCTTGAAGCCCGGCAT 366
DB 400 TACTTTTGGCAATGAGGGAAGATTAATTGATTAACGACTTCAAGAGCTTGAAGCCCGGCAT 459
QY 367 TTTCTATGACACTGACATGCAATGATGATGATGATTAAGAACTTGTGTGAGCCGTG 426
DB 460 TTTCTATGACACTGACATGATGATGATGATGATTAAGAACTTGTGTGAGCCGTG 519
QY 427 ATTTGCTGACTCTGGGACAGCCCTCAGAAAGCAATTTTAAAGTCAAGAGAGAGAGAGAG 486
DB 520 ATTTGCTGACTCTGGGACAGCCCTCAGAAAGCAATTTTAAAGTCAAGAGAGAGAGAGAG 579
QY 487 ATTAAGTGGGCACTCCCGGTGGGATCACTGTGACTCTTGAAGACAGAGCTTGAAGTCA 546
DB 580 ATTAAGTGGGCACTCCCGGTGGGATCACTGTGACTCTTGAAGACAGAGCTTGAAGTCA 639
QY 547 GAGCTGCTACACATTTGAATCTCAAGTCTGAGCTTCTGAGATTCGATGATTCAGGAAGAA 606
DB 640 GAGCTGCTACACATTTGAATCTCAAGTCTGAGCTTCTGAGATTCGATGATTCAGGAAGAA 699
QY 607 GATTCGAGGTTTGAAGCAAAATGCAATGAGACAGCAACCAATCCATGTTGTAATTGA 666
DB 700 GATTCGAGGTTTGAAGCAAAATGCAATGAGACAGCAACCAATCCATGTTGTAATTGA 759
QY 667 GACTTTGAGTCTCACTTACCCGTTGGGATACCCCACTCTCAAGCCCTCTGAATATT 726
DB 760 GACTTTGAGTCTCACTTACCCGTTGGGATACCCCACTCTCAAGCCCTCTGAATATT 819
QY 727 CCTGTTTACCCCGCAAAATTTTACAGATACATCTGACAGAGTCTCTTGGCCAGAGAA 786
DB 820 CCTGTTTACCCCGCAAAATTTTACAGATACATCTGACAGAGTCTCTTGGCCAGAGAA 879
QY 787 AGCCAAATCTGTGATCTTCAAGATCCAGTTTTCAGTGGCAATTTCAAGGCAATT 846
DB 880 AGCCAAATCTGTGATCTTCAAGATCCAGTTTTCAGTGGCAATTTCAAGGCAATT 939
QY 847 CAATCTACTACGAATGATGCAATTAACCAACTCTGCTGGTAAATTTGACATTTCAAT 906
DB 940 CAATCTACTACGAATGATGCAATTAACCAACTCTGCTGGTAAATTTGACATTTCAAT 999
QY 907 ACAGACTTTTCTATCAGCTGAGATGCTTCAAGCTGATCTGCTTACAGTGAATCT 966
DB 1000 ACAGACTTTTCTATCAGCTGAGATGCTTCAAGCTGATCTGCTTACAGTGAATCT 1059
QY 967 GAGGTACAAAGCTTACTCAAGAGCTGCAAGCTTGAAGATTAAGAGAGAGAGAGAG 1026
DB 1060 GAGGTACAAAGCTTACTCAAGAGCTGCAAGCTTGAAGATTAAGAGAGAGAGAGAG 1119
QY 1027 TTGAAATTAAGGCAACCAAGAAAGAGAGCTACCTTACCCAGCATTAATCTGAG 1086
DB 1120 TTGAAATTAAGGCAACCAAGAAAGAGAGCTACCTTACCCAGCATTAATCTGAG 1179
QY 1087 GGAATGTTCTCTCAAGTCAATTTTACCTGCTGCTTGAATCCGAGCAATCTCTAATAAG 1146
DB 1180 GGAATGTTCTCTCAAGTCAATTTTACCTGCTGCTTGAATCCGAGCAATCTCTAATAAG 1239
QY 1147 GCATTTTGGAGCCCTTGTGACATTAACAGTGAAGTGTGTAAGAGAGAGAGAGAG 1206
DB 1240 GCATTTTGGAGCCCTTGTGACATTAACAGTGAAGTGTGTAAGAGAGAGAGAGAG 1299
QY 1207 GAGCTGTGAGTAACAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1266
DB 1300 GAGCTGTGAGTAACAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1359
QY 1267 TGTCTTGTGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1326
DB 1360 TGTCTTGTGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1419
QY 1327 GAAATCTTCTTAACTTCAACCCAGAGCAATATTCGTGTGAGAGAGAGAGAGAGAG 1386
DB 1420 GAAATCTTCTTAACTTCAACCCAGAGCAATATTCGTGTGAGAGAGAGAGAGAGAG 1479

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QY 1387 CCAGAAAGCTCCATTTTGTCTTCAACATTTGGAATTTTCTGTCTACCTCCACAAAGAG 1446
DB 1480 CCAGAAAGCTCCATTTTGTCTTCAACATTTGGAATTTTCTGTCTACCTCCACAAAGAG 1539
QY 1447 GTTCTGCGAAGAGATATGTAACAGCTGTGCTGCTTGTGTGCTTCAAGTTCTTCAAG 1506
DB 1540 GTTCTGCGAAGAGATATGTAACAGCTGTGCTGCTTGTGTGCTTCAAGTTCTTCAAG 1599
QY 1507 CCAACATACATGATCCCATGAAGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1566
DB 1600 CCAACATACATGATCCCATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1659
QY 1567 TCTCTCGAACAACAATTTCTTCACTTACAGATGAGACCCCTCAATCCCATATATG 1626
DB 1660 TCTCTCGAACAACAATTTCTTCACTTACAGATGAGACCCCTCAATCCCATATATG 1719
QY 1627 GTGGGTCCAGAAACCGGATAGCCCGCTTATTTGGTCTTACACATAGAGAGAACTC 1686
DB 1720 GTGGGTCCAGAAACCGGATAGCCCGCTTATTTGGTCTTACACATAGAGAGAACTC 1779
QY 1687 CAAGAACACACCCAGATGGAATTTTGGAGCAATGTTGTTTGGCTGAGAGAT 1746
DB 1780 CAAGAACACACCCAGATGGAATTTTGGAGCAATGTTGTTTGGCTGAGAGAT 1839
QY 1747 AAGATAGGATTAATCTATTCAGAAAGAGCTCAGACATTTCTTAAGATGAGATCTTA 1806
DB 1840 AAGATAGGATTAATCTATTCAGAAAGAGCTCAGACATTTCTTAAGATGAGATCTTA 1899
QY 1807 ACTCATTAAGGTTTCTTCTTCAAGAGATGCTCTGTGTTGGAGAGAGAGAGAGAGAG 1866
DB 1900 ACTCATTAAGGTTTCTTCTTCAAGAGATGCTCTGTGTTGGAGAGAGAGAGAGAGAG 1959
QY 1867 AAGTATGTCAAGACAACTCAGAGCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1926
DB 1960 AAGTATGTCAAGACAACTCAGAGCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2019
QY 1927 GAGAACGGCATTATTTATGTGTGAGAGATGCAAGAAATATGAGAGATGATACATGAT 1986
DB 2020 GAGAACGGCATTATTTATGTGTGAGAGATGCAAGAAATATGAGAGATGATACATGAT 2079
QY 2047 CTGGCCACTTTTAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2097
DB 2140 CTGGCCACTTTTAAAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2190

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RESULT 8

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US-10-741-600-693
; Sequence 693, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 693
; LENGTH: 3274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-693

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Query Match 50.6%; Score 1062; DB 21; Length 3274;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 2012; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 67 TGTGAGCAAGCTGTGTACATGATTTTCTGCAAGATCTTCACTGTATTAATGATCCGAT 126

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178 TGTGAGCAAGCTGTGATCAATGATTTTCTGCAGATCTTCACTGTATTTATGTATCCGAT 237
127 AAGTATGACCTTAAAAACCGAAGAGCTCTCTTGTGTGTGTGTCTACACAGGACAC 186
238 AAGTATGACCTTAAAAACCGAAGAGCTCTCTTGTGTGTGTGTCTACACAGGACAC 297
187 GGAAGACCCACCCGACACAGCCCGGAGTTGTTAAGAAATACAAACCAACATCTGCC 246
298 GGAAGACCCACCCGACACAGCCCGGAGTTGTTAAGAAATACAAACCAACATCTGCC 357
247 GTTGAATTTCTTGTCTACCTGGGATAGGTTACTGGGCTCGGTGATTCAGAAATCAC 306
358 GTTGAATTTCTTGTCTACCTGGGATAGGTTACTGGGCTCGGTGATTCAGAAATCAC 417
307 TACTTTTGCAGTGGGGGAGATTAATGTATTAACGACTTCAGAGCTTGGAGCCCGCAT 366
418 TACTTTTGCAGTGGGGGAGATTAATGTATTAACGACTTCAGAGCTTGGAGCCCGCAT 477
367 TTTCTATGACACTGGAACATGAGATGACTGTGTAGAGTTAAGCTTGTGTGAGCCGTG 426
478 TTTCTATGACACTGGAACATGAGATGACTGTGTAGAGTTAAGCTTGTGTGAGCCGTG 537
427 ATTGCTGGAATCTGGCCGACCTCAGAAAGCATTTTATGTCAGAGCAGAGGACAAAGGAG 486
538 ATTGCTGGAATCTGGCCGACCTCAGAAAGCATTTTATGTCAGAGCAGAGGACAAAGGAG 597
487 ATAAAGTGGCAGCTCCCGGTGGATCACTGACATCTTGTAGAGACAGACTTGTGAAGTCA 546
598 ATAAAGTGGCAGCTCCCGGTGGATCACTGACATCTTGTAGAGACAGACTTGTGAAGTCA 657
547 GAGCTGCTACATTTGAATCTCAAGTGTAGAGCTTGTGAATTCAGATTAAGAAAG 606
658 GAGCTGCTACATTTGAATCTCAAGTGTAGAGCTTGTGAATTCAGATTAAGAAAG 717
607 GATTCTGAGGTTTGAAGAAATGAGTGAACAGCAACCAATTCATTTGTAATTGA 666
718 GATTCTGAGGTTTGAAGAAATGAGTGAACAGCAACCAATTCATTTGTAATTGA 777
667 GACTTTGAGTCTCACTTACCCGTTCCGGTACCCCACTCTCAAGAGCTCTGTAATAT 726
778 GACTTTGAGTCTCACTTACCCGTTCCGGTACCCCACTCTCAAGAGCTCTGTAATAT 837
727 CTTGTTTACCCCGGAAATTTTACAGTACATCTGCAAGAGTCTTGGCCAGAGGAA 786
838 CTTGTTTACCCCGGAAATTTTACAGTACATCTGCAAGAGTCTTGGCCAGAGGAA 897
787 AGCCAAGTATCTGATCTTCAAGAGATCCAGTTTTCAGATGCAATTTGAAGGAGT 846
898 AGCCAAGTATCTGATCTTCAAGAGATCCAGTTTTCAGATGCAATTTGAAGGAGT 957
847 CAATTTACTACGATGTGCAATTAACCACTCTGCTGTAGAAATGACATTTCAAT 906
958 CAATTTACTACGATGTGCAATTAACCACTCTGCTGTAGAAATGACATTTCAAT 1017
907 ACAGACTTTTCTTACGCTCGAGATGCTTCAAGCTGATCTGCCCTTAACAGTATCT 966
1018 ACAGACTTTTCTTACGCTCGAGATGCTTCAAGCTGATCTGCCCTTAACAGTATCT 1077
967 GAGGTACAAAGCCCTACCAAGCTGAGCTTGAAGATTAAGAGAGCACTGGTCTT 1026
1078 GAGGTACAAAGCCCTACCTCAAGCTGAGCTTGAAGATTAAGAGAGCACTGGTCTT 1137
1027 TTGAAATTAAGGACGACACAAAGAAAGAGAGCTTACCCGACATATATCTGCG 1086
1138 TTGAAATTAAGGACGACACAAAGAAAGAGAGCTTACCCGACATATATCTGCG 1197
1087 GGAATGTTCTCTCCAGTCTATTTTACTGCTGTCTTGAATTCGAGCAATTCCTAAAAG 1146
1198 GGAATGTTCTCTCCAGTCTATTTTACTGCTGTCTTGAATTCGAGCAATTCCTAAAAG 1257
1147 GCATTTTGGAGCCCTTGTGACTATATACAGTGAAGTCTGAAAGCCGACGCTACAG 1206

1258 GCATTTTTCGAGCCCTTGTGACTATACAGTGAAGTGTGAAAAGCCGACGCTACAG 1317
1207 GAGCTGTGACGTAAACAAAGGGGACCGAGATTATAGCCGCTTGTGTACAGATGCTGTGCC 1266
1318 GAGCTGTGACGTAAACAAAGGGGACCGAGATTATAGCTGCTTGTGTACAGATGCTGTGCC 1377
1267 TGTGTTTGTGATCTCTCTCGCTTTCCTTCTTGTGCAAGCAGCACTCATGCTCTCTGCTC 1326
1378 TGTGTTTGTGATCTCTCTCGCTTTCCTTCTTGTGCAAGCAGCACTCATGCTCTCTGCTC 1437
1327 GAAATCTTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1386
1438 GAAATCTTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1497
1387 CCAGAAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTTCTGTCTACCTGCAACAGAG 1446
1498 CCAGAAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTTCTGTCTACCTGCAACAGAG 1557
1447 GTTCTGCGAAGGAGATATGATAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1506
1558 GTTCTGCGAAGGAGATATGATAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1617
1507 CCAGAAATATCATGATCCCATGAGACAGAGGAGAAAGCCCTGAGCTCTAAGATATCATC 1566
1618 CCAGAAATATCATGATCCCATGAGACAGAGGAGAAAGCCCTGAGCTCTAAGATATCATC 1677
1567 TCTCTCTGAAACAAATTTCTTCACTTACAGATGACCCCTCAATTCCTCATATATG 1626
1678 TCTCTCTGAAACAAATTTCTTCACTTACAGATGACCCCTCAATTCCTCATATATG 1737
1627 GTGGGTTCAGAAACCGGATAGCCCGTTTATTTGGTTCTTACAACTAGAGAAATC 1686
1738 GTGGGTTCAGAAACCGGATAGCCCGTTTATTTGGTTCTTACAACTAGAGAAATC 1797
1687 CAAGAACAAACCCAGATGAAATTTTGGAGCAATGTGTTTGTGTTTGTGCTCAGGAT 1746
1798 CAAGAACAAACCCAGATGAAATTTTGGAGCAATGTGTTTGTGTTTGTGCTCAGGAT 1857
1747 AAGATAGGATTTATTTATTTAGAAAAAGCTCAGACATTTCTTAAAGATGGATCTTA 1806
1858 AAGATAGGATTTATTTATTTAGAAAAAGCTCAGACATTTCTTAAAGATGGATCTTA 1917
1807 ACTCATCTAAAGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAAAGCCAGCA 1866
1918 ACTCATCTAAAGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAAAGCCAGCA 1977
1867 AAGTATGTAACAAGACATCCAGCTTCAATGAGCAGAGGTGAGAGATCTCTCAG 1926
1978 AAGTATGTAACAAGACATCCAGCTTCAATGAGCAGAGGTGAGAGATCTCTCAG 2037
1927 GAGAACGGCCATATTTATGTTGTGAGATGCAAGAAATATGAGATGTAATGAT 1986
2038 GAGAACGGCCATATTTATGTTGTGAGATGCAAGAAATATGAGATGTAATGAT 2097
1987 GCCCTGTGCAATTAATTAAGCAAGAGTTGAGTTGAAATTAAGCAATGAAATC 2046
2098 GCCCTGTGCAATTAATTAAGCAAGAGTTGAGTTGAAATTAAGCAATGAAATC 2157
2047 CTGGCCACTTTAAAGAAAGAAAGAAAGCTTACAGATATTTGTGATTA 2097
2158 CTGGCCACTTTAAAGAAAGAAAGAAAGCTTACAGATATTTGTGATTA 2208

RESULT 9
US-10-029-386-6369
; Sequence 6369, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GE
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 6369
LENGTH: 591
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008727.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.45
OTHER INFORMATION: NT HIT: AF121205.1, EVALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUE 3.30e+00
OTHER INFORMATION: EST_HUMAN HIT: AU132586.1, EVALUE 0.00e+00
US-10-029-386-6369

Query Match 15.7%; Score 330; DB 16; Length 591;
Best Local Similarity 99.7%; Pred. No. 1.2e-169;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGTTGAGCCCTGATTCCTGAGACTTCGCGCCAGCCCTCAGAAAGATT 460
DB 38 GTTTAGAACTTGTGTTGAGCCCTGATTCCTGAGACTTCGCGCCAGCCCTCAGAAAGATT 97
QY 461 TTAGGTCAAGCAGAGCAGAGAGAGATTAAGTGGCGCACTCCCGGTGGATCAGCTGCAAT 520
DB 98 TTAGGTCAAGCAGAGCAGAGAGAGATTAAGTGGCGCACTCCCGGTGGATCAGCTGCAAT 157
QY 521 CCTTGAAGCAGAGCCTTGTGAAGTCAAGCTGCTACATTAATCAATCAAGTCAAGCTTC 580
DB 158 CCTGAGAGCAGAGCCTTGTGAAGTCAAGCTGCTACATTAATCAATCAAGTCAAGCTTC 217
QY 581 TGAAGTTCATGATTTAGAGAGAGAGATTTCTGAGTTTGAAGCAAAATGCGTGAACA 640
DB 218 TGAAGTTCATGATTTAGAGAGAGAGATTTCTGAGTTTGAAGCAAAATGCGTGAACA 277
QY 641 GCAACCAATCCAAATGTTGATTAATGAAGACTTGAAGTCTCACTTACCCGTTGGTACCCC 700
DB 278 GCAACCAATCCAAATGTTGATTAATGAAGACTTGAAGTCTCACTTACCCGTTGGTACCCC 337
QY 701 CACTCTCACAAGCCTCTCGAATATTCCTGGTTACCCCGAGATATTTTACAGGTACATC 760
DB 338 CACTCTCACAAGCCTCTCGAATATTCCTGGTTACCCCGAGATATTTTACAGGTACATC 397
QY 761 TGCAGAGTCTCTTGGCCAGG 781
DB 398 TGCAGAGTCTCTTGGCCAGG 418

RESULT 10
US-10-029-386-20100
Sequence 20100, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AEMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20100
LENGTH: 379
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008727.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.45
OTHER INFORMATION: NT HIT: g114729757, EVALUE 0.00e+00

OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUE 1.80e+00
OTHER INFORMATION: EST_HUMAN HIT: AU132586.1, EVALUE 0.00e+00
US-10-029-386-20100

Query Match 15.6%; Score 328; DB 16; Length 379;
Best Local Similarity 99.7%; Pred. No. 1.4e-168;
Matches 378; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 402 TTTAGAACTTGTGTTGAGCCCTGATTCCTGAGACTTCGCGCCAGCCCTCAGAAAGATT 461
DB 1 TTTAGAACTTGTGTTGAGCCCTGATTCCTGAGACTTCGCGCCAGCCCTCAGAAAGATT 60
QY 462 TAGGTCAAGCAGAGCAGAGAGAGATTAAGTGGCGCACTCCCGGTGGATCAGCTGCAAT 521
DB 61 TAGGTCAAGCAGAGCAGAGAGAGATTAAGTGGCGCACTCCCGGTGGATCAGCTGCAAT 120
QY 522 CTTGAGAGCAGAGCCTTGTGAAGTCAAGCTGCTACATTAATCTCAAGTCAAGCTTCT 581
DB 121 CTTGAGAGCAGAGCCTTGTGAAGTCAAGCTGCTACATTAATCTCAAGTCAAGCTTCT 180
QY 582 GAGATTCGATGATTCAGAGAGAGAGATTCAGAGTTTGAAGCAAAATGCGTGAACAAG 641
DB 181 GAGATTCGATGATTCAGAGAGAGAGATTCAGAGTTTGAAGCAAAATGCGTGAACAAG 240
QY 642 CAACCAATCCAAATGTTGATTAATGAAGACTTGAAGTCTCACTTACCCGTTGGTACCCC 701
DB 241 CAACCAATCCAAATGTTGATTAATGAAGACTTGAAGTCTCACTTACCCGTTGGTACCCC 300
QY 702 ACTCTCACAAGCCTCTCGAATATTCCTGGTTACCCCGAGATATTTTACAGGTACATC 761
DB 301 ACTCTCACAAGCCTCTCGAATATTCCTGGTTACCCCGAGATATTTTACAGGTACATC 360
QY 762 GCAGAGTCTCTTGGCCAG 780
DB 361 GCAGAGTCTCTTGGCCAG 379

RESULT 11
US-10-029-386-1735
Sequence 1735, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AEMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 1735
LENGTH: 591
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC021609.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
OTHER INFORMATION: NT HIT: AF121205.1, EVALUE 0.00e+00
OTHER INFORMATION: EST_HUMAN HIT: AU132586.1, EVALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUE 3.30e+00
US-10-029-386-1735

Query Match 13.3%; Score 279; DB 16; Length 591;
Best Local Similarity 99.5%; Pred. No. 1.2e-141;
Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGGTGAAGCCGTGAGTTCGTGCACTCTGGCCAGCCCTTCAGAAAGCATT 460
DB 38 GTTTAGAACTTGTGGTGAAGCCGTGAGTTCGTGCACTCTGGCCAGCCCTTCAGAAAGCATT 97
QY 461 TTGAGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCGGTGGCATCACTGGCAT 520
DB 98 TTGAGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCGGTGGCATCACTGGCAT 157
QY 521 CCTTGAAGCAGACCTTGTGAAGTCAAGAGTGTCAACATTTGAATCTCAAGTCAAGCTTC 580
DB 158 CCTGAGAGCAGACCTGTGAAGTCAAGAGTGTCAACATTTGAATCTCAAGTCAAGCTTC 217
QY 581 TGAGATTCAATGATTCAGAAAGAAAGATTTCTGAAGTTTGAACCAAAATGCACTGACA 640
DB 218 TGAGATTCAATGATTCAGAAAGAAAGATTTCTGAAGTTTGAACCAAAATGCACTGACA 277
QY 641 GCAACCAATCCAAATGTTGAATTAAGATCTTGAAGTCTCACTTACCCGTTGGTACCCC 700
DB 278 GCAACCAATCCAAATGTTGAATTAAGATCTTGAAGTCTCACTTACCCGTTGGTACCCC 337
QY 701 CACTTCACAAGCCTCTGTAATTTCTGATTTACCCCAAGATATTTACAGGTACATC 760
DB 338 CACTTCACAAGCCTCTGTAATTTCTGATTTACCCCAAGATATTTACAGGTACATC 397
QY 761 TGCAGAGTCTCTTGGCCAGG 781
DB 398 TGCAGAGTCTCTTGGCCAGG 418

RESULT 12

US-10-029-386-15435
; Sequence 15435, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 15435
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021609.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
; OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUE 1.80e+00
; OTHER INFORMATION: EST HUMAN HIT: AU132586.1, EVALUE 0.00e+00
; OTHER INFORMATION: NT HIT: g14729757, EVALUE 0.00e+00
US-10-029-386-15435

Query Match 13.2%; Score 277; DB 16; Length 379;
Best Local Similarity 99.5%; Pred. No. 1.4e-140;

Matches 377; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 402 TTTTGAACCTTGTGTGAGCCGTGAGTTCGTGACTCTGGCCAGCCCTTCAGAAAGCATT 461
DB 1 TTTTGAACCTTGTGTGAGCCGTGAGTTCGTGACTCTGGCCAGCCCTTCAGAAAGCATT 60
QY 462 TAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCGGTGGCATCACTGGATC 521
DB 61 TAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCGGTGGCATCACTGGATC 120

QY 522 CTGAGAGCAGACCTTGTGAAGTCAAGCTCTACACATTTGAATCTCAAGTCAAGCTTC 581
DB 121 CTGAGAGCAGACCTTGTGAAGTCAAGCTCTACACATTTGAATCTCAAGTCAAGCTTC 180
QY 582 GAGATTCAATGATTCAGAAAGAAAGATTTCTGAAGTTTGAACCAAAATGCACTGACA 641
DB 181 GAGATTCAATGATTCAGAAAGAAAGATTTCTGAAGTTTGAACCAAAATGCACTGACA 240
QY 642 CAACCAATCCAAATGTTGAATTAAGATCTTGAAGTCTCACTTACCCGTTGGTACCCC 701
DB 241 CAACCAATCCAAATGTTGAATTAAGATCTTGAAGTCTCACTTACCCGTTGGTACCCC 300
QY 702 ACTTCACAAGCCTCTGTAATTTCTGATTTACCCCAAGATATTTACAGGTACATC 761
DB 301 ACTTCACAAGCCTCTGTAATTTCTGATTTACCCCAAGATATTTACAGGTACATC 360
QY 762 GCAGAGTCTCTTGGCCAG 780
DB 361 GCAGAGTCTCTTGGCCAG 379

RESULT 13

US-10-741-600-17757
; Sequence 17757, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17757
; LENGTH: 43985
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-17757

Query Match 12.7%; Score 266; DB 21; Length 43985;
Best Local Similarity 99.5%; Pred. No. 2e-134;

Matches 366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGTGAGCCGTGAGTTCGTGCACTCTGGCCAGCCCTTCAGAAAGCATT 460
DB 14836 GTTTAGAACTTGTGTGAGCCGTGAGTTCGTGCACTCTGGCCAGCCCTTCAGAAAGCATT 14895
QY 461 TTGAGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCGGTGGCATCACTGGCAT 520
DB 14896 TTGAGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCGGTGGCATCACTGGCAT 14955
QY 521 CCTTGAAGCAGACCTTGTGAAGTCAAGAGTGTCAACATTTGAATCTCAAGTCAAGCTTC 580
DB 14956 CCTTGAAGCAGACCTTGTGAAGTCAAGAGTGTCAACATTTGAATCTCAAGTCAAGCTTC 15015
QY 581 TGAGATTCAATGATTCAGAAAGAAAGATTTCTGAAGTTTGAACCAAAATGCACTGACA 640
DB 15016 TGAGATTCAATGATTCAGAAAGAAAGATTTCTGAAGTTTGAACCAAAATGCACTGACA 15075
QY 641 GCAACCAATCCAAATGTTGAATTAAGATCTTGAAGTCTCACTTACCCGTTGGTACCCC 700
DB 15076 GCAACCAATCCAAATGTTGAATTAAGATCTTGAAGTCTCACTTACCCGTTGGTACCCC 15135
QY 701 CACTTCACAAGCCTCTGTAATTTCTGATTTACCCCAAGATATTTACAGGTACATC 760
DB 15136 CACTTCACAAGCCTCTGTAATTTCTGATTTACCCCAAGATATTTACAGGTACATC 15195
QY 761 TGCAGAGG 768
DB 15196 TGCAGAGG 15203

RESULT 14
US-10-029-386-633/c
; Sequence 633, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 633
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021609.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.48
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.58
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.52
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.57
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.79
; OTHER INFORMATION: SWISSPROT HIT: P37039, EVALUOR 1.00e-06
; OTHER INFORMATION: EST_HUMAN HIT: BF346446.1, EVALUOR 1.00e-98
; OTHER INFORMATION: NT HIT: AF121212.1, EVALUOR 0.00e+00
US-10-029-386-633

Query Match 9.0%; Score 188; DB 16; Length 525;
Best Local Similarity 100.0%; Pred. No. 1.1e-91;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1765 TTCAGAAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAATCATCTAAAGTTTCC 1824
DB 234 TTCAGAAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAATCATCTAAAGTTTCC 175
QY 1825 TTCTCAAGAGATGCTCTGTTGGGAGAGAAAGCCCGAGCAAGATATGTAACAAGCAAC 1884
DB 174 TTCTCAAGAGATGCTCTGTTGGGAGAGAAAGCCCGAGCAAGATATGTAACAAGCAAC 115
QY 1885 ATCCAGCTTCATGGCCAGACAGTGGGAGATCTCTCCAGAGAAAGGCCATATTTAT 1944
DB 114 ATCCAGCTTCATGGCCAGACAGTGGGAGATCTCTCCAGAGAAAGGCCATATTTAT 55
QY 1945 GTGTGTGG 1952
DB 54 GTGTGTGG 47

RESULT 15
US-10-029-386-14338/c
; Sequence 14338, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 14338
; LENGTH: 175
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021609.3

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.48
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.58
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.52
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.57
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.79
; OTHER INFORMATION: SWISSPROT HIT: O61608, EVALUOR 4.00e-04
; OTHER INFORMATION: EST_HUMAN HIT: AA085543.1, EVALUOR 7.00e-94
; OTHER INFORMATION: NT HIT: g113325067, EVALUOR 5.00e-94
US-10-029-386-14338

Query Match 8.3%; Score 175; DB 16; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.4e-84;

Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1770 AAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAATCATCTAAAGTTTCCCTTC 1829
DB 175 AAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAATCATCTAAAGTTTCCCTTC 116
QY 1830 AAGAGATGCTCTGTTGGGAGAGAAAGCCCGAGCAAGATATGTAACAAGCAATCCA 1889
DB 115 AAGAGATGCTCTGTTGGGAGAGAAAGCCCGAGCAAGATATGTAACAAGCAATCCA 56
QY 1890 GCTTCATGGCCAGACAGTGGGAGATCTCTCCAGAGAAAGGCCATATTTAT 1944
DB 55 GCTTCATGGCCAGACAGTGGGAGATCTCTCCAGAGAAAGGCCATATTTAT 1

Search completed: August 27, 2005, 17:33:25
Job time : 903.401 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 23:18:31 ; Search time 4546.04 Seconds
(without alignments)
17558.328 Million cell updates/sec

Title: US-09-371-347a-43

Perfect score: 2097
Sequence: 1 atgagagaggttcctgtctact.....ttcagagatattggtcacaataa 2097

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032314700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hcg:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gest1:*
9: gb_gest2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1592	75.9	3100	3	BC062577 Homo sapi
2	905	43.2	3143	3	BC035977 Homo sapi
3	719	34.3	908	5	BX348674 BX348674
4	638	30.4	874	4	BM801462 AGENCOURT
5	623	29.7	646	7	CN260357 170004241
6	586	27.9	852	5	BQ431497 AGENCOURT
7	565	26.9	865	1	AU279788 AU279788
8	543	25.9	877	1	AU124440 AU124440
9	531	25.3	1061	5	BQ218755 AGENCOURT
10	507	24.2	834	5	BU941078 AGENCOURT
11	470	22.4	521	6	CB164340 K-EST0225
12	466	22.2	826	4	BI772430 603055786
13	461	22.0	776	6	CB997527 AGENCOURT
14	455	21.7	822	1	AU132586 AU132586
15	448	21.4	591	2	AM965709 EST37782
16	446	21.3	818	6	CD559384 AGENCOURT
17	434	20.7	591	4	BI025283 RCS-MT025
18	399	19.4	710	5	BU570323 AGENCOURT
19	389	19.0	974	5	BX375211 BX375211
20	384	18.3	527	4	BI025277 RCS-MT025
21	374	17.8	579	7	CN260360 170006001
22	367	17.5	642	2	BF346446 602020302
23	361	17.2	692	7	CN260359 170004706
24	359	17.1	499	6	CD704108 EST20635

25	354	16.9	386	1	AA279726 2892410.1
26	351	16.7	839	2	BG531787 BG531787
27	340	16.2	526	4	AW952883 EST346953
28	337	16.1	818	7	CP985233 AGENCOURT
29	335	16.0	413	2	BF810368 BF810368
30	335	16.0	413	2	BF810479 RCS-CI014
31	332	15.8	366	1	AA085543 2n44h1.1
32	311	14.8	478	4	BM754488 K-EST0031
33	309	14.7	685	4	BM049352 603626120
34	308	14.7	620	7	CK002453 AGENCOURT
35	302	14.4	420	4	BG877205 QV3-HT046
36	292	13.9	528	2	BE301292 ba89b07.x
37	290	13.8	395	4	BM838530 K-EST0114
38	272	13.0	301	1	AL704780 DKFZP686M
39	264	12.6	366	6	CB298361 220019.re
40	257	12.3	366	2	BF808461 QV1-CI017
41	257	12.3	368	1	AA355001 EST63417
42	252	12.0	324	1	AA469901 zc94b04.r
43	249	11.9	664	7	CR768694 DKFZP459K
44	249	11.9	667	7	CR770923 DKFZP469N
45	249	11.9	767	7	CR557482 DKFZP469K

ALIGNMENTS

RESULT 1	BC062577	3100 bp	mRNA	linear	HTC 25-NOV-2003
LOCUS	BC062577				
DEFINITION	Homo sapiens cDNA clone IMAGE:5189058, containing frame-shift errors.				
ACCESSION	BC062577				
VERSION	BC062577.1	GI:38511756			
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 3100) Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenker, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshnyk, S., Carninci, P., Prange, C., Raha, S.S., Loguigliano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McGowan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hu, L., Hu, L., Gibb, R.A., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibb, R.A., Fahy, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalske, U., Smalls, D.E., Scherf, A., Schein, U.E., Jones, S.J. and Marra, M.A.				
TITLE	human and initial analyses of more than 15,000 full-length				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
MEDLINE	22388257				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 3100)				
AUTHORS	Strausberg, R.				
TITLE	Direct Submissions				
JOURNAL	Submitted (24-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgabs-rc@mail.nih.gov Tissue Procurement: Life Technologies, Inc.				

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_ungcngrl.nih.gov
Ahter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Boufard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietsch, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lurie, P., Legaspi, R.,
Maduro, O.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDonnell, J., Pearson, R., Stantirpop, S., Thomas, P.J., Touchman, J.W.,
Tsaurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H., and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LIML at: <http://image.liml.gov>
Series: IRAC Plate: 135 Row: e Column: 21
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA 91: 4505278
This clone has the following problem: frame shifted.

FEATURES

source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5189058"
/tissue_type="Colon, Kidney, Stomach, adult, whole pooled"
/clone_id="NIH_MGC_116"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 75.9%; Score 1592; DB 3; Length 3100;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 283 GGTCTCGGTATTCAGAAATACCTACTTTCAGATGGGGGAGAGATTAATGATTAACGA 342
DB 172 GGTCTCGGTATTCAGAAATACCTACTTTCAGATGGGGGAGAGATTAATGATTAACGA 231
QY 343 CTTCAGAGCTTGGAGCCCGCATTTTCTATGACCTGACATGAGATGACTGTGTAGT 402
DB 232 CTTCAGAGCTTGGAGCCCGCATTTTCTATGACCTGACATGAGATGACTGTGTAGT 291
QY 403 TTGAACTTGTGTTGACCGGTGATTTGCTGACTCTGGCAGCCCTCAGAAAGCATTTT 462
DB 292 TTGAACTTGTGTTGACCGGTGATTTGCTGACTCTGGCAGCCCTCAGAAAGCATTTT 351
QY 463 AGGTCAAGCAGAGCAGAGAGATTAAGTGGCGCACTCCCGGTGAGCATCACTGCATCC 522
DB 352 AGGTCAAGCAGAGCAGAGAGATTAAGTGGCGCACTCCCGGTGAGCATCACTGCATCC 411
QY 523 TTGAGCAGACCTTGGAGTCAAGTCTGCTACATTTGAATTCGAAGTCGAGCTTCG 582
DB 412 TCGAGCAGACCTTGGAGTCAAGTCTGCTACATTTGAATTCGAAGTCGAGCTTCG 471
QY 583 AGATTGATGATTCAGAGAGAAAGATTTCTGAGGTTTGAAGCAAAATGACGTGACAGC 642
DB 472 AGATTGATGATTCAGAGAGAAAGATTTCTGAGGTTTGAAGCAAAATGACGTGACAGC 531
QY 643 AACCAATCCAAATGTTGAATTTGAAGATTTGAGTCTCACTTACCCGTTGGATACCCCA 702
DB 532 AACCAATCCAAATGTTGAATTTGAAGATTTGAGTCTCACTTACCCGTTGGATACCCCA 591
QY 703 CTCTCAAGGCTCTCGAATATTCCTGTTTACCCCAAGATTAATTTTACAGTACATTCG 762
DB 592 CTCTCAAGGCTCTCGAATATTCCTGTTTACCCCAAGATTAATTTTACAGTACATTCG 651
QY 763 CAGGAGCTCTTGGCAGAGAAAGCAAGTATCTGACTTCAAGAGATTCAGTTT 822
DB 652 CAGGAGCTCTTGGCAGAGAAAGCAAGTATCTGACTTCAAGAGATTCAGTTT 711

QY 823 CAAATCCAAATTTCAAGGAGTTCACTTACTAGCAATGATCCATTAACCACTCTG 882
DB 712 CAAATCCAAATTTCAAGGAGTTCACTTACTAGCAATGATCCATTAACCACTCTG 771
QY 883 CTGTTGAATTTGACATTTCAAAATACAGCTTTTCTATCAAGCTGAGATGCTTCAGC 942
DB 772 CTGTTGAATTTGACATTTCAAAATACAGCTTTTCTATCAAGCTGAGATGCTTCAGC 831
QY 943 GTGATCTGCTTAACTGATATTTGAGATTAAGAGCTTCTCAAGAGCTGACGTTGAA 1002
DB 832 GTGATCTGCTTAACTGATATTTGAGATTAAGAGCTTCTCAAGAGCTGACGTTGAA 891
QY 1003 GATTAAGAGAGCACTGCGCTCTTTGAAATTAAGGACAGACCAAGAAAGAGAGCT 1062
DB 892 GATTAAGAGAGC-CTGCGCTCTTTGAAATTAAGGACAGACCAAGAAAGAGAGCT 950
QY 1063 ACCTTACCCAGATATTAATCTGCGGAGATGTTCTCAAGTCAATTTTACCTGCTGCTT 1122
DB 951 ACCTTACCCAGATATTAATCTGCGGAGATGTTCTCAAGTCAATTTTACCTGCTGCTT 1010
QY 1123 GAAATCCGAGCATTTCTTAAGAAAGGATTTTGGAGAGCCCTTGTGACTATACAGTGAC 1182
DB 1011 GAAATCCGAGCATTTCTTAAGAAAGGATTTTGGAGAGCCCTTGTGACTATACAGTGAC 1070
QY 1183 AGTCTGAAAGGCGCAGGCTACAGAGCTGTGAGTAAACAGGGGACGCCATTTAGC 1242
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QY 1243 CGCTTTGTAAGAGATGCTGTGCTGCTGTTGAGATCTGCTGCTGCTGCTGCTGCTGCTG 1302
DB 1131 CGCTTTGTAAGAGATGCTGTGCTGCTGTTGAGATCTGCTGCTGCTGCTGCTGCTGCTG 1190
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QY 1363 TGTGCAAGCTCAAGTTTATTTTCAACCAAGAAAGCTTCATTTTGTCTTCAACATTTG 1422
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DB 1311 TTTCTGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1370
QY 1483 TTGTTGTTGCTTCAAGTTCTTCAAGCCAAATATCATGATTCCTATGAGACAGCGGAAA 1542
DB 1371 TTGTTGTTGCTTCAAGTTCTTCAAGCCAAATATCATGATTCCTATGAGACAGCGGAAA 1430
QY 1543 GCCCTGCTCTTAAGATATCATCTCTCTGCAACCAAAATCTTTTCCACTTACAGAT 1602
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DB 1491 GACCCCTCAATCCCAATCAATGATGAGGCTGCGAGAAACCGGCACTAGCCCGTTATTGGG 1550
QY 1663 TTCTTCAATATGAGAGAAATCTCAAGAAACCAACCCAGATGAGAAATTTTGGAGCAATG 1722
DB 1551 TTCTTCAATATGAGAGAAATCTCAAGAAACCAACCCAGATGAGAAATTTTGGAGCAATG 1610
QY 1723 TGGTTGTTTGGCTGCGAGGATTAAGATAGGATTTATCTATTCAGAAAGAGCTCAGA 1782
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QY 1783 CATTTCTTAAGAGAGGATTTTAATCTCAATCTTAAGAGTTTCTTCAAGAGATGCTCT 1842
DB 1671 CATTTCTTAAGAGAGGATTTTAATCTCAATCTTAAGAGTTTCTTCAAGAGATGCTCT 1730
QY 1843 GTTGGAG 1902
DB 1731 GTTGGAG 1790

QY 1903 CAGTGGCCAGATCTCTCCAGAGAAAGCCCATATTATGTTGTGAGATGCAAG 1962
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DB 1791 CAGGTGGCGAGATCTCTCCAGAGAAAGCCCATATTATGTTGTGAGATGCAAG 1850
| | | | |
QY 1963 AATATGGCCAGATGATGATGCTCTTGTGCAATATTAAGCAAGGTTGAGATT 2022
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DB 1851 AATATGGCCAGATGATGATGCTCTTGTGCAATATTAAGCAAGGTTGAGATT 1910
| | | | |
QY 2023 GAAAACTGAAGCATGAAAAACCTGGCCACTTTAAAGAAAGAAAGGCTTACCTTCAG 2082
| | | | |
DB 1911 GAAAACTGAAGCATGAAAAACCTGGCCACTTTAAAGAAAGAAAGGCTTACCTTCAG 1970
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QY 2083 GATATTGGTCATTA 2097
| | | | |
DB 1971 GATATTGGTCATTA 1985
| | | | |
RESULT 2
BC035977 3143 bp mRNA linear HTC 20-SEP-2002
LOCUS BC035977 Home sapiens, clone IMAGE:461253, mRNA.
DEFINITION BC035977
ACCESSION BC035977 GI:23243305
VERSION BC035977.1
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 3143)
Strausberg, R.
Direct Submission
Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-ehgc.stanford.edu
Contact: (Dickson, Mark) mcd@pdxl.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRML Plate: 41 Row: 9 Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4505278
This clone has the following problem: frame shifted.
FEATURES
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/lab_note="DH10B"
/note="Vector: pDNR-LIB"
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Best Local Similarity 99.7%; Pred. No 0;
Matches 1055; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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DB 52 ATGAGAGAGTTTCTGTTACTATATGCTACACAGACGAGGACAAAGCCATCGAGAA 111
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QY 61 GAAATGTGAGCAAGCTGTGTGATGATGATTTTCTGAGATCTTCACTATATTAGTGA 120
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DB 112 GAAATGTGAGCAAGCTGTGTGATGATGATTTTCTGAGATCTTCACTATATTAGTGA 171
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QY 121 TCCGATTAAGTATGACCTAAACCCGAAACAGCTCTCTGTGTGTGTGTTCTACACG 180
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DB 172 TCCGATTAAGTATGACCTAAACCCGAAACAGCTCTCTGTGTGTGTGTTCTACACG 231
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QY 241 CTGCGGTTGATTTCTTTGCTCACTGCGGTATGAGTTTCTGCGGTATTCAGAA 300
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DB 292 CTGCGGTTGATTTCTTTGCTCACTGCGGTATGAGTTTCTGCGGTATTCAGAA 351
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| | | | |
DB 472 CCGTGAATGCTGACACTGCGCAGAGCCCTCAGAAAGCAATTTAGTCAAGACAGACAA 531
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DB 712 ATTGAAGACTTTGAGTCTCACTTACCCGCTGAGTACCCCACTCTCAGAGCTCTCTG 771
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DB 772 AATATTCTGCTTTTACCCCAAGATTTTACAGATTCATCTGCAAGAGTCTCTGACCAG 831
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QY 781 GAGGAAGCCAGATATCTGAGCTTCAGAGATTCAGGTTTCAAGTGCATTTCAAG 840
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DB 832 GAGGAAGCCAGATATCTGAGCTTCAGAGATTCAGGTTTCAAGTGCATTTCAAG 891
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| | | | |
DB 892 GCGATTCAACTTACTACGATGATGCAATTAACCACTCTGCTGTAGATTTGACATT 951
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QY 901 TCAATATCAGACTTTTCTATACGCTTGAAGATGCTTCAAGCTGATCTGCTTACAGT 960
| | | | |
DB 952 TCAATATCAGACTTTTCTATACGCTTGAAGATGCTTCAAGCTGATCTGCTTACAGT 1011
| | | | |
QY 961 GATTCTGAGGTACAAAGCTTACCAAGATGCAAGCTTGAAGATTAAGAGAGCACTGC 1020
| | | | |
DB 1012 GATTCTGAGGTACAAAGCTTACCAAGATGCAAGCTTGAAGATTAAGAGAGCACTGC 1071
| | | | |
QY 1021 GTCTTTTGAATAAAGCAGACACAAAGAAAGG 1058
| | | | |
DB 1072 GTCTTTTGAATAAAGCAGACACAAAGAAAGG 1109
| | | | |
RESULT 3
BX348674 908 bp mRNA linear EST 08-APR-2004
LOCUS BX348674

DEFINITION BX348674 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
CDNA clone CS00C010Y111 5-PRIME, mRNA sequence.
ACCESSION BX348674
VERSION BX348674.1 GI:30375301
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 908)
AUTHORS Li, W. B., Gruber, C., Jesse, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Creteil, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3392.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CS0BA006ZB02_CS00490_1&c=3392.f

FEATURES
source
Location/Qualifiers
1..908
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC010Y111"
/issue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 34.3%; Score 719; DB 5; Length 908;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 674 AGTCTCACTTACCGGTTGGTACCCCACTTCACAAAGCTCTGTAATTCCTGTT 733
DB 28 AGTCTCACTTACCGGTTGGTACCCCACTTCACAAAGCTCTGTAATTCCTGTT 87
QY 734 TACCCCAAGTAATTTACAGTACATCTGCAGAGGCTCTTGGCAGAGAAAGCCAG 793
DB 88 TACCCCAAGTAATTTACAGTACATCTGCAGAGGCTCTTGGCAGAGAAAGCCAG 147
QY 794 TATCTGAGCTTACAGAGATCCAGTTTTCAGAGTCCAAATTTCAAGAGCAGTTCACTTA 853
DB 148 TATCTGAGCTTACAGAGATCCAGTTTTCAGAGTCCAAATTTCAAGAGCAGTTCACTTA 207
QY 854 CTACGAATGATGCATATAAAACACTCTGCTGTAGATTTGACATTTCAATACAGACT 913
DB 208 CTACGAATGATGCATATAAAACACTCTGCTGTAGATTTGACATTTCAATACAGACT 267
QY 914 TTTTCTATCAGCTGAGATGCTTTCAGCTGATCTGCCCTTAACAGTATTCAGGTAC 973
DB 268 TTTTCTATCAGCTGAGATGCTTTCAGCTGATCTGCCCTTAACAGTATTCAGGTAC 327
QY 974 AAAGCTACTCCAAAGACTGAGCTTGAGATTAAGAGAGCAGTGGCTCTTTGAAA 1093
DB 328 AAAGCTACTCCAAAGACTGAGCTTGAGATTAAGAGAGCAGTGGCTCTTTGAAA 387
QY 1034 TAAAGGAGACAAAGAAAGAGAGTACCTTACCCAGCATATACCTGCGGATGT 1093
DB 388 TAAAGGAGACAAAGAAAGAGAGTACCTTACCCAGCATATACCTGCGGATGT 447
QY 1094 CTCCTCAGTTATTTTACCTGCTGTGTAATCCAGCAATTCCTTAAGAGCATTTT 1153

DB 448 CTCCTCAGTTATTTTACCTGCTGTGTAATCCAGCAATTCCTTAAGAGCATTTT 507
QY 1154 TGGAGCCCTTGTGACTATACAGTACAGTGTCTGAAAAGCGAGCTACAGAGCTGT 1213
DB 508 TGGAGCCCTTGTGACTATACAGTACAGTGTCTGAAAAGCGAGCTACAGAGCTGT 567
QY 1214 GCAGTAACAGAGGGGAGCCGATTTATAGCCGCTTTGTACAGATGCTGCTGTTGT 1273
DB 568 GCAGTAACAGAGGGGAGCCGATTTATAGCCGCTTTGTACAGATGCTGCTGTTGT 627
QY 1274 TGGATCTCCCTCGCTTCCCTTCCCTTGGCAGCAGCAGTCTGCTGTCGATC 1333
DB 628 TGGATCTCCCTCGCTTCCCTTCCCTTGGCAGCAGCAGTCTGCTGTCGATC 687
QY 1334 TTCTTAACCTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTATTTACCCAGA 1392
DB 688 TTCTTAACCTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTATTTACCCAGA 746

RESULT 4
LOCUS BM801462
DEFINITION AGENCOURT_6459212 NIH_MGC_88 Homo sapiens cDNA IMAGE:5560477
5', mRNA sequence.
ACCESSION BM801462
VERSION BM801462.1 GI:19118285
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 874)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1AM12286 row: 1 column: 14
High quality sequence stop: 710.

FEATURES
source
Location/Qualifiers
1..874
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5560477"
/issue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 30.4%; Score 638; DB 4; Length 874;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 738; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAGAGGTTTGTGTTACTATATGCTACACAGAGGAGACGCAAGCCATGCGAGAA 60
DB 50 ATGAGAGGTTTGTGTTACTATATGCTACACAGAGGAGACGCAAGCCATGCGAGAA 109
QY 61 GAATGTGAGAGAGCTGTGTGATGATTTTTCGACAGATCTTCACTATATTAGGAA 120

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Db      110 GAAATATGTAGCAAGCTGTGATCATGATTTTCTGCAGATCTTCACTGATTAATGAA 169
Qy      121 TCCGATTAAGTATGACCTTAAACCCGAAACAGCTCCCTTGTGTGTGTTCTTACAG 180
Db      170 TCCGATTAAGTATGACCTTAAACCCGAAACAGCTCCCTTGTGTGTGTTCTTACAG 229
Qy      181 GGCACCCGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACGAAACCAACA 240
Db      230 GGCACCCGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACGAAACCAACA 289
Qy      241 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGAGTTAAGTTGCTCGGTATTCAGAA 300
Db      290 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGAGTTAAGTTGCTCGGTATTCAGAA 349
Qy      301 TACACTTACTTTTGCAATGGGGGAGATTAATGATTAACGACTTCAAGCTTGAAGCC 360
Db      350 TACACTTACTTTTGCAATGGGGGAGATTAATGATTAACGACTTCAAGCTTGAAGCC 409
Qy      361 CCGCATTTCTATGACACTGACATGACATGACATGACATGACATGACATGACATGAC 420
Db      410 CCGCATTTCTATGACACTGACATGACATGACATGACATGACATGACATGACATGAC 469
Qy      421 CCGTGATTTCTGAGCTGTGCGCAGCCCTTCAAGACATTTTAAAGTCAAGACAGACA 480
Db      470 CCGTGATTTCTGAGCTGTGCGCAGCCCTTCAAGACATTTTAAAGTCAAGACAGACA 529
Qy      481 GAGGATTAAGTGGCCGACCTCCCGGTGATCACTGACATCTTGAAGACAGACCTTGG 540
Db      530 GAGGATTAAGTGGCCGACCTCCCGGTGATCACTGACATCTTGAAGACAGACCTTGG 589
Qy      541 AAGTCAGAGCTGTACATGATTAATCTCAAGTCAAGCTTCTGATTTGATGATTCAGAA 600
Db      590 AAGTCAGAGCTGTACATGATTAATCTCAAGTCAAGCTTCTGATTTGATGATTCAGAA 649
Qy      601 AGAAGATTTCTGAGTTTGAACAAATGACAGTGAACAGAACCAATCCAAATGTTGA 660
Db      650 AGAAGATTTCTGAGTTTGAACAAATGACAGTGAACAGAACCAATCCAAATGTTGA 709
Qy      661 ATTGAAGACTTTGAGTCTCACTTACCCGTTGGGTACCCCACTTCAAGAGCTCTCTG 720
Db      710 ATTGAAGACTTTGAGTCTCACTTACCCGTTGGGTACCCCACTTCAAGAGCTCTCTG 769
Qy      721 AATATCTGTGTTTACCCCC 740
Db      770 AATATCTGTGTTTACCCCC 789

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RESULT 5
CN260357          646 bp      mRNA      linear      EST 16-MAY-2004
LOCUS             17000424179730 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
DEFINITION       CN260357
ACCESSION        CN260357.1 GI:47276771
VERSION          EST.
KEYWORDS         Homo sapiens (human)
SOURCE           Homo sapiens
ORGANISM         Homo sapiens (human)
REFERENCE        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
                  1 (bases 1 to 646)
                  Brandenberger, R., Wei, H., Zhang, S., Lei, S., Muraige, J., Fiek, G. J.,
                  Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R.,
                  Lebkoweki, J. and Stanton, L. M.
                  Transcriptional characterization and elucidates signaling networks that
                  control human ES cell growth and differentiation
                  Nat. Biotechnol. 22 (6), 707-716 (2004)
                  Contact: Brandenberger R
                  Regenerative Medicine
                  Geron Corporation
                  230 Constitution Drive, Menlo Park, CA 94025, USA
                  Tel: 650 473 8658
                  Fax: 650 473 7760
                  Email: rbrandenberger@geron.com
                  Insert Length: 646 Std Error: 0.00.

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FEATURES

source

Location/Qualifiers

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1..646
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
H9"
/clone_1ib="GRN ES"
/note="oligo dt primed, full-length enriched cDNA library
from undifferentiated hbs cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"

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ORIGIN

Query Match 29.7%; Score 623; DB 7; Length 646;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      987 AAGACTGACGCTTGAAGATTAAGAGAGACAGCTGCTTTTGAATAAAGGACAGAC 1046
Db      24 AAGACTGACGCTTGAAGATTAAGAGAGACAGCTGCTTTTGAATAAAGGACAGAC 83
Qy      1047 AAGAAGAAAGAGCTACTTACCCAGATATATCTGGGGATGTTCTTCACTTCAAT 1106
Db      84 AAGAAGAAAGAGCTACTTACCCAGATATATCTGGGGATGTTCTTCACTTCAAT 143
Qy      1107 TTTTACCTGCTGCTTGAATCCAGCAATTCCTTAAAGCAATTTTTCGAGCCCTTGT 1166
Db      144 TTTTACCTGCTGCTTGAATCCAGCAATTCCTTAAAGCAATTTTTCGAGCCCTTGT 203
Qy      1167 GGAATATACAGTGAAGTGTGAAAGGCGAGGCTTACAGAGCTGTGACATTAACAAG 1226
Db      204 GGAATATACAGTGAAGTGTGAAAGGCGAGGCTTACAGAGCTGTGACATTAACAAG 263
Qy      1227 GGCAGCCGATTAATAGCCGCTTTGTACAGATGCTGTGCTGTTTGTGATTCCTCT 1286
Db      264 GGCAGCCGATTAATAGCCGCTTTGTACAGATGCTGTGCTGTTTGTGATTCCTCT 323
Qy      1287 CGCTTCCCTTCTGTCAGACCACTGAGTCTGCTGCTGAAATCTTCTTAACTTCA 1346
Db      324 CGCTTCCCTTCTGTCAGACCACTGAGTCTGCTGCTGAAATCTTCTTAACTTCA 383
Qy      1347 ACCAGACCAATATTCGTGCAAGCTCAAGTTATTTTCAACCCAGAAAGCTCCATTTGT 1406
Db      384 ACCAGACCAATATTCGTGCAAGCTCAAGTTATTTTCAACCCAGAAAGCTCCATTTGT 443
Qy      1407 CTTCACATTTGGAATTTCTGTCTACTGCAACAGAGGTTCTGCGAAGGAGATATG 1466
Db      444 CTTCACATTTGGAATTTCTGTCTACTGCAACAGAGGTTCTGCGAAGGAGATATG 503
Qy      1467 TACAGGCTGCTGAGGCTTGTGCTTCAAGTTCTTCAAGCCAAATACATCATCATCCCA 1526
Db      504 TACAGGCTGCTGAGGCTTGTGCTTCAAGTTCTTCAAGCCAAATACATCATCATCCCA 563
Qy      1527 TGAAGACAGCGGAAAGCCCTGCTCTTAAGATATCATCTCTCTGAAACAAATTC 1586
Db      564 TGAAGACAGCGGAAAGCCCTGCTCTTAAGATATCATCTCTCTGAAACAAATTC 623
Qy      1587 TTTTCACTTACCATGATGACCCCT 1609
Db      624 TTTTCACTTACCATGATGACCCCT 646

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RESULT 6

BQ431497

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

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BQ431497          852 bp      mRNA      linear      EST 24-MAY-2002
LOCUS             AGENCOURT 7894690 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6158144
DEFINITION       5', mRNA sequence.
ACCESSION        BQ431497
VERSION          BQ431497.1 GI:21170583
KEYWORDS         EST.
SOURCE           Homo sapiens (human)
ORGANISM         Homo sapiens

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Db 241 AGCTACTTACCCAGCATATATCTGGGGAGTGTCTCTCCAGTTTCAATTTTACCTGTG 300

Qy 1119 TCTTGAATCCGAGCAATTCCTAAAGGCAATTTTGGAGCCCTTGGAGCTATACGAG 1178

Db 301 TCTTGAATCCGAGCAATTCCTAAAGGCAATTTTGGAGCCCTTGGAGCTATACGAG 360

Qy 1179 TGACAGTGTGTAAGGCGAGGCTACAGAGGCTGTGTCAGTAAACAAGGGGCGAGCCGATTA 1238

Db 361 TGACAGTGTGTAAGGCGAGGCTACAGAGGCTGTGTCAGTAAACAAGGGGCGAGCCGATTA 420

Qy 1239 TAGCCGCTTGTGACGAGATGCTGCTGCTGCTTGTGATCTCTCTGCTTCCCTTC 1298

Db 421 TAGCCGCTTGTGACGAGATGCTGCTGCTGCTTGTGATCTCTCTGCTTCCCTTC 480

Qy 1299 TTGCCAGGACCACTGAGTCTGCTGCAACATCTCTTAACTTCAACCCAGACATTA 1358

Db 481 TTGCCAGGACCACTGAGTCTGCTGCAACATCTCTTAACTTCAACCCAGACATTA 540

Qy 1359 TTGCTGTGCAAGCTCAAGTTTATT 1383

Db 541 TTGCTGTGCAAGCTCAAGTTTATT 565

RESULT 8

LOCUS AU124440 877 bp mRNA linear EST 01-AUG-2002

DEFINITION AU124440 NT2RM4 Homo sapiens cDNA clone NT2RM400010 5', mRNA sequence.

ACCESSION AU124440

VERSION AU124440.1 GI:10949156

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 877)

AUTHORS Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and Isogai,T.

TITLE HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)

JOURNAL Unpublished (2000)

COMMENT Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5', & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES

Location/Qualifiers

1..877

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="NT2RM400010"

/cell_type="teratocarcinoma"

/cell_line="NT2"

/clone_lib="NT2RM4"

/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells"

ORIGIN

Query Match 25.9%; Score 543; DB 1; length 877;

Best Local Similarity 100.0%; Pred.No.1.2e-286;

Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1143 AAGGCAATTTTGGAGCCCTTGTGACTATACAGTGAAGTGAAGGCGAGGCT 1202

Db 192 AAGGCAATTTTGGAGCCCTTGTGACTATACAGTGAAGTGAAGGCGAGGCT 251

Qy 1203 AAGGAGCTGTGAGTAAACAAGGGGAGCCGATTAATAGCCGCTTGTGAGATGCTG 1262

Db 252 AAGGAGCTGTGAGTAAACAAGGGGAGCCGATTAATAGCCGCTTGTGAGATGCTG 311

Qy 1263 TGCCTGTGTTGATATCTCTCTGCTTCCCTTCTTCCAGGACCACTGATCTCT 1322

Db 312 TGCCTGTGTTGATATCTCTCTGCTTCCCTTCTTCCAGGACCACTGATCTCT 371

Qy 1323 GCTGAAACATCTTCTTAACTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTATT 1382

Db 372 GCTGAAACATCTTCTTAACTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTATT 431

Qy 1383 TGACCGAAGAAAGCTCCATTTGTCTTCAACATTTGGAATTTCTGTACTGCGCAAC 1442

Db 432 TGACCGAAGAAAGCTCCATTTGTCTTCAACATTTGGAATTTCTGTACTGCGCAAC 491

Qy 1443 AAGAGTTCTGCGGAAGGAGATGTATACAGGCTGAGCTTGTGTTGCTTCAAGTTCT 1502

Db 492 AAGAGTTCTGCGGAAGGAGATGTATACAGGCTGAGCTTGTGTTGCTTCAAGTTCT 551

Qy 1503 TGAGCCAAACATATGATGATCCCATGAGACAGCGGAAAGCCCTGCTCTTAAGATATC 1562

Db 552 TGAGCCAAACATATGATGATCCCATGAGACAGCGGAAAGCCCTGCTCTTAAGATATC 611

Qy 1563 CATCTCTCTGCAACAAATTTCTTCCACTTACAGATGACCCCTCAATCCCATCAT 1622

Db 612 CATCTCTCTGCAACAAATTTCTTCCACTTACAGATGACCCCTCAATCCCATCAT 671

Qy 1623 AATGAGGTGTCAGGAAACCGGATAGCCCGTTTATTTGGTTCTTACAAATAGAGAGA 1682

Db 672 AATGAGGTGTCAGGAAACCGGATAGCCCGTTTATTTGGTTCTTACAAATAGAGAGA 731

Qy 1683 ACT 1685

Db 732 ACT 734

RESULT 9

LOCUS BQ218755 1061 bp mRNA linear EST 02-MAY-2002

DEFINITION AGENCOURT 7565843 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6041670 5', mRNA sequence.

ACCESSION BQ218755

VERSION BQ218755.1 GI:20400155

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 1061)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE NIH-MGC

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: <http://image.llnl.gov>

Place: LAM13279 row: n column: 07

High quality sequence stop: 518.

Location/Qualifiers

1..1061

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6041670"

/issue_type="embryonal carcinoma, cell line"

/lab host="DH10B (phage-resistant)"
/clone lib="NIH_MGC_92"
/note="Organ: testis; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 25.3%; Score 531; DB 5; Length 1061;
Best Local Similarity 100.0%; Pred. No. 5.2e-280;
Matches 531; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 995 AGCTTGAAGTAAAGAGACACTGCGCTCTTTGAAATTAAGGACACAAAGAGA 1054
Db 1 AGCTTGAAGTAAAGAGACACTGCGCTCTTTGAAATTAAGGACACAAAGAGA 60

QY 1055 AAGGAGCTACCTTACCCAGCATTTACCTGCGGAGATTTCTTCCAGTTATTTTAACT 1114
Db 61 AAGGAGCTACCTTACCCAGCATTTACCTGCGGAGATTTCTTCCAGTTATTTTAACT 120

QY 1115 GGATGCTTGAATCCGAGCAATTCCTAAAGGCAATTTTTCGAGCCCTTGTGAGACTATA 1174
Db 121 GGATGCTTGAATCCGAGCAATTCCTAAAGGCAATTTTTCGAGCCCTTGTGAGACTATA 180

QY 1175 CCAAGTACAGTGTCTGAAAGGCGAGGCTACAGAGCTGTGCAAGTAAACAAAGGCGAGCCG 1234
Db 181 CCAAGTACAGTGTCTGAAAGGCGAGGCTACAGAGCTGTGCAAGTAAACAAAGGCGAGCCG 240

QY 1235 ATTATACCGCTTTTATACAGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1294
Db 241 ATTATACCGCTTTTATACAGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300

QY 1295 CTCTCTGCGAGCCGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1354
Db 301 CTCTCTGCGAGCCGACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

QY 1355 CATATTCGTGTGCAAGCTCAAGTTATTTCAACCCAGGAAAGCTCATTTTGTCTTCAACA 1414
Db 361 CATATTCGTGTGCAAGCTCAAGTTATTTCAACCCAGGAAAGCTCATTTTGTCTTCAACA 420

QY 1415 TTGTGGAATTTCTGTCTTACTGCGCAACAGAGTTTTCGCGAAGGAGTATATACAGGCT 1474
Db 421 TTGTGGAATTTCTGTCTTACTGCGCAACAGAGTTTTCGCGAAGGAGTATATACAGGCT 480

QY 1475 GGCTGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1525
Db 481 GGCTGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 531

RESULT 10
BU941078 834 bp mRNA linear EST 18-OCT-2002
LOCUS
DEFINITION AGNCOURT_10540067 NIH_MGC_128 Homo sapiens cDNA clone
IMAGE:6712893 5', mRNA sequence.
ACCESSION BU941078
VERSION BU941078.1 GI:24129897
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 834)
NIH-MGC http://mhc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@db-remail.nih.gov
Tissue Procurement: NCI
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNCM3022 row: e column: 21
High quality sequence stop: 586.
Location/Qualifiers

FEATURES

source

1. 834
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6712893"
/tissue_type="mixed (pool of 40 RNAs)"
/lab host="DH10B (T1-phage-resistant)"
/clone lib="NIH_MGC_128"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattagcgc);
Site 2: SfiI (ggccgcctgcgc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AAGAGTGTATCAACGACAGAGGCGCATTAAGCGCGG-3' and
5'-ATTCTAGAGCGGAGGCGCGCATTAAG-3' (30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART Kit and size-selected to contain the >2 kb
size fraction (other fractions present in NIH_MGC_126 and
NIH_MGC_127). Library created in the laboratory of T.
Udén, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
Library."

ORIGIN

Query Match 24.2%; Score 507; DB 5; Length 834;
Best Local Similarity 99.7%; Pred. No. 8.3e-267;
Matches 607; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 379 GGAATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 438
Db 3 GGAATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 62

QY 439 TGAGCAGCCCTCGAAGCAATTTAGTCAAGCAGAGAGCAAGAGAGATTAAGTGGCGCA 498
Db 63 TGAGCAGCCCTCGAAGCAATTTAGTCAAGCAGAGAGCAAGAGAGATTAAGTGGCGCA 122

QY 499 CTCGCGGTGATCACTGATCTTGAAGACAGACCTTGTGAAGTCAAGCTGCTACAC 558
Db 123 CTCGCGGTGATCACTGATCTTGAAGACAGACCTTGTGAAGTCAAGCTGCTACAC 182

QY 559 ATTGAATCTCAAGTCAAGCTTCTGAATTCGATGATTCAGAGAGAGAGATTTCTGAGTT 618
Db 183 ATTGAATCTCAAGTCAAGCTTCTGAATTCGATGATTCAGAGAGAGAGATTTCTGAGTT 242

QY 619 TTGAAGCAAAATGACAG 678
Db 243 TTGAAGCAAAATGACAG 302

QY 679 TCACTTACCGGTCGGTACCCCACTCTCAAGAGCTTCTGAAATTTCTGTTTACCC 738
Db 303 TCACTTACCGGTCGGTACCCCACTCTCAAGAGCTTCTGAAATTTCTGTTTACCC 362

QY 739 CCAAGATATTTACAGATCACTGCAAGAGTCTTGGCGAGAGAGAGAGAGAGAGATCT 798
Db 363 CCAAGATATTTACAGATCACTGCAAGAGTCTTGGCGAGAGAGAGAGAGAGAGATCT 422

QY 799 GTACCTTACAGATCAAGTTTTCAGTGGCAATTTCAAGGAGTTCACCTTACTACG 858
Db 423 GTACCTTACAGATCAAGTTTTCAGTGGCAATTTCAAGGAGTTCACCTTACTACG 482

QY 859 AATGATGCAATTAACCACTGCTGTGATGAATTTGACATTTCAATACAGACTTTTCC 918
Db 483 AATGATGCAATTAACCACTGCTGTGATGAATTTGACATTTCAATACAGACTTTTCC 542

QY 919 TATACGCTGGAAGATGCTTACGCGTATCTGCCCTTACAGATATTTCTGAGTACAAAGC 978

Db	543	TATAGCTGAGATGCTTGAAGCTATCTGCTTAACAGTATTTGAGTACAAAGC	602
Qy	979	CTACTCCAA 987	
Db	603	CTACTCCAA 611	
RESULT 11			
CB164340			
LOCUS			
DEFINITION	CB164340	521 bp mRNA linear EST 30-JAN-2003	
ACCESSION	K-EST0225498	LI17N670205n1 Homo sapiens cDNA clone	
VERSION	LI17N670205n1-39-F02 5'	mRNA sequence.	
KEYWORDS	CB164340.1	GI:28150466	
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 521)		
	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,		
	Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and		
	Kim,Y.S.		
TITLE	21c Frontier Korean EST Project 2001		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: Kim YS		
	Genome Research Center		
	Korea Research Institute of Bioscience & Biotechnology		
	52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea		
	Tel.: +82-42-860-4470		
	Fax: +82-42-860-4409		
	Email: yongsung@mail.krdb.re.kr		
	Plate: 39 row: F column: 02		
	High quality sequence stop: 521.		
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Source	1..521		
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	/sex="F"		
	/lab_host="Top10F"		
	/clone_idb="LI17N670205n1"		
	/note="Organ: Liver; Vector: pT73-Pac; Site 1: SCORI;		
	Site 2: NotI; The library was contributed by the Scors		
	laboratory and it was constructed as described by Bonaldo,		
	M.F., Lennon, G. and Soares, M.B. (1996), Genome Research		
	6(9): 791-806. RNA was prepared from harvested cell		
	culture."		
ORIGIN			
Query Match	22.4%	Score 470; DB 6; Length 521;	
Best Local Similarity	99.8%;	Fred. No. 1.9e-246;	
Matches 520; Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
Qy	1540	AAAGCCCGGCTCCCTAAGATATCCATCTCTCTGGAACAAGAAATTTCTTCCACTTACCA	1599
Db	1	AAAGCCCTGGCTCTTAAGATATCCATCTCTCTGGAACAAGAAATTTCTTCCACTTACCA	60
Qy	1600	GATGACCCCTCAATCCCATCATATATATGTTGGGTCGAGAACCGGCATAGCCCGTTTAT	1659
Db	61	GATGACCCCTCAATCCCATCATATATATGTTGGGTCGAGAACCGGCATAGCCCGTTTAT	120
Qy	1660	GGGTTCCTTACAACTATGAGAGAAACTCCAAAGAACCAACCCAGATGGAAATTTTGGAGCA	1719
Db	121	GGGTTCCTTACAACTATGAGAGAAACTCCAAAGAACCAACCCAGATGGAAATTTTGGAGCA	180
Qy	1720	ATGTGGTTGTTTGGCTGCGAGCATTAAGATTAAGATTAATCTATTGAGAAAGAGCTC	1779
Db	181	ATGTGGTTGTTTGGCTGCGAGCATTAAGATTAAGATTAATCTATTGAGAAAGAGCTC	240
Qy	1780	AGACATTTCTTAAAGCATGGATCTTAACTCATCTTAAAGTTTCTTCTTCAGAGAGTCT	1839

Db	241	AGATATTTCCTTAAGCATGGGATTTTAACTCATCTTAAGAAGTTTCCTCTCAAGAGATGCT	300
Qy	1840	CCTGTGTGGGAGAGGAAGCCCCCAGCAAAGTAATACAGACAACATCCAGCTTCATGCG	1899
Db	301	CCTTGTGGGAGAGGAAGCCCCCAGCAAAGTAATACAGACAACATCCAGCTTCATGCG	360
Qy	1300	CAGAGAGTGCGAGAAATCCCTCCACAGAGAAGCGGCATAATTTATGTGTGTGAGATGCA	1959
Db	361	CAGAGAGTGCGAGAAATCCCTCCACAGAGAAGCGGCATAATTTATGTGTGTGAGATGCA	420
Qy	1960	AAGAATATGCGCAAGATGTACATGATGCCCTTGTGCAAAATATATAGCAAGAGTTGGA	2019
Db	421	AAGAATATGCGCAAGATGTACATGATGCCCTTGTGCAAAATATATAGCAAGAGTTGGA	480
Qy	2020	GTTGAAAAACTAGAAAGCAATGAAAACCCTGGCCAATTAA	2060
Db	481	GTTGAAAAACTAGAAAGCAATGAAAACCCTGGCCAATTAA	521
RESULT 12			
LOCUS	B1772430	826 bp	mRNA linear EST 25-SEP-2001
DEFINITION	603055786F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5205285 5'		
ACCESSION	B1772430		
VERSION	B1772430.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	NIH-MGC http://mgc.nci.nih.gov/		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs@wmail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E.R. Consortium (LMNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.R. Consortium/LMNL at: http://image.lmnl.gov Plate: LMAM1514 row: 1 column: 22 High quality sequence stop: 824.		
FEATURES	Location/Qualifiers		
Source	1..826		
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	/clone="IMAGE:5205285"		
	/lab_host="DH10B"		
	/clone_id="NIH_MGC_122"		
	/note="Organ: pooled lung and spleen; Vector: pCMV-Sport6 Site 1: NotI; Site 2: BcoRI (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (BcoRI site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC library."		
ORIGIN			
Query Match	22.2%; Score 466; DB 4; Length 826;		
Best Local Similarity	99.5%; Pred. No. 3,2e+24;		
Matches	616; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
Qy	1 ATGAGAGGTTTCCTTAATCTATATGCTACACAGACGAGACGGAAGGCATATGGCAAA	60	

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Db 53 ATGAGAGGTTTCTGTTACTATATGCTACACAGAGGAGACAGCAAGGCAATCGACAA 112
Qy 61 GAAATGTGTAGCAGAGCTGTGTATCATATGATTTTCTGCAGATCTTCACTATATTATGAA 120
Db 113 GAAATATGTAGCAGAGCTGTGTATCATATGATTTTCTGCAGATCTTCACTATATTATGAA 112
Qy 121 TCCGATTAAGTATGACCTTAATAAACCGAAACAGCTCTCTTGTGTGTGTGTTTCTACACG 180
Db 173 TCCGATTAAGTATGACCTTAATAAACCGAAACAGCTCTCTTGTGTGTGTGTTTCTACACG 232
Qy 181 GGCACCGGAGACCCACCCGACACAGCCCGAAGTTTGTAAAGAAATACAGAACCAACA 240
Db 233 GGCACCGGAGACCCACCCGACACAGCCCGAAGTTTGTAAAGAAATACAGAACCAACA 232
Qy 241 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGGGTTTACTGCGTCTCGGTGATTCAGAA 300
Db 293 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGGGTTTACTGCGTCTCGGTGATTCAGAA 352
Qy 301 TACACCTACTTTTGCATATGGGGGAGATTAATGATTAACGACTTCAAGCTTGGAGCC 360
Db 353 TACACCTACTTTTGCATATGGGGGAGATTAATGATTAACGACTTCAAGCTTGGAGCC 412
Qy 361 CGGATTTCTATGACATGACATGACATGACATGACATGACATGACATGACATGACATGAC 420
Db 413 CGGATTTCTATGACATGACATGACATGACATGACATGACATGACATGACATGACATGAC 472
Qy 421 CCGTGAATGCTGACCTCTGCGCAGCCCTCAGAAAGATTTTAAAGTCAAGACAGAGCAA 480
Db 473 CCGTGAATGCTGACCTCTGCGCAGCCCTCAGAAAGATTTTAAAGTCAAGACAGAGCAA 532
Qy 481 GAGGAGATTAAGTGGCGCACTCCCGGTGGCATCACCTGCACTCTTGAAGACAGACCTTGTG 540
Db 533 GAGGAGATTAAGTGGCGCACTCCCGGTGGCATCACCTGCACTCTTGAAGACAGACCTTGTG 592
Qy 541 AAGTCAGAGCTGCTACATTTGAATCTCAAGTGGAGCTTCGAGATTTCAGATTTCAGGA 600
Db 593 AAGTCAGAGCTGCTACATTTGAATCTCAAGTGGAGCTTCGAGATTTCAGATTTCAGGA 652
Qy 601 AGAAGGATTTCTGAGGTTT 619
Db 653 AGAAGGATTTCTGAGGTTT 671

RESULT 13
LOCUS CB997527 776 bp mRNA linear EST 01-MAY-2003
DEFINITION AGENCOURT 13620640 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30338684 5', mRNA sequence.
ACCESSION CB997527
VERSION CB997527.1 GI:30292047
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 776)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: egarbs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: NDAM365 row: 1 column: 21
High quality sequence stop: 564.
Location/Qualifiers
1..776
FEATURES
SOURCE
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:30338684"
/issue_type="pre-clamptic placenta"
/lab_host="DH10B Tona"
/clone_idb="NIH_MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
all-XhoI; Site_2: BamH; Library is oligo-dT primed and
directionally cloned using primer
5'-TTTTTTTTTTTTTNN-3', size-selected for average insert
size 2.3 kb and normalized to ROT 5. This is a primary
library enriched for full-length clones and constructed
using the Cap-trapper method (Carninci, in preparation).
Library constructed by M. Brownstein (NIH/NHGRI,
National Institutes of Health). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 22.0%; Score 461; DB 6; Length 776;
Best Local Similarity 99.5%; Pred. No. 1,8e-241;
Matches 611; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGAGAGGTTTCTGTTACTATATGCTACACAGAGGAGACAGCAAGGCAATCGACAA 60
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Qy 61 GAAATGTGTAGCAGAGCTGTGTATCATATGATTTTCTGCAGATCTTCACTATATTATGAA 120
Db 148 GAAATGTGTAGCAGAGCTGTGTATCATATGATTTTCTGCAGATCTTCACTATATTATGAA 207
Qy 121 TCCGATTAAGTATGACCTTAATAAACCGAAACAGCTCTCTTGTGTGTGTGTTTCTACACG 180
Db 208 TCCGATTAAGTATGACCTTAATAAACCGAAACAGCTCTCTTGTGTGTGTGTTTCTACACG 267
Qy 181 GGCACCGGAGACCCACCCGACACAGCCCGAAGTTTGTAAAGAAATACAGAACCAACA 240
Db 268 GGCACCGGAGACCCACCCGACACAGCCCGAAGTTTGTAAAGAAATACAGAACCAACA 327
Qy 241 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGGGTTTACTGGGTCTCGGTGATTCAGAA 300
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Qy 301 TACACCTACTTTTGCATATGGGGGAGATTAATGATTAACGACTTCAAGCTTGGAGCC 360
Db 388 TACACCTACTTTTGCATATGGGGGAGATTAATGATTAACGACTTCAAGCTTGGAGCC 447
Qy 361 CCGCATTTCTATGACATGACATGACATGACATGACATGACATGACATGACATGACATGAC 420
Db 448 CCGCATTTCTATGACATGACATGACATGACATGACATGACATGACATGACATGACATGAC 507
Qy 421 CCGTGAATGCTGACCTCTGCGCAGCCCTCAGAAAGATTTTAAAGTCAAGACAGAGCAA 480
Db 508 CCGTGAATGCTGACCTCTGCGCAGCCCTCAGAAAGATTTTAAAGTCAAGACAGAGCAA 567
Qy 481 GAGGAGATTAAGTGGCGCACTCCCGGTGGCATCACCTGCACTCTTGAAGACAGACCTTGTG 540
Db 568 GAGGAGATTAAGTGGCGCACTCCCGGTGGCATCACCTGCACTCTTGAAGACAGACCTTGTG 627
Qy 541 AAGTCAGAGCTGCTACATTTGAATCTCAAGTGGAGCTTCGAGATTTCAGATTTCAGGA 600
Db 628 AAGTCAGAGCTGCTACATTTGAATCTCAAGTGGAGCTTCGAGATTTCAGATTTCAGGA 687
Qy 601 AGAAGGATTTCTGA 614
Db 688 AGAAGGATTTCTGA 701

RESULT 14
LOCUS AUI32586 822 bp mRNA linear EST 01-AUG-2002
DEFINITION AUI32586 NT2RPA Homo sapiens cDNA clone NT2RPA000141 5', mRNA
sequence.
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ACCESSION  AUI32586
VERSION     AUI32586.1  GI:10992940
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 822)
            Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y., Salto, K., Yamamoto, J.,
            Nishikawa, T., Nakamura, Y., Nagai, T., Sugano, S., Maehuo, Y. and
            Isogai, T.
            HRI human cDNA project (Ota, T., Sugiyama, T., Ishii, S., Suzuki, Y.,
            Salto, K., Yamamoto, J., Nishikawa, T., Nakamura, Y., Nagai, T.,
            Sugano, S., Maehuo, Y., Isogai, T.)
            Unpublished (2000)
JOURNAL
COMMENT      Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            153-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3975
            Fax: 81-438-52-3986
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES
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Best Local Similarity 99.6%; Pred. No. 3.6e-238;
Matches 555; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 343 CTTCAGAGCTTGGAGCCCGCATTTCTATGACATGACATGACAGATGATGCTGTAGGT 402
DB 242 CTTCAGAGCTTGGAGCCCGCATTTCTATGACATGACATGACAGATGATGCTGTAGGT 301
QY 403 TTAGAACTTGTGGTGGCCGTGATGCTGTGACATCTGCGCAGCCCTCAAGAAAGCATTTT 462
DB 302 TTAGAACTTGTGGTGGCCGTGATGCTGTGACATCTGCGCAGCCCTCAAGAAAGCATTTT 361
QY 463 AGGTCAAGAGAGAGAAAGAGAGATTAAGTGGGGCATCCCGGTGGCATCCTGTGATCC 522
DB 362 AGGTCAAGAGAGAGAAAGAGAGATTAAGTGGGGCATCCCGGTGGCATCCTGTGATCC 421
QY 523 TTGAGAGACAGACCTTGTGAAGTCAGAGCTGCTACATTTGAATCTCAAGTCCAGCTTCTG 582
DB 422 TGGAGAGACAGACCTTGTGAAGTCAGAGCTGCTACATTTGAATCTCAAGTCCAGCTTCTG 481
QY 583 AGATTGATGATTCAGAGAAAGAGATTTGAGGTTTGAAGCAAAATGCAAGTGAACAGC 642
DB 482 AGATTGATGATTCAGAGAAAGAGATTTGAGGTTTGAAGCAAAATGCAAGTGAACAGC 541
QY 643 AACCAATCAATGTTTAATTAAGACTTGAAGTCTTACCGGTCGTGATCCGCCA 702
DB 542 AACCAATCAATGTTTAATTAAGACTTGAAGTCTTACCGGTCGTGATCCGCCA 601
QY 703 CTCTCAAGACCTCTCTGATATATCTGTGTTTACCCCGAGAAATTTTACAGGTACATCTG 762

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DB 602 CTCTCAAGACCTCTCTGATATATCTGTGTTTACCCCGAGAAATTTTACAGGTACATCTG 661
QY 763 CAGAGTCTCTTGGCCAGAGAGAAAGCAAGATGCTGACTTCAGCAGATCCAGTTT 822
DB 662 CAGAGTCTCTTGGCCAGAGAGAAAGCAAGATGCTGACTTCAGCAGATCCAGTTT 721
QY 823 CAAGTCCCAATTTTCAA 839
DB 722 CAAGTCCCAATTTTCAA 738
RESULT 15
AM965709
LOCUS       EST377782 MAGE resequenes, MAGI Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION  AM965709.1  GI:8155545
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 591)
            Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
            Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and
            Quackenbush, J.
            Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
            Unpublished (2000)
JOURNAL
COMMENT      Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@igr.org
            Plate: 218
            Seq primer: Reverse.
FEATURES
    source          1..591
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ORIGIN
Query Match      21.4%; Score 448; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.5e-234;
Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1192 AAGCCAGGCTACAGAGCTGTGCACTAAACAAGGGGAGCCGATTAATAGCCGCTTTGTA 1251
DB 1 AAGCCAGGCTACAGAGCTGTGCACTAAACAAGGGGAGCCGATTAATAGCCGCTTTGTA 60
QY 1252 CGAGATGCTGTGCGCTGTGTGATCTCCCTCGCTTCCCTTCCGACGACCA 1311
DB 61 CGAGATGCTGTGCGCTGTGTGATCTCCCTCGCTTCCCTTCCGACGACCA 120
QY 1312 CTCAAGTCTCTGCTGAAACATCTTCTTAACTTCAACCCAGACATATTCGTGTGAAC 1371
DB 121 CTCAAGTCTCTGCTGAAACATCTTCTTAACTTCAACCCAGACATATTCGTGTGAAC 180
QY 1372 TCAAGTTTATTTACCCGAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCT 1431
DB 181 TCAAGTTTATTTACCCGAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCT 240
QY 1432 ACTGCACAACAGAGGTTCTGCGAAGGAGATGATACAGGCTGCTGCTTGTGTT 1491
DB 241 ACTGCACAACAGAGGTTCTGCGAAGGAGATGATACAGGCTGCTGCTTGTGTT 300
QY 1492 GCTTCAAGTCTTCAACCAATACATGATCCATGAAAGACGCGGAAAGCCCTGGCT 1551
DB 301 GCTTCAAGTCTTCAACCAATACATGATCCATGAAAGACGCGGAAAGCCCTGGCT 360

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Qy 1552 CCTAAGATATCCATCTCTCTCGAACAATAATTCTTCCACTTACCAATGACCCCTCA 1611
Db 361 CCTAAGATATCCATCTCTCTCGAACAATAATTCTTCCACTTACCAATGACCCCTCA 420
Qy 1612 ATCCCATCATATATGATGGTCCAGGAA 1639
Db 421 ATCCCATCATATATGATGGTCCAGGAA 448

Search completed: August 27, 2005, 15:58:35
Job time : 4548.04 sec8

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 19:17:21 ; Search time 6007.21 Seconds

(without alignments)
16914.771 Million cell updates/sec

Title: US-09-371-347A-43

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*\n2: gb_hcg:*\n3: gb_in:*\n4: gb_om:*\n5: gb_ov:*\n6: gb_pat:*\n7: gb_ph:*\n8: gb_pl:*\n9: gb_pr:*\n10: gb_ro:*\n11: gb_sts:*\n12: gb_sy:*\n13: gb_un:*\n14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2046	97.6	3259	6	AR144976 Sequence
2	2046	97.6	3259	6	AX050463 Sequence
3	2046	97.6	3259	6	AF025794 Homo sapi
4	2046	97.6	3259	6	AF121214 Homo sapi
5	1944	92.7	3241	6	CQ726091 Sequence
6	1893	90.3	3310	9	BC054816 Homo sapi
7	1338	63.8	2933	11	BV177620 Homo sapi
8	1338	63.8	2933	11	BV178010 Homo sapi
9	386	18.4	390	6	BD077780 5' EST of
10	381	18.2	1353	9	AF121202S04
11	330	15.7	109626	9	AC010346 Homo sapi
12	330	15.7	110756	9	AC025174 Homo sapi
13	279	13.3	158199	2	AC022921 Homo sapi
14	279	13.3	167237	2	AC021609 Homo sapi
15	279	13.3	177536	2	AC091945 Homo sapi
16	189	9.0	1156	9	AF121210 Homo sapi
17	188	9.0	1034	9	AF121202S09
18	188	9.0	167237	2	AC021609 Homo sapi
19	188	9.0	177536	2	AC091945 Homo sapi

20	183	8.7	1432	9	AF121202S07
21	161	7.7	158199	2	AC022921 Homo sapi
22	158	7.5	1256	9	AF121202S02
23	158	7.5	2475	6	AR454615 Sequence
24	158	7.5	2475	6	AX375651 Sequence
25	155	7.4	2011	9	AF121202S06
26	146	7.0	2214	9	AF121202S12
27	125	6.0	969	9	AF121202S05
28	121	5.8	1119	9	AF121202S10
29	119	5.7	1200	9	AF121202S03
30	109	5.2	4506	9	AF121202S01
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32	63	3.0	63	6	AX611833 Sequence
33	60	2.9	60	6	CO539377 Sequence
34	54	2.6	54	6	AX611839 Sequence
35	54	2.6	54	6	AX611843 Sequence
36	51	2.4	51	6	AX162161 Sequence
37	48	2.3	48	6	AX611835 Sequence
38	48	2.3	48	6	AX611841 Sequence
39	47	2.2	183	6	CO670532 Sequence
40	44	2.1	650	9	AF121202S08
41	41	2.0	41	6	AX611845 Sequence
42	38	1.8	38	6	AX611837 Sequence
43	38	1.8	63	6	AX611834 Sequence
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45	32	1.5	271339	2	AC131637 Rattus no

ALIGNMENTS

RESULT 1	AR144976	Sequence 23 from patent US 6210950.	DNA	linear	PAT 08-AUG-2001
LOCUS	AR144976	3259 bp			
DEFINITION	Sequence 23 from patent US 6210950.				
ACCESSION	AR144976				
VERSION	AR144976.1	GI:15106843			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 3259)				
AUTHORS	Johnson, W.G. and Stenroos, E.Scott.				
TITLE	Method for diagnosing, preventing, and treating developmental disorders due to a combination of genetic and environmental factors				
JOURNAL	Patent: US 6210950-A 23 03-APR-2001;				
FEATURES	Location/Qualifiers				
source	1..3259				
ORIGIN	/organism="unknown"				
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Query Match	97.6%; Score 2046; DB 6; Length 3259;				
Best Local Similarity	100.0%; Pred. No. 0;				
Matches 2096; Conservative	0; Mismatches 1; Indels 0; Gaps 0;				
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DB	80	ATGAGGAGGTTTCTGTATATATGCTACACGAGGACGAGCAAGGCCATCCGAGAA	139		
QY	61	GAATGTGTGACAGCTGTGTATGATGATTTTGTGAGATCTTCACTATTTAGTGA	120		
DB	140	GAATGTGTGACAGCTGTGTATGATGATTTTGTGAGATCTTCACTATTTAGTGA	199		
QY	121	TCGATTAAGTATGACCTAAACCGAAGCAGCTCTTGTGTTGTGTTCTACACG	180		
DB	200	TCGATTAAGTATGACCTAAACCGAAGCAGCTCTTGTGTTGTGTTCTACACG	259		
QY	181	GGCAGCGGAGACCCGACGACGAGCCGCAAGTTTGAAGAAATAGAACCAACAA	240		
DB	260	GGCAGCGGAGACCCGACGAGCCGCAAGTTTGAAGAAATAGAACCAACAA	319		
QY	241	CTGCCGTTGATTTCTTCTCACTGCGGTATGAGGTTACTGGGTTCTCGTATTCAGAA	300		

Db	320	CTGCCGGTGAATTTCTTTGCTCACTCGGGATATGGGTTACTGGGTTCTCGGATTCAGAA	379
Qy	301	TACACCTTACTTTTGCAATG999999AAGTAATTGATAAACAATTCAAGACTTGAAGCC	360
Db	380	TACACCTTACTTTTGCAATG999999AAGTAATTGATAAACAATTCAAGACTTGAAGCC	439
Qy	361	CGGCATTTCTATGACATCGAGCATATGCAATGACATCTGTATAGGTTTATGAACTTGTGGTGA	420
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Qy	421	CCGTGATATGCTGACCTCTG9CCAGACCCTCAGAAAGCAATTTAGGTCAAGCAGAGCA	480
Db	500	CCGTGATATGCTGACCTCTG9CCAGACCCTCAGAAAGCAATTTAGGTCAAGCAGAGCA	559
Qy	481	GAGAGATATGATGGCGCACTCCCGTGGCATCACTGATCCTTGAAGACAGACTTGTG	540
Db	560	GAGAGATATGATGGCGCACTCCCGTGGCATCACTGATCCTTGAAGACAGACTTGTG	619
Qy	541	AAATCAGAGCTGCTTACATATGAAATCTCAAGTCCAGCTTCTGAATTCGATGATTCAGAA	600
Db	620	AAATCAGAGCTGCTTACATATGAAATCTCAAGTCCAGCTTCTGAATTCGATGATTCAGAA	679
Qy	601	AGAAAGATTTCTAGAGTTTGTAGCAAAATCAGATGAAACAGCAACCAATCAATGTTGTA	660
Db	680	AGAAAGATTTCTAGAGTTTGTAGCAAAATCAGATGAAACAGCAACCAATCAATGTTGTA	739
Qy	661	ATTGAAAGCTTTGAGTCTCACTTACCCGTTCCGTAACCCCACTCTCAAGACCTCTCTG	720
Db	740	ATTGAAAGCTTTGAGTCTCACTTACCCGTTCCGTAACCCCACTCTCAAGACCTCTCTG	799
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Qy	781	GAGGAAAGCCAAAGTATCTGTACCTCAGCAGATCCAGTTTTCAGAGGCCAATTTCAAG	840
Db	860	GAGGAAAGCCAAAGTATCTGTACCTCAGCAGATCCAGTTTTCAGAGGCCAATTTCAAG	919
Qy	841	GCAGTTCAACTTACATCAGATGATGCCATAAAAAACACTCTGCTGTGATGAAATTTGACATT	900
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Qy	901	TCAAAATCAGACTTTTCTATACCTGATGCTGAGATGCTTACAGCTGATCTGCCCTPACAGT	960
Db	980	TCAAAATCAGACTTTTCTATACCTGATGCTGAGATGCTTACAGCTGATCTGCCCTPACAGT	1039
Qy	961	GATTCGTAGGTACAAAGCTTACTCCAAAGATCGACGCTTGAAGATTAAGAAGACACATGC	1020
Db	1040	GATTCGTAGGTACAAAGCTTACTCCAAAGATCGACGCTTGAAGATTAAGAAGACACATGC	1099
Qy	1021	GTCCTTTGAAAATTAAGGACAGACACAAGAAGAAAGAGCTTACTTACCACACATATA	1080
Db	1100	GTCCTTTGAAAATTAAGGACAGACACAAGAAGAAAGAGCTTACTTACCACACATATA	1159
Qy	1081	CTGCGGGAGTGTCTCTCCAGTTCAATTTTACCTGTGTCTTGAATCCAGACATTTCT	1140
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Db	1280	CTACAGAGCTGTGACATTAACAAGGGGACAGCCCATTTATACCGCTTTGTACAGATATCC	1339
Qy	1261	TGTGCTGCTTGTGGATCTCTCTCTGCTTTCCTTCTTTCAGCCCACTAGTCTC	1320
Db	1340	TGTGCTGCTTGTGGATCTCTCTCTGCTTTCCTTCTTTCAGCCCACTAGTCTC	1399
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Qy	1381	TTTCACCCAGAAAAGCTTCCATTTTGTCTTCAACATTTGTGAAATTTCTGTCTACTGCCACA	1440
Db	1460	TTTTCAACCCAGAAAAGCTTCCATTTTGTCTTCAACATTTGTGAAATTTCTGTCTACTGCCACA	1519
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Db	1520	ACAGAGGTTCTGCGGGAAGGGAAGTATGTACAGAGCGGTGCGCTTGTGTGTGTGCTTCAGTT	1579
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Db	1580	CTTCAGGCAAAACATACATGATCCCATGAAGACAGCGGGAAGAGCCCTGGCTCTTAAGATA	1639
Qy	1561	TCCATCTCTCTCGAACAACAAATTCCTTCCACTTACCAAGATGACCCCTCAATCCCATC	1620
Db	1640	TCCATCTCTCTCGAACAACAAATTCCTTCCACTTACCAAGATGACCCCTCAATCCCATC	1699
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Db	1760	AAACTCCAGAACCAACCCAGATGAAATTTTGGACAAATGTGTGTTTTTGGCTGC	1819
Qy	1741	AGGCAATAGGATAGGATTAATCTATTTCAGAAAAGGCTCAGACATTTCTTAAGCATGG	1800
Db	1820	AGGCAATAGGATAGGATTAATCTATTTCAGAAAAGGCTCAGACATTTCTTAAGCATGG	1879
Qy	1801	ATCTTAACTCATCTTAAAGGTTTTCTTTCAGAGATGCTCTGTGTGGGAGAGAGAACCC	1860
Db	1880	ATCTTAACTCATCTTAAAGGTTTTCTTTCAGAGATGCTCTGTGTGGGAGAGAGAACCC	1939
Qy	1861	CCAGCAAAAGTATGTACAAAGCAACATCCAGCTTCATGGCCAGCAGTGGAGAGATCTC	1920
Db	1940	CCAGCAAAAGTATGTACAAAGCAACATCCAGCTTCATGGCCAGCAGTGGAGAGATCTC	1999
Qy	1921	CTCCAGAGAAACGGCCATATTTATGTGTGTGTGAGATCAAAAGATATATGGCCAAAGATGTA	1980
Db	2000	CTCCAGAGAAACGGCCATATTTATGTGTGTGTGAGATCAAAAGATATATGGCCAAAGATGTA	2059
Qy	1981	CATGATGCTCTGTGCAATATATAGCAAGAGTTGGAGTTGAAAACTTGAAGCAATG	2040
Db	2060	CATGATGCTCTGTGCAATATATAGCAAGAGTTGGAGTTGAAAACTTGAAGCAATG	2119
Qy	2041	AAACCCCTGGCACTTTTAAAAAGAAAACGCTACCTTCAGAGATATTTGTCTATA	2097
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LOCUS	AX050463	3259 bp	DNA	linear	PAT 12-JAN-2001
DEFINITION	Sequence 23 from Patent WO0071754.				
ACCESSION	AX050463				
VERSION	AX050463.1 GI:12226668				
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 Johnson, W.G. and Stenroos, E.S.				
AUTHORS	Methods for diagnosing, preventing, and treating developmental				
TITLE	disorders due to a combination of genetic and environmental factors				
JOURNAL	Patent: WO 0071754-A 23 30-NOV-2000;				
FEATURES	University of Medicine and Dentistry of New Jersey (US)				
SOURCE	location/Qualifiers				
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ORIGIN

97.6%; Score 2046; DB 6; Length 3259;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db	140	GAATATGATGACAGAGCTGTGTAT	GATGATTTTCTGCAGATCTTCACTATATATGAGAA	139
QY	121	TCCGATATGATATGACCTTAA	AAACCGAAACAGCTCTCTGTGTGTGTGTGTCTACACAGC	180
Db	200	TCCGATATGATATGACCTTAA	AAACCGAAACAGCTCTCTGTGTGTGTGTGTCTACACAGC	259
QY	181	GGCACCGGAGACCCACCCG	ACACAGCCCGCAGTTTGTATAGAAATATACAAACCAACA	240
Db	260	GGCACCGGAGACCCACCCG	ACACAGCCCGCAGTTTGTATAGAAATATACAAACCAACA	319
QY	241	CTGCCTGTGTAATTTCTT	GTCTCACCTGCGGTATATGAGTTATCTGCGTATTCAGAA	300
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QY	301	TACACCTTACTTTTGCA	TATGAGGAGATTAATTAACGACTTCAAGACTTGAAGCC	360
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Db	800	AATATCTCGGTTTAC	CCCCGAAATTTTACAGATCATCTGACGAGGTCTTTGGCCAG	859
QY	781	GAGGAAGCCAGATAT	CTGTGACTTCAGACAGATCCAGATTTTCAAGTGCACATTTCAAG	840
Db	860	GAGGAAGCCAGATAT	CTGTGACTTCAGACAGATCCAGATTTTCAAGTGCACATTTCAAG	919
QY	841	GCAATTCACATTA	CTACAGATGATGCTCAATTAACATCTGTGCTGTGTGAATTTGACATT	900
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1981	CATGATGCCCT	GTGTGCAATATATAGCAAAAGGTGTGAAGTGTGAAGCAATG	2040
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Db 1400 CTGCTGAACATCTTCTTAACTTCAACCCAGACATATTCGTGTCAAGCTCAAGTTA 1459
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RESULT 4
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LOCUS Homo sapiens methionine synthase reductase (MTRR) mRNA, complete
DEFINITION cds.
ACCESSION AF121214
VERSION AF121214.1 GI:6561338
KEYWORDS

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3291)
AUTHORS Leclerc,D., Odleyre,M., Wu,Q., Wilson,A., Huizenga,J.J., Rozen,R., Scherer,S.W. and Gravel,R.A.
TITLE Molecular cloning, expression and physical mapping of the human methionine synthase reductase gene
JOURNAL Gene 240 (1), 75-88 (1999)
MEDLINE 20033550
PUBMED 10564814
REFERENCE 2 (bases 1 to 3291)
AUTHORS Leclerc,D., Odleyre,M.-H., Wu,Q., Wilson,A., Huizenga,J.J., Johns,T., Shoubiridge,E.A., Rosenblatt,D.S., Scherer,S.W., Rozen,R. and Gravel,R.A.
TITLE Direct Submission
JOURNAL Submitted (18-JAN-1999) Human Genetics, Montreal Children's Hospital, 4060 Ste-Catherine West, Montreal, Quebec H3Z 2Z3, Canada
FEATURES
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DEFINITION Sequence 12025 from Patent WO02068579.
ACCESSION CO726091
VERSION CO726091.1 GI:42288134
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kite, such as nucleic acid arrays, comprising a majority of
humaneurons or transcripts, for detecting expression and other uses
hereof
JOURNAL Patent: WO 02068579-A 12025 06-SEP-2002;
PB Corporation (NY) (US)
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RESULT 6
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DEFINITION
Homo sapiens 5-methyltetrahydrofolate-homocysteine
methyltransferase reductase, mRNA (cDNA clone IMAGE:5205285),
partial cds.
BC054816
VERSION
BC054816.1 GI:33392775
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 3310)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,J., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marisina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Chapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramsen,R.D., Muliyil,S.J., Bosak,S.A., McSwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywicki,M.T., Skalska,U., Smalins,D.E.,
Schmeich,A., Schein,J.B., Jones,S.V. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED
22388257
12477932
2 (bases 1 to 3310)
Strausberg,R.
Direct Submission
Submitted (03-JUL-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

REMARK
COMMENT

DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@ngri.nih.gov
Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-D., Karlina,E., Kwong,P., Laric,P., Legaapi,R.,
Maduro,O.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantipop,S., Thomas,P.J., Touchman,J.W.,
Tsurgent,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAK Plate: 115 Row: d Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4505278.

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ACCESSION	BV177620
VERSION	BV177620.1 GI:48013757
KEYWORDS	STS.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 2933)
AUTHORS Nelson,R.M., Marnellos,G., Kemmerer,S., Hoyal,C.R., Shi,M.M.,
Cantor,C.R. and Braun,A.
TITLE Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
JOURNAL Genome Res. (2004) In press
COMMENT Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 2933.

FEATURES
source Location/Qualifiers
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1778; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

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LOCUS sqm97986 Human DNA (Sequencem) Homo sapiens STS genomic, sequence
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ACCESSION BV178010.1 GI:48014252
VERSION BV178010.1
KEYWORDS STS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2933)
Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
Canfor,C.R. and Braun,A.
Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
Genome Res. (2004) In press

JOURNAL COMMENT
Contact: Andreas Braun
Pharmaceuticals division
Sequencem, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequencem.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 2933

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
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ORIGIN
STS
Query Match 63.8%; Score 1338; DB 11; Length 2933;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1778; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

Qy 315 CAATGGGGGAGAGATATGATTAACGACTTCAAGAGCTTGGAGCCCGGCAATTTATATA 374
Db 2846 CAATGGGGGAGAGATATGATTAACGACTTCAAGAGCTTGGAGCCCGGCAATTTATATA 2787
Qy 375 CACTGGAACATGACGATGATCTGTAGTTTAAAGAACTTGTGTTGAGCCCGTGAATTCCTGG 434
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DEFINITION Homo sapiens methionine synthase reductase (MTRR) gene, exon 5.					
ACCESSION AF121205					
VERSION AF121205.1	GI:6572530				
KEYWORDS					
SOURCE	4 of 12				
ORGANISM Homo sapiens (human)					
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
AUTHORS 1 (bases 1 to 1353)					
Leclerc,D., Odleyev,M., Wu,Q., Wilson,A., Huizenga,J.J., Rozen,R., Scherer,S.W. and Gravel,R.A.					
Molecular cloning, expression and physical mapping of the human methionine synthase reductase gene					
Gene 240 (1), 75-88 (1999)					
MEDLINE 20033550					
PUBMED 10564814					
REFERENCE 2 (bases 1 to 1353)					
AUTHORS Leclerc,D.					
TITLE Direct Submission					
JOURNAL Submitted (20-JAN-1999) Human Genetics, Montreal Children's Hospital, 4060 Ste-Catherine West, Montreal, Quebec H3Z 2Z3, Canada					
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AC010346
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DEFINITION HTG.
ACCESSION
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 109626)
JOURNAL DOB Joint Genome Institute and Stanford Human Genome Center.
REFERENCE
AUTHORS Unpublished
TITLE 2 (bases 1 to 109626)
JOURNAL DOB Joint Genome Institute.
REFERENCE
AUTHORS Direct Submission
TITLE DOB Joint Genome Institute.
JOURNAL Submitted (15-SEP-1999) Production Sequencing Facility, DOB Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 109626)
REFERENCE
AUTHORS DOB Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-2000) DOB Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Nov 10, 2000 this sequence version replaced gi:9256196.
Draft Sequence Produced by DOB Joint Genome Institute
www.jgi.doe.gov
www-shgc.stanford.edu
SFS Content:
Quality: Phrap Quality >=40 99.9% of Sequence;
WT-9255 G05749.

FEATURES

source

1. 109626
Location/Qualifiers
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ORIGIN

Query Match 15.7%; Score 330; DB 9; Length 109626;
Best Local Similarity 99.7%; Pred. No. 1.3e-168;
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AC025174
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VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 110756)
JOURNAL DOB Joint Genome Institute and Stanford Human Genome Center.
REFERENCE
AUTHORS Unpublished
TITLE 2 (bases 1 to 110756)
JOURNAL DOB Joint Genome Institute.
REFERENCE
AUTHORS Direct Submission
TITLE DOB Joint Genome Institute.
JOURNAL Submitted (07-MAR-2002) Production Sequencing Facility, DOB Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 110756)
REFERENCE
AUTHORS DOB Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-2002) Production Sequencing Facility, DOB Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 110756)
REFERENCE
AUTHORS DOB Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-2002) DOB Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 28, 2002 this sequence version replaced gi:19224767.
Draft Sequence Produced by DOB Joint Genome Institute
www.jgi.doe.gov
www-shgc.stanford.edu
SFS Content:
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.

FEATURES

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Query Match 15.7%; Score 330; DB 9; Length 110756;
Best Local Similarity 99.7%; Pred. No. 1.3e-168;
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Qy 461 TTAGTCAACAGAGAGCAAGAGAGATAGTGGCGCACTCCGTTGGCATCCTGCAT 520
Db 20100 TTAGTCAACAGAGAGCAAGAGAGATAGTGGCGCACTCCGTTGGCATCCTGCAT 20159
Qy 521 CCTTGAAGAGAGACCTTGTGAAGTCAAGCTGCTACACATTGAATCTCAAGTGAAGCTTC 580
Db 20160 CCTCGAGAGAGACCTTGTGAAGTCAAGCTGCTACACATTGAATCTCAAGTGAAGCTTC 20219
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Db 20220 TGAGATTCAGTGAATTCAGAAAGAGATTCGAGGTTTGAAGCAAAATGACAGTGAACA 20279
Qy 641 GCAACCAATCAATGTTGTAATTAAGACATTTGAGTCCATTCACCTTCCGTTACCCC 700
Db 20280 GCAACCAATCAATGTTGTAATTAAGACATTTGAGTCCATTCACCTTCCGTTACCCC 20339
Qy 701 CACTCTCAACAGCTCTCTGAATTTCTCGTTTACCCCAAGAAATTTTACAGTATCATC 760
Db 20340 CACTCTCAACAGCTCTCTGAATTTCTCGTTTACCCCAAGAAATTTTACAGTATCATC 20399
Qy 761 TGCAGAGTCTCTTGCCAGG 781
Db 20400 TGCAGAGTCTCTTGCCAGG 20420

RESULT 13
AC022921 158199 bp DNA linear HTG 12-MAR-2000
LOCUS Homo sapiens clone RP11-138P20, WORKING DRAFT SEQUENCE, 12
DEFINITION Unordered pieces.
AC022921
AC022921.2 GI:7229868
HTG; HTGS PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 158199)
Britten, B., Linton, L., Nussbaum, C. and Lander, E.
Homo sapiens, clone RP11-138P20
2 (bases 1 to 158199)
Britten, B., Linton, L., Nussbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckert, R., Beda, F., Boguslavsky, L., Bouhgalter, B., Brown, A., Burkett, G., Casle, A., Choedel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Darelano, K., Dewar, K., Domino, M., Doyle, M., Fenesor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hages, B., Heaford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lander, T., Lehoczy, J., Levine, R., Liu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N., McEwan, P., McGurk, A., McKernan, K., McPheters, R., Meldrum, J., Meneses, L., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, J. M., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Turrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Mar 12, 2000 this sequence version replaced gi:6921909.
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information
Center project name: L6314
Center clone name: 138_P20
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 152656 bases at least Q40
Consensus quality: 155474 bases at least Q30
Consensus quality: 156388 bases at least Q20
Insert size: 178000; agarose-fp
Insert size: 157099; sum-of-ctnigs
Quality coverage: 4.4 in Q20 bases; agarose-fp
Quality coverage: 5.0 in Q20 bases; sum-of-ctnigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 ctnigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the ctnigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 1283: contig of 1283 bp in length
* 1284 1383: gap of 100 bp
* 1384 4203: contig of 2820 bp in length
* 4204 4303: gap of 100 bp
* 4304 6786: contig of 2483 bp in length
* 6787 6886: gap of 100 bp
* 6887 9683: contig of 2797 bp in length
* 9684 9783: gap of 100 bp
* 9784 12902: contig of 3119 bp in length
* 12903 13002: gap of 100 bp
* 13003 16429: contig of 3427 bp in length
* 16430 16529: gap of 100 bp
* 16530 25201: contig of 8672 bp in length
* 25202 25301: gap of 100 bp
* 25302 36759: contig of 11458 bp in length
* 36760 36859: gap of 100 bp
* 36860 53921: contig of 17062 bp in length
* 53922 54021: gap of 100 bp
* 54022 72054: contig of 18033 bp in length
* 72055 72154: gap of 100 bp
* 72155 102527: contig of 30373 bp in length
* 102528 158199: contig of 55572 bp in length.
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4304. 6786
/note="assembly_fragment"
6887. 9683
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vector_side:left
/note="assembly_fragment"
13003. 16429
/note="assembly_fragment"
16530. 25201
/note="assembly_fragment"
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vector_side:right
25302. 36759
/note="assembly_fragment"

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ORIGIN

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Query Match      13.3%; Score 279; DB 2; Length 158199;
Best Local Similarity 99.5%; Pred. No. 1.1e-140;
Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 401 GTTTGAATCTGTTGGTGGCCGTGATCTGGAATCTGGCCAGCCCTCAGAAAGCAT 460
DB 3446 GTTTGAATCTGTTGGTGGCCGTGATCTGGAATCTGGCCAGCCCTCAGAAAGCAT 3505
QY 461 TTAGGTCAAGCAGAGCAGAGAGATAGTGGCAGCTCCCGGTGATCAGCTGCAT 520
DB 3506 TTAGGTCAAGCAGAGCAGAGAGATAGTGGCAGCTCCCGGTGATCAGCTGCAT 3565
QY 521 CCTTGAAGCAGAGCCTTGTGAAGTCAAGCTGCTACATTAATCTCAAGTCAAGCTTC 580
DB 3566 CCTTGAAGCAGAGCCTTGTGAAGTCAAGCTGCTACATTAATCTCAAGTCAAGCTTC 3625
QY 581 TGAAGTCAATGATTTCAAGAAAGAAATTTCTGAGTTTGAAGCAAAATGCAATGAACA 640
DB 3626 TGAAGTCAATGATTTCAAGAAAGAAATTTCTGAGTTTGAAGCAAAATGCAATGAACA 3685
QY 641 GCACCAATCCATGTTGTAATGAAGACTTGAAGTCTCACTTACCCGCTGGTACCCC 700
DB 3686 GCACCAATCCATGTTGTAATGAAGACTTGAAGTCTCACTTACCCGCTGGTACCCC 3745
QY 701 CACTCTCACAAGCCTCTCTGAATATTCCTGTTTACCCCGAATATTTACAGATCATC 760
DB 3746 CACTCTCACAAGCCTCTCTGAATATTCCTGTTTACCCCGAATATTTACAGATCATC 3805
QY 761 TGCAGAGTCTCTTGGCCAGG 781
DB 3806 TGCAGAGTCTCTTGGCCAGG 3826

```

```

RESULT 14
AC021609 LOCUS      167237 bp      DNA      linear      HTG 12-MAR-2000
DEFINITION      Homo sapiens clone RP11-259D10, WORKING DRAFT SEQUENCE, 6 unordered
ACCESSION      AC021609.3 GI:7230210
VERSION      AC021609
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
REFERENCE
AUTHORS      Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
TITLE      Mammalian Butcheria; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL      1 (bases 1 to 167237)
REFERENCE      2 (bases 1 to 167237)
AUTHORS      Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE      Homo sapiens, clone RP11-259D10
JOURNAL      Unpublished

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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Bede,F.,
 Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G., Castle,A.,
 Choedel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
 Dearlano,K., Dewar,K., Domini,M., Doyle,M., Fensholt,J.,
 Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J.,
 Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
 Howland,J.C., Johnson,R., Jones,C., Kann,L., Karasik,A., Klein,J.,
 Lander,E., Lehotzky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
 MacDonald,P., Margulis,N., McMan,P., McGurk,A., McKernan,K.,
 McPheters,R., Meldrum,J., Menus,L., Morrow,J., Naylor,J.,
 Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K.,
 Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,

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TITLE
JOURNAL
COMMENT

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Roy,A., Santos,R., Severy,P., Spencer,B., Strange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 12, 2000 this sequence version replaced gi:6899697.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L5818
Center clone name: 259_D_10
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 161183 bases at least Q40
Consensus quality: 164380 bases at least Q30
Consensus quality: 165590 bases at least Q20
Insert size: 164000; agarose-fp
Insert size: 166737; sum-of-contigs
Quality coverage: 5.1 in Q20 bases; sum-of-contigs
Quality coverage: 5.0 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 3656: contig of 3656 bp in length
* 3657 3756: gap of 100 bp
* 3757 9436: contig of 5680 bp in length
* 9437 9536: gap of 100 bp
* 9537 27768: contig of 1832 bp in length
* 27769 27868: gap of 100 bp
* 27869 52058: contig of 24190 bp in length
* 52059 52158: gap of 100 bp
* 52159 80100: contig of 27942 bp in length
* 80101 80200: gap of 100 bp
* 80201 167237: contig of 87037 bp in length.
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/note="assembly_fragment"

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ORIGIN

Query Match 13.3%; Score 279; DB 2; Length 167237;
Best Local Similarity 99.5%; Pred. No. 1.1e-140;
Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGGTGGACCGTGGATTGCTGAGCTTGGCCAGCCCTCAGAAAGCATT 460
DB 62083 GTTTAGAACTTGTGGTGGACCGTGGATTGCTGAGCTTGGCCAGCCCTCAGAAAGCATT 62142
QY 461 TTAGGTCAAGCAGAGCAGAGAGAGATTAAGTGGCGCACTCCGGTGGCATCCTGCAT 520
DB 62143 TTAGGTCAAGCAGAGCAGAGAGAGATTAAGTGGCGCACTCCGGTGGCATCCTGCAT 62202
QY 521 CCTGAGAGACAGACCTTGTGAAGTCAGAGCTGTACACATTGAATCTCAAGTCAGAGCTTC 580
DB 62203 CCTGAGAGACAGACCTTGTGAAGTCAGAGCTGTACACATTGAATCTCAAGTCAGAGCTTC 62262
QY 581 TGAATTCGATGATTCAGAGAAAGATTTCTGAGCTTTGAAGCAAAATGCAGTGAACA 640
DB 62263 TGAATTCGATGATTCAGAGAAAGATTTCTGAGCTTTGAAGCAAAATGCAGTGAACA 62322
QY 641 GCAACCAATCCAAATGTGTAATGAAGACTTGTGAGCTCACTTACCCGTTGGTACCCC 700
DB 62323 GCAACCAATCCAAATGTGTAATGAAGACTTGTGAGCTCACTTACCCGTTGGTACCCC 62382
QY 701 CACTCTCACAAGCCTCTCTGAATATTCCTGTGTTACCCCGAATATTTACAGGTATC 760
DB 62383 CACTCTCACAAGCCTCTCTGAATATTCCTGTGTTACCCCGAATATTTACAGGTATC 62442
QY 761 TGCAGAGTCTCTTGGCCAG 781
DB 62443 TGCAGAGTCTCTTGGCCAG 62463

RESULT 15

AC091945 177596 bp DNA linear HTG 09-JUN-2001
LOCUS Homo sapiens chromosome 5 clone RP11-35616, WORKING DRAFT SEQUENCE,
DEFINITION 27 unordered pieces.
AC091945
AC091945.1 GI:14333881
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 177596)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE DOB Joint Genome Institute.
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 177596)
REFERENCE DOB Joint Genome Institute.
TITLE Direct Submission.
JOURNAL Submitted (09-JUN-2001) Production Sequencing Facility, DOB Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

Project Information
Center Project Name: 543267
Center clone name: RP11-35616

Summary Statistics
Consensus quality: 152700 bases at least Q40
Consensus quality: 168451 bases at least Q30
Consensus quality: 170419 bases at least Q20
Estimated insert size: 226080; agarose-fp estimation
Estimated insert size: 174996; sum-of-contigs estimation
Quality coverage: 7.75 in Q20 bases; agarose-fp estimation
Quality coverage: 10.01 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 27 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1207: contig of 1207 bp in length
1208 1307: gap of unknown length
1308 3385: contig of 2078 bp in length
3386 3485: gap of unknown length
3486 5553: contig of 2068 bp in length
5554 5653: gap of unknown length
5654 7030: contig of 1377 bp in length
7031 7130: gap of unknown length
7131 9069: contig of 1939 bp in length
9070 9169: gap of unknown length
9170 11452: contig of 2283 bp in length
11453 11552: gap of unknown length
11553 16002: contig of 4450 bp in length
16003 16102: gap of unknown length
16103 21083: contig of 4981 bp in length
21084 21884: gap of unknown length
21884 26893: contig of 5710 bp in length
26894 26993: gap of unknown length
26993 29987: contig of 2994 bp in length
29988 30088: gap of unknown length
30088 32949: contig of 2862 bp in length
32950 33049: gap of unknown length
33050 38757: contig of 5708 bp in length
38758 38857: gap of unknown length
38858 45202: contig of 6345 bp in length
45203 45302: gap of unknown length
45303 50911: contig of 5609 bp in length
50912 51011: gap of unknown length
51012 55880: contig of 4865 bp in length
55881 55980: gap of unknown length
55981 63189: contig of 7209 bp in length
63190 63289: gap of unknown length
63290 69632: contig of 6343 bp in length
69633 69732: gap of unknown length
69733 76373: contig of 6645 bp in length
76374 76477: gap of unknown length
76478 83051: contig of 6574 bp in length
83052 83151: gap of unknown length
83152 94929: contig of 11778 bp in length
94930 95029: gap of unknown length
95030 104346: contig of 9317 bp in length
104347 104446: gap of unknown length
104447 115275: contig of 10829 bp in length
115276 115375: gap of unknown length
115376 123488: contig of 8113 bp in length
123489 123588: gap of unknown length
123589 133172: contig of 9584 bp in length
133173 133272: gap of unknown length
133273 145495: contig of 12223 bp in length
145496 145595: gap of unknown length
145596 160270: contig of 14675 bp in length
160271 160370: gap of unknown length
160371 177596: contig of 17226 bp in length.

FEATURES

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/mol_type="genomic DNA"
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/chromosome="5"
/clone="RP11-35616"
/clone_lib="RP11 human BAC library 11"

ORIGIN

Query Match 13.3%; Score 279; DB 2; Length 177596;
Best Local Similarity 99.5%; Pred. No. 1.1e-140;

Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTGAAGCTTGTGGTGGAGCGGTGATGTTGGAAGCTTGGGCGAGCCCTCAGAAAGCAT 460
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Db 83524 GTTGAAGCTTGTGGTGGAGCGGTGATGTTGGAAGCTTGGGCGAGCCCTCAGAAAGCAT 83583
|||
QY 461 TTAGGTCAAGCAGAGGACAAAGAGATTAAGTGGCGCACTCCCGGTGGCATCACTGCAT 520
|||
Db 83584 TTAGGTCAAGCAGAGGACAAAGAGATTAAGTGGCGCACTCCCGGTGGCATCACTGCAT 83643
|||
QY 521 CCTGAGAGCAGACCTTGTGAAGTCAGAGCTGCTACACTTGAATCTCAAGTCAGCTTC 580
|||
Db 83644 CCTGAGAGCAGACCTTGTGAAGTCAGAGCTGCTACACTTGAATCTCAAGTCAGCTTC 83703
|||
QY 581 TGAGATTGATGATTCAGAGAGAAAGATTCAGAGCTTTTGAAGCAAAATGAGTGAACA 640
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Db 83704 TGAGATTGATGATTCAGAGAGAAAGATTCAGAGCTTTTGAAGCAAAATGAGTGAACA 83763
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Db 83824 CACTTCACAGGCTCTCTGAATATTCCTGTTTACCCCGAATATTTACAGGTACATC 83883
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QY 761 TGCAGAGTCTCTTGGCCAGG 781
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Db 83884 TGCAGAGTCTCTTGGCCAGG 83904
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Search completed: August 27, 2005, 09:38:56
Job time : 6010.21 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 13:32:20 ; Search time 733.49 Seconds
(without alignments)
16924.161 Million cell updates/sec

Title: US-09-371-347A-43

Perfect score: 2097
Sequence: 1 atgagagaggttcctgctact.....ttcagatatttgctcataa 2097

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn19808:*
2: geneseqn19908:*
3: geneseqn20008:*
4: geneseqn20018:*
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10: geneseqn20038:*
11: geneseqn20038:*
12: geneseqn20048:*
13: geneseqn20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2094	99.9	2094	11	Adm43212 Human met
2	2046	97.6	3259	5	Aa65070 DNA encod
3	2046	97.6	3259	5	Aa65070 DNA encod
4	2046	97.6	3259	11	Adm43206 Human ech
5	2043	97.4	2094	11	Adm43208 Human wil
6	1992	95.0	2094	11	Adm43209 Human met
7	1944	92.7	3259	3	Aa58935 DNA encod
8	1893	90.3	3270	13	Adm87538 Human tum
9	1800	85.8	2091	11	Adm43216 Human met
10	1800	85.8	2091	11	Adm43216 Human met
11	1701	81.1	3256	3	Aa58977 A human m
12	1640	78.2	3256	3	Aa58976 A human m
13	1018	48.5	3256	13	Adm39029 Human SNP
14	1018	48.5	3274	13	Adm39030 Human SNP
15	905	43.2	3189	4	Adm42470 Human dia
16	805	38.4	1986	4	Aa541064 cDNA enco
17	427	20.4	1663	4	Aa541602 cDNA enco
18	386	18.4	390	2	Aa541820 Human sec
19	330	15.7	591	12	Adm73174 Human gen
20	328	15.6	379	12	Adm86905 Human gen

21	279	13.3	591	12	Adm86540 Human gen
22	277	13.2	379	12	Adm82240 Human gen
23	225	10.7	503	5	Aa65069 DNA encod
24	188	9.0	525	12	Adm67438 Human gen
25	175	8.3	175	12	Adm81143 Human gen
26	158	7.5	2475	6	Adm32365 Human lun
27	158	7.5	2475	13	Adm161720 Human CDN
28	137	6.5	525	12	Adm73117 Human gen
29	124	5.9	175	12	Adm86848 Human gen
30	124	5.9	244	3	Aa42736 Human 5'
31	69	2.9	60	6	Adm36264 Human sp1
32	51	2.4	51	4	Adm178548 Human s11
33	30	1.4	1681	11	Adm131127 Human CDN
34	27	1.3	1835	5	Aa65071 DNA encod
35	26	1.2	26	3	Aa58955 PCR prime
36	26	1.2	26	3	Aa58939 PCR prime
37	26	1.2	26	6	Adm09549 Arteriosc
38	26	1.2	26	6	Adm43713 Pregestat
39	26	1.2	26	11	Adm43205 Human met
40	26	1.2	26	11	Adm43189 Human met
41	25	1.2	25	3	Aa58952 PCR prime
42	25	1.2	25	3	Aa58937 PCR prime
43	25	1.2	25	3	Aa58947 PCR prime
44	25	1.2	25	11	Adm43187 Human met
45	25	1.2	25	11	Adm43202 Human met

ALIGNMENTS

RESULT 1	ADm43212	ADm43212 standard; cDNA; 2094 BP.
ID	ADm43212	ADm43212 standard; cDNA; 2094 BP.
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AC	ADm43212	
XX	ADm43212	
DT	03-JUN-2004	(first entry)
XX		
DE	Human methionine synthase reductase CDS G110A variant.	
XX		
KW	Human; ss; Methionine synthase reductase polypeptide; HsMTRR; cancer;	
KW	cardiovascular disease; neural tube defect; hyperhomocysteinemia;	
KW	chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.	
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OS	Homo sapiens.	
XX		
EH	Key	Location/Qualifiers
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FT		/product= "HsMTRR"
FT		/partial
FT		/note= "No stop codon shown"
FT	variation	replace(66, A)
FT		/*tag= b
FT		/standard_name= "Single_nucleotide_polymorphism"
FT	variation	replace(110, G)
FT		/*tag= c
FT		/standard_name= "Single_nucleotide_polymorphism"
XX		
PN	US2003082676-A1.	
XX		
PD	01-MAY-2003.	
XX		
XX	10-AUG-1999;	99US-00371347.
XX		
PR	16-JAN-1998;	98US-0071622P.
XX		
PR	15-JAN-1999;	99US-00232028.
XX		
PA	(GRAY/) GRAVEL R. A.	
PA	(ROZE/) ROZEN R.	
PA	(LECL/) LECLERC D.	
PA	(WILS/) WILSON A.	
PA	(ROSE/) ROSENBLATT D.	

XX Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
PI MPI: 2003-57610/54.
XX P-PSDB; ADM43213.
XX
XX New substantially pure nucleic acid encoding a mammalian methionine
PT synthase reductase polypeptide, useful for diagnosing, preventing or
PT treating conditions associated with altered methionine synthase activity,
PT e.g. cancer.
XX
XX
XX Disclosure; SEQ ID NO 43; 26pp; English.

XX The invention relates to a substantially pure nucleic acid that encodes a
CC mammalian methionine synthase reductase polypeptide, hMTFR, or that
CC hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
CC ADM43209. Also included are a non-human animal where one or both genetic
CC alleles encoding the methionine synthase reductase polypeptide are
CC mutated, an antibody that specifically binds the above methionine
CC synthase reductase polypeptide, a method of detecting the presence of the
CC above polypeptide, a method for detecting sequence variants for
CC methionine synthase reductase in a mammal, methods of treating or
CC preventing cancer (or cardiovascular disease or neural tube defects) in a
CC subject, methods of screening for a compound that modulates methionine
CC synthase reductase biological activity and a method for detecting an
CC increased risk of developing a neural tube defect in a mammalian embryo
CC or foetus. The nucleic acid is useful in diagnosing, preventing or
CC treating conditions associated with altered methionine synthase activity,
CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are
CC also associated with hyperhomocysteinaemia. The gene for hMTFR is
CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
CC sequence of a variant human hMTFR cDNA.
XX

XX Sequence 2094 BP; 592 A; 489 C; 480 G; 533 T; 0 U; 0 Other;

Query Match 99.9%; Score 2094; DB 11; Length 2094;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2094; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGGTTCTGTTACTATATGCTACACAGAGGAGACAGGAAAGGCATCGCGAA 60
DB 1 ATGAGAGGTTCTGTTACTATATGCTACACAGAGGAGACAGGAAAGGCATCGCGAA 60
QY 61 GAATGTGTAGCAAGCTGTGTATCATGATTTCTGCAGATCTTCACTATATTAGTAA 120
DB 61 GAATGTGTAGCAAGCTGTGTATCATGATTTCTGCAGATCTTCACTATATTAGTAA 120
QY 121 TCCGATTAAGTATGACTTAATAAACCAGAAACAGCTCTCTGTTGTGTGTTTCTACACG 180
DB 121 TCCGATTAAGTATGACTTAATAAACCAGAAACAGCTCTCTGTTGTGTGTTTCTACACG 180
QY 181 GGACCCGGAGACCAACCCGACACAGCCCGGAAAGTTTAAAGAAATACAGAACCAACA 240
DB 181 GGACCCGGAGACCAACCCGACACAGCCCGGAAAGTTTAAAGAAATACAGAACCAACA 240
QY 241 CTGCGGTTGATTTCTTGTCTCACTCGGTATGGTTACTCGGTTCTCGGTGATTCAGAA 300
DB 241 CTGCGGTTGATTTCTTGTCTCACTCGGTATGGTTACTCGGTTCTCGGTGATTCAGAA 300
QY 301 TACACCTACTTTTTCGAAATGGGGGAGATTAATTGATAACGACTTCAAGAGCTTGAAGC 360
DB 301 TACACCTACTTTTTCGAAATGGGGGAGATTAATTGATAACGACTTCAAGAGCTTGAAGC 360
QY 361 CGGATTTCTATGACATGACATGACATGACATGACATGACATGACATGACATGACATGAC 420
DB 361 CGGATTTCTATGACATGACATGACATGACATGACATGACATGACATGACATGACATGAC 420
QY 421 CCGTGATTCGTGAGCTCTGGCAGCCCTCAGAAAGATTTTATAGTCAAGAGAGACAA 480
DB 421 CCGTGATTCGTGAGCTCTGGCAGCCCTCAGAAAGATTTTATAGTCAAGAGAGACAA 480

QY 481 GAGAGATTAAGTGGCGCACTCCCGTGGCATCACTGATCTCTTGAGACAGACTTTG 540
DB 481 GAGAGATTAAGTGGCGCACTCCCGTGGCATCACTGATCTCTTGAGACAGACTTTG 540
QY 541 AAGTCAGCTGTATACATTAATGAAATCTCAAGTCAAGTCTGATTCATGATTCAGGA 600
DB 541 AAGTCAGCTGTATACATTAATGAAATCTCAAGTCAAGTCTGATTCATGATTCAGGA 600
QY 601 AGAAGATTCGTAGGTTTGAAGCAAAATGCAAGTCAAGCAACCAATCCATGTTGTA 660
DB 601 AGAAGATTCGTAGGTTTGAAGCAAAATGCAAGTCAAGCAACCAATCCATGTTGTA 660
QY 661 ATTGAAGACTTGAAGTCTTCACTTACCCGTTGGTATCCCACTCTCAAGCTCTCTG 720
DB 661 ATTGAAGACTTGAAGTCTTCACTTACCCGTTGGTATCCCACTCTCTCAAGCTCTCTG 720
QY 721 AATATCTGTTTACCCCAAGATTTTAACAGTATCTGCAAGAGTCTCTGGCCAG 780
DB 721 AATATCTGTTTACCCCAAGATTTTAACAGTATCTGCAAGAGTCTCTGGCCAG 780
QY 781 GAGAAAGCCAGTATCTGTGACTTCAAGATCCAGATCCAGTTTTCAGTGCATTTCAAG 840
DB 781 GAGAAAGCCAGTATCTGTGACTTCAAGATCCAGATCCAGTTTTCAGTGCATTTCAAG 840
QY 841 GCAGTTCAATTCTATCAAGATGATGCAATTAACCACTCTGCTGATGATTTGACATT 900
DB 841 GCAGTTCAATTCTATCAAGATGATGCAATTAACCACTCTGCTGATGATTTGACATT 900
QY 901 TCAATTAACAGCTTTTCTATCAAGCTGAGATGCTTCAAGCTGATGCTTCAAGT 960
DB 901 TCAATTAACAGCTTTTCTATCAAGCTGAGATGCTTCAAGCTGATGCTTCAAGT 960
QY 961 GATTCTGAGTCAAGACCTTACTCAAGATCTGACAGCTTGAAGATTAAGAGACACTGC 1020
DB 961 GATTCTGAGTCAAGACCTTACTCAAGATCTGACAGCTTGAAGATTAAGAGACACTGC 1020
QY 1021 GTCTTTTGAATTAAGGACACACAAAGAAAGAGACTTCTTATCCCGCATATA 1080
DB 1021 GTCTTTTGAATTAAGGACACACAAAGAAAGAGACTTCTTATCCCGCATATA 1080
QY 1081 CCGTGGGATGTTCTCTCCAGTCAATTTTACCTGAGTCTTGAATTCGAGCAATTCCT 1140
DB 1081 CCGTGGGATGTTCTCTCCAGTCAATTTTACCTGAGTCTTGAATTCGAGCAATTCCT 1140
QY 1141 AAAAAGCAATTTTGGAGACCTTGTGACTATACAGTACAGTGTGTAAGGCGCAG 1200
DB 1141 AAAAAGCAATTTTGGAGACCTTGTGACTATACAGTACAGTGTGTAAGGCGCAG 1200
QY 1201 CTACAGAGCTGTGCACTTAACAAAGGAGACCGGATTAATGCGCTTTGTACAGATGCC 1260
DB 1201 CTACAGAGCTGTGCACTTAACAAAGGAGACCGGATTAATGCGCTTTGTACAGATGCC 1260
QY 1261 TGTGCTGCTGTGTGATCTCTCTGCTGCTTCTTCTTCCCTTTCGACGACCACTCACTC 1320
DB 1261 TGTGCTGCTGTGTGATCTCTCTGCTGCTTCTTCTTCCCTTTCGACGACCACTCACTC 1320
QY 1321 CTGCTGAAATCTTCTTAACTTCAACCCAGACATATTCGTGTCAGACTCAAGTTTA 1380
DB 1321 CTGCTGAAATCTTCTTAACTTCAACCCAGACATATTCGTGTCAGACTCAAGTTTA 1380
QY 1381 TTTTCAACCAAGAAAGCTCAATTTTGTCTTCAATTTGTGAATTTCTGTACTGACACA 1440
DB 1381 TTTTCAACCAAGAAAGCTCAATTTTGTCTTCAATTTGTGAATTTCTGTACTGACACA 1440
QY 1441 ACAGAGTTCTGGAAGGAGATGATGACAGCTGAGCTGTTGTGTTGTTGCTCAGTT 1500
DB 1441 ACAGAGTTCTGGAAGGAGATGATGACAGCTGAGCTGTTGTGTTGTTGCTCAGTT 1500
QY 1501 CTTCAAGCAAACTATCATGATCCATGAAAGCAGGCGGAAAGCCCTGCTCTTAAGATA 1560
DB 1501 CTTCAAGCAAACTATCATGATCCATGAAAGCAGGCGGAAAGCCCTGCTCTTAAGATA 1560
QY 1561 TCCATCTCTCTGAAACAATAATCTTTCACCTTACAGATGACCCCTCAATCCCATC 1620

DB 1561 TCATCTCTCTGGAACAACAAATTCCTTCACTTACAGATGACCCCTCAATCCCCTC 1620
QY 1621 ATTAATGTGGTCCAGAAACCGGCATAGCCCTTTATTTGGTCTTACAACTAAGAG 1680
DB 1621 ATTAATGTGGTCCAGAAACCGGCATAGCCCTTTATTTGGTCTTACAACTAAGAG 1680
QY 1681 AAATCTCAAGAACCAACCAAGATGGAATTTTGGAGCATGTGTTGTTTGGCTGC 1740
DB 1681 AAATCTCAAGAACCAACCAAGATGGAATTTTGGAGCATGTGTTGTTTGGCTGC 1740
QY 1741 AGGCATTAAGATTAAGGATTAATCTATTCAGAAAAGCTCAGACATTTCTTAAGCATG 1800
DB 1741 AGGCATTAAGATTAAGGATTAATCTATTCAGAAAAGCTCAGACATTTCTTAAGCATG 1800
QY 1801 ATCTTAATCATCTTAAGGTTTCTTCTCAAGAGATGCTCTTGGGAGAGAGAGCC 1860
DB 1801 ATCTTAATCATCTTAAGGTTTCTTCTCAAGAGATGCTCTTGGGAGAGAGAGCC 1860
QY 1861 CCAAGCAAGATGATGTAACAAGCAATCCAGCTTCATGGCCAGAGGTTGGAGATCTTC 1920
DB 1861 CCAAGCAAGATGATGTAACAAGCAATCCAGCTTCATGGCCAGAGGTTGGAGATCTTC 1920
QY 1921 CTCGAGAGAACCGCCATATTTATGTGTGTGAGATGCAAAAGATATGGCCAGATGTA 1980
DB 1921 CTCGAGAGAACCGCCATATTTATGTGTGTGAGATGCAAAAGATATGGCCAGATGTA 1980
QY 1981 CATGATGCTCTTGTGCAATATTAAGCAAAAGCTTGGAGTTGAAAACTAAGCATG 2040
DB 1981 CATGATGCTCTTGTGCAATATTAAGCAAAAGCTTGGAGTTGAAAACTAAGCATG 2040
QY 2041 AAAACCTGGCCCTTTAAAGAAAGAAAAGCTACCTTCAGGATTTTGGTCA 2094
DB 2041 AAAACCTGGCCCTTTAAAGAAAGAAAAGCTACCTTCAGGATTTTGGTCA 2094

RESULT 2
AAS65070
AAS65070 standard; cDNA; 3259 BP.
XX
AC AAS65070;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #874.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001MO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX
PA (HYSB-) HYSBQ INC.
XX
PI Dmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX P-PSDB; ABG00883.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 874; 103pp; English.

XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostic as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 3259 BP; 944 A; 695 C; 674 G; 946 T; 0 U; 0 Other;

Query Match 97.6%; Score 2046; DB 5; Length 3259;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2086; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGAGAGTTCTCTTATATATGCTTACACAGCAGGAGCAAGGCAAGCCATGAGAA 60
DB 80 ATGAGAGAGTTCTCTTATATATGCTTACACAGCAGGAGCAAGGCAAGCCATGAGAA 139
QY 61 GAAATGTGAGCAAGCTGTGTACATGATTTTTCGAGATTTTCACTATATATGAA 120
DB 140 GAAATGTGAGCAAGCTGTGTACATGATTTTTCGAGATTTTCACTATATATGAA 199
QY 121 TCGATATATGATGACCTTAAACCCGAAACAGCTCTCTTGTGTGTTGCTTACACG 180
DB 200 TCGATATATGATGACCTTAAACCCGAAACAGCTCTCTTGTGTGTTGCTTACACG 259
QY 181 GGCACCGAGAGCCCAACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAAACA 240
DB 260 GGCACCGAGAGCCCAACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAAACA 319
QY 241 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGAGTTTCTGCTGATTTCAAG 300
DB 320 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGAGTTTCTGCTGATTTCAAG 379
QY 301 TACACCTACTTTTGGCAATGGGGGGAATATGATTAACGACTTCAAGGCTTGAAGCC 360
DB 380 TACACCTACTTTTGGCAATGGGGGGAATATGATTAACGACTTCAAGGCTTGAAGCC 439
QY 361 CGGCATTTCTATGACACTGACATGAGATGACTGTAGTTTAAACTTGTGTGAG 420
DB 440 CGGCATTTCTATGACACTGACATGAGATGACTGTAGTTTAAACTTGTGTGAG 499
QY 421 CCGTGATTTCTGAGACTTGGCCAGCTCTCAGAAAGCATTTTNGTCAAGAGAGCAA 480
DB 500 CCGTGATTTCTGAGACTTGGCCAGCTCTCAGAAAGCATTTTNGTCAAGAGAGCAA 559
QY 481 GAGGATATAGTGGCCACTCCCGGTGGATCACTGCAATCTTGAAGAGACAGCTTGTG 540
DB 560 GAGGATATAGTGGCCACTCCCGGTGGATCACTGCAATCTTGAAGAGACAGCTTGTG 619
QY 541 AAGTCAGAGCTGCTACATTAATCTCAAGTCAAGCTTCTGAGATTCAGATTCAGGA 600
DB 620 AAGTCAGAGCTGCTACATTAATCTCAAGTCAAGCTTCTGAGATTCAGATTCAGGA 679
QY 601 AGAAAGATTTCTGAGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCATGTTGTA 660
DB 680 AGAAAGATTTCTGAGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCATGTTGTA 739

QY 661 ATTGAAGCTTTGAGTCTCACTTACCCGTTCCGTAACCCCACTCTCAAGCCTCTCTG 720
 Db 740 ATTGAAGCTTTGAGTCTCACTTACCCGTTCCGTAACCCCACTCTCTCAAGCCTCTCTG 799
 QY 721 AATATTCCTGGTTAATCCCGAGATATTTACAGTACATCTGACGAGAGTCTCTTGGCAG 780
 Db 800 AATATTCCTGGTTAATCCCGAGATATTTACAGTACATCTGACGAGAGTCTCTTGGCAG 859
 QY 781 GAGAAAGCCAGATATCTGACTTCAGAGATCCAGTCTTTCAGAGTCCCAATTTCAAG 840
 Db 860 GAGAAAGCCAGATATCTGACTTCAGAGATCCAGTCTTTCAGAGTCCCAATTTCAAG 919
 QY 841 GCAGTTCAATTTACTAGATGATGCAATTAACCACTCTGCTGGTAATTTGACAT 900
 Db 920 GCAGTTCAATTTACTAGATGATGCAATTAACCACTCTGCTGGTAATTTGACAT 979
 QY 901 TCAATTCAGACTTTCTCTACAGCTGAGATGCTTACGCGTATCTGCTCCCAAGT 960
 Db 980 TCAATTCAGACTTTCTCTACAGCTGAGATGCTTACGCGTATCTGCTCCCAAGT 1039
 QY 961 GATTTGAGGTACAAAGCCTTCTCAAGACCTGACGCTTGAAGTAAAGAGACACTGC 1020
 Db 1040 GATTTGAGGTACAAAGCCTTCTCAAGACCTGACGCTTGAAGTAAAGAGACACTGC 1099
 QY 1021 GTCTTTGAAATTAAGGAGACACAAAGAAAGAGACTTACCTTACCCAGCATATA 1080
 Db 1100 GTCTTTGAAATTAAGGAGACACAAAGAAAGAGACTTACCTTACCCAGCATATA 1159
 QY 1081 CTTGCGGGAGTGTCTCTCCAGTTCATTTTACCGGTGTCTGAAATCCGAGCAATTCCT 1140
 Db 1160 CTTGCGGGAGTGTCTCTCCAGTTCATTTTACCGGTGTCTGAAATCCGAGCAATTCCT 1219
 QY 1141 AAAAAGCATTTTTCGAGCCCTTGTGACTATACAGTACAGTGTCTGAAAAGCGCAG 1200
 Db 1220 AAAAAGCATTTTTCGAGCCCTTGTGACTATACAGTACAGTGTCTGAAAAGCGCAG 1279
 QY 1201 CTACAGAGCTGTGACATTAACAAGGGGCGAGCGATTAATGACCGCTTTTACAGATGCC 1260
 Db 1280 CTACAGAGCTGTGACATTAACAAGGGGCGAGCGATTAATGACCGCTTTTACAGATGCC 1339
 QY 1261 TGTGCTGCTGTGTGATCTCTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
 Db 1340 TGTGCTGCTGTGTGATCT 1399
 QY 1321 CTGCTGACATCTTCTTAACTTCAACCCAGACCATATTCGTGTGACAGCTCAAGTTTA 1380
 Db 1400 CTGCTGACATCTTCTTAACTTCAACCCAGACCATATTCGTGTGACAGCTCAAGTTTA 1459
 QY 1381 TTTTACCCAGAAAGCTTCCATTTTGTCTTCAACCTTGTGAAATTTCTGTCTACCTGCCACA 1440
 Db 1460 TTTTACCCAGAAAGCTTCCATTTTGTCTTCAACCTTGTGAAATTTCTGTCTACCTGCCACA 1519
 QY 1441 ACAGAGGTTCTGCGGAGGAGTATGTACAGGCTGCGGCTTGTGTTGTTGCTTCAAGT 1500
 Db 1520 ACAGAGGTTCTGCGGAGGAGTATGTACAGGCTGCGGCTTGTGTTGTTGCTTCAAGT 1579
 QY 1501 CTTTACGCAACATATCATGATCCCATGAAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
 Db 1580 CTTTACGCAACATATCATGATCCCATGAAGACGCGGAAAGCCCTGCTCTTAAGATA 1639
 QY 1561 TCCATCTCTCTCTGAAACAAATTTCTTTCATCTTACCATGATGACCCCTCATCTCCATC 1620
 Db 1640 TCCATCTCTCTCTGAAACAAATTTCTTTCATCTTACCATGATGACCCCTCATCTCCATC 1699
 QY 1621 ATATATGTTGGTTCAGAGACCGGATGACCCCGTTTATTTGGGTCTTACAAATAGAGAG 1680
 Db 1700 ATATATGTTGGTTCAGAGACCGGATGACCCCGTTTATTTGGGTCTTACAAATAGAGAG 1759
 QY 1681 AAATCTCAAGAAACAACCCAGATGAAATTTTGAACAAATGTGTGTTTGTGCTGC 1740
 Db 1760 AAATCTCAAGAAACAACCCAGATGAAATTTTGAACAAATGTGTGTTTGTGCTGC 1819
 QY 1741 AGGCAATAGATAGGATATCTATTCAAGAAAGAGCTCAGACATTTCTTAAGCATGG 1800

Db 1820 AGGCAATAGATAGGATATCTATTCAAGAAAGAGCTCAGACATTTCTTAAGCATGG 1879
 QY 1801 ATCTTAATCATCTTAAAGGTTTCTTCTCAGAGATGCTCTGTTGGGAGAGAAAGCC 1860
 Db 1880 ATCTTAATCATCTTAAAGGTTTCTTCTCAGAGATGCTCTGTTGGGAGAGAAAGCC 1939
 QY 1861 CCAGCAAGATATGTACAAACAATCCAGCTTATGCGCAGAGAGTGGCAGATCTTC 1920
 Db 1940 CCAGCAAGATATGTACAAACAATCCAGCTTATGCGCAGAGAGTGGCAGATCTTC 1999
 QY 1921 CTCACAGAGAGGCGCATTTATGTGTGTGAGATGCAAGAAATATGGCCAGATGTA 1980
 Db 2000 CTCACAGAGAGGCGCATTTATGTGTGTGAGATGCAAGAAATATGGCCAGATGTA 2059
 QY 1981 CATGATGCTCTGTGCAATTAATTAACCAAGAGTGTGAGTTGAAAACTAGAACAAATG 2040
 Db 2060 CATGATGCTCTGTGCAATTAATTAACCAAGAGTGTGAGTTGAAAACTAGAACAAATG 2119
 QY 2041 AAAACCTTGCCACTTTAAAGAAAGAAACCGTACCTTCAGATATTTGTCTATA 2097
 Db 2120 AAAACCTTGCCACTTTAAAGAAAGAAACCGTACCTTCAGATATTTGTCTATA 2176

RESULT 3
 AAC91226
 ID AAC91226 standard; DNA; 3259 BP.
 XX AAC91226;
 AC 20-MAR-2001 (first entry)
 DT 20-MAR-2001 (first entry)
 XX
 XX Human schizophrenia related gene SEQ ID NO: 23.
 DE
 XX Human; schizophrenia; developmental disorder; spina bifida cystica;
 KM Tourette's syndrome; bipolar illness; autism; conduct disorder;
 KM attention deficit disorder; obsessive compulsive disorder;
 KM chronic multiple tic syndrome; learning disorder; polymorphism; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0200071754-A1.
 XX
 PD 30-NOV-2000.
 XX
 XX 24-MAY-2000; 2000MO-US014354.
 PF
 XX 25-MAY-1999; 99US-00318448.
 PR
 XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
 PA
 XX Johnson WG, Stenroos ES;
 PI
 XX
 XX WPI; 2001-025174/03.
 DR
 XX
 XX Diagnosing a developmental disorder, e.g. schizophrenia, by forming
 PT datasets (DS) of genetic (e.g. genotypes of folate metabolism alleles)
 PT and environmental variables affecting an individual and then comparing
 PT these DS with reference DS.
 PT
 XX
 XX Disclosure; Page 142-143; 156pp; English.
 PS
 XX The present invention provides a novel method of estimating the
 CC susceptibility of an individual to a developmental disorder using genetic
 CC and environmental variables. The method can be used in the diagnosis,
 CC prevention and treatment of disorders such as schizophrenia, spina bifida
 CC cystica, Tourette's syndrome, bipolar illness, autism, conduct disorders,
 CC attention deficit disorder, obsessive compulsive disorder, chronic
 CC multiple tic syndrome and learning disorders such as dyslexia
 CC
 XX Sequence 3259 BP; 944 A; 695 C; 674 G; 946 T; 0 U; 0 Other;
 SQ

Query Match 97.6%; Score 2046; DB 5; Length 3259;

ID ADM43206 standard, cDNA, 3259 BP.
XX
XX ADM43206;
XX
DT 03-JUN-2004 (first entry)
XX
XX Human full length cDNA encoding methionine synthase reductase.
XX
XX Human; ss; gene; Methionine synthase reductase polypeptide; HmTRR;
KM cancer; cardiovascular disease; neural tube defect;
KM hyperhomocysteinemia; chromosome 5p15.2-p15.3; SNP;
KM single nucleotide polymorphism.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FH CDS 80..2176
FT /*tag= a
FT /product= "hmTRR"
FT variation replace(145,A)
FT /*tag= b
FT /standard_name= "Single_nucleotide_polymorphism"
FT variation replace(189,A)
FT /*tag= c
FT /standard_name= "Single_nucleotide_polymorphism"
XX US2003082676-A1.
XX 01-MAY-2003.
XX 10-AUG-1999; 99US-00371347.
XX 16-JAN-1998; 98US-0071622P.
XX 15-JAN-1999; 99US-00232028.
XX
XX (GRAV/) GRAVEL R A.
XX (ROZE/) ROZEN R.
XX (LECL/) LECLEERC D.
XX (WILS/) WILSON A.
XX (ROSE/) ROSENBLATT D.
XX
XX Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX
XX WPI, 2003-576610/54.
XX P-PSDB; ADM43207.
XX
XX New substantially pure nucleic acid encoding a mammalian methionine
XX synthase reductase polypeptide, useful for diagnosing, preventing or
XX treating conditions associated with altered methionine synthase activity,
XX e.g. cancer.
XX
XX Example 2; SEQ ID NO 24; 26bp; English.
XX
XX The invention relates to a substantially pure nucleic acid that encodes a
XX mammalian methionine synthase reductase polypeptide, HmTRR, or that
XX hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
XX ADM43209. Also included are a non-human animal where one or both genetic
XX alleles encoding the methionine synthase reductase polypeptide are
XX mutated, an antibody that specifically binds the above methionine
XX synthase reductase polypeptide, a method of detecting the presence of the
XX above polypeptide, a method for detecting sequence variants for
XX methionine synthase reductase in a mammal, methods of treating or
XX preventing cancer (or cardiovascular disease or neural tube defects) in a
XX subject, methods of screening for a compound that modulates methionine
XX synthase reductase biological activity and a method for detecting an
XX increased risk of developing a neural tube defect in a mammalian embryo
XX or foetus. The nucleic acid is useful in diagnosing, preventing or
XX treating conditions associated with altered methionine synthase activity,
XX such as cancer, cardiovascular disease or neural tube defects, or in
XX screening for a compound that modulates methionine synthase reductase
XX biological activity. Naturally occurring variants of the polypeptide are
XX also associated with hyperhomocysteinemia. The gene for HmTRR is
XX located on chromosome 5p15.2-p15.3. The present sequence is full length

CC sequence of the wild-type human hmTRR cDNA.
XX
SQ Sequence 3259 BP; 944 A; 695 C; 674 G; 946 T; 0 U; 0 Other;
Query Match 97.6%; Score 2046; DB 11; Length 3259;
Best Local Similarity 100.0%; Pred No. 0;
Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAGAGGTTCTCTGTTACTATATGCTACACAGCAGGACAGGCAAGCCATCGAGAA 60
DB 80 ATGAGAGGTTCTCTGTTACTATATGCTACACAGCAGGACAGGCAAGCCATCGAGAA 139
QY 61 GAAATGTGAGCAGAGCTGTGTACATGATTTTTCGAGATTTTCACTATATTAATGAA 120
DB 140 GAAATGTGAGCAGAGCTGTGTACATGATTTTTCGAGATTTTCACTATATTAATGAA 199
QY 121 TCCGATTAAGTATGACCTTAATAAACCGAAACAGCTCCTCTGTTGTTGTTCTACACG 180
DB 200 TCCGATTAAGTATGACCTTAATAAACCGAAACAGCTCCTCTGTTGTTGTTCTACACG 259
QY 181 GGCACCGAGACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
DB 260 GGCACCGAGACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 319
QY 241 CTGCGCGTTGATTTCTTTGCTCACTCGCGTATGCGTTACTGCGTCTCGGTATTCAGAA 300
DB 320 CTGCGCGTTGATTTCTTTGCTCACTCGCGTATGCGTTACTGCGTCTCGGTATTCAGAA 379
QY 301 TACACCTACTTTTGGCAATGGGGGAGATTAATGATTAACGACTTCAGAGCTTGGAGCC 360
DB 380 TACACCTACTTTTGGCAATGGGGGAGATTAATGATTAACGACTTCAGAGCTTGGAGCC 439
QY 361 CGGCAATTTCTATGACACTGGACATGCAATGACTGTGTAGTTTGAACCTTGTGTAG 420
DB 440 CGGCAATTTCTATGACACTGGACATGCAATGACTGTGTAGTTTGAACCTTGTGTAG 499
QY 421 CCGTGATTTCTGATCTGTGCGCCAGCCCTCAGAAAGCATTTTATGTCAGAGACAGAA 480
DB 500 CCGTGATTTCTGATCTGTGCGCCAGCCCTCAGAAAGCATTTTATGTCAGAGACAGAA 559
QY 481 GAGAGATTAAGTGGGCGACCTCCGCGGATCACTGATCCTTGAAGGACAGACCTTGTG 540
DB 560 GAGAGATTAAGTGGGCGACCTCCGCGGATCACTGATCCTTGAAGGACAGACCTTGTG 619
QY 541 AAGTCAGAGCTGTACACATTTGATCTCAAGTCAGACCTTCTGAGATTCGATTCAGAA 600
DB 620 AAGTCAGAGCTGTACACATTTGATCTCAAGTCAGACCTTCTGAGATTCGATTCAGAA 679
QY 601 AGAAAGATTTCTGAGTTTGAAGCAAAATGCAGTGAACAGCAACCAATCCAAATGTTGA 660
DB 680 AGAAAGATTTCTGAGTTTGAAGCAAAATGCAGTGAACAGCAACCAATCCAAATGTTGA 739
QY 661 ATGAAGACTTTGAGTCTCACTTACCCGTTCCGTTCCGTTCCGTTCCGTTCCGTTCCG 720
DB 740 ATGAAGACTTTGAGTCTCACTTACCCGTTCCGTTCCGTTCCGTTCCGTTCCGTTCCG 799
QY 721 AATATTCCTGTTTACCCCGCAAAATTTTACAGATCAATTCGAGAGTCTTGGCCAG 780
DB 800 AATATTCCTGTTTACCCCGCAAAATTTTACAGATCAATTCGAGAGTCTTGGCCAG 859
QY 781 GAGAAAGCCCAATATCTGTGACTTCAGCAGATCCAGTTTTCAGTGCCTAATTTCAAG 840
DB 860 GAGAAAGCCCAATATCTGTGACTTCAGCAGATCCAGTTTTCAGTGCCTAATTTCAAG 919
QY 841 GCAGTTCACTTACTCGAATGATGTCATTAATAACCACTCTGCTGGATTAATGACATT 900
DB 920 GCAGTTCACTTACTCGAATGATGTCATTAATAACCACTCTGCTGGATTAATGACATT 979
QY 901 TCAATATCAGACTTTTCTATCAGCCTGAGATGCTTCAAGCCTGATCTGCTCAACAGT 960
DB 980 TCAATATCAGACTTTTCTATCAGCCTGAGATGCTTCAAGCCTGATCTGCTCAACAGT 1039
QY 961 GATTCTGAGTACAAAGCCTTCTCAAAAGACTGACGTTGAAGATTAAGAGAGCACTGC 1020

DB 1040 GATTCGAGGTACAAAGCTTATCCAAAGCTGAGCTTGAGATTAAGAGAGCTGC 1099
1021 GTCTTTTGAATAAAGGACACAAAGAAAGAGCTTACTTACCCAGCATATA 1080
1100 GTCTTTTGAATAAAGGACACAAAGAAAGAGCTTACTTACCCAGCATATA 1159
1081 CCGGGGGAGTGTCTCTCAAGTTCAATTTTACTGAGTCTTGAATCCGAGCAATTCCT 1140
1160 CCGGGGGAGTGTCTCTCAAGTTCAATTTTACTGAGTCTTGAATCCGAGCAATTCCT 1219
1141 AAAAGGCAATTTTGGAGCCCTTGTGACTATACAGTACAGTCTGAAAAAGCCAG 1200
1220 AAAAGGCAATTTTGGAGCCCTTGTGACTATACAGTACAGTCTGAAAAAGCCAG 1279
1201 CTACAGAGCTGTGACGTAAACAGAGGGGACCGGATTAATAGCCGCTTTGTACAGATGCC 1260
1280 CTACAGAGCTGTGACGTAAACAGAGGGGACCGGATTAATAGCCGCTTTGTACAGATGCC 1339
1261 TGTGCTGTGTGTGATCTCTCTCTGCTTCCCTTCCCTTCCAGGACACACTCAGTCTC 1320
1340 TGTGCTGTGTGTGATCTCTCTCTGCTTCCCTTCCCTTCCAGGACACACTCAGTCTC 1399
1321 CTGCTGAAATCTTCTTAACTTCAACCCAGACATATTCGTGTCAAGTCAAGTTTA 1380
1400 CTGCTGAAATCTTCTTAACTTCAACCCAGACATATTCGTGTCAAGTCAAGTTTA 1459
1381 TTTCACCAAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTCTGTCTACGACCA 1440
1460 TTTCACCAAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTCTGTCTACGACCA 1519
1441 ACAGAGTTCTGGGAGAGAGATATGTACAGGCTGGCTGGCTTGTGTGTGTCTTCAAGTT 1500
1520 ACAGAGTTCTGGGAGAGAGATATGTACAGGCTGGCTGGCTTGTGTGTGTCTTCAAGTT 1579
1501 CTTCAGCAAAATATCATGATCCCATGAGACAGGAGGAAAGCCCTGGCTCTTAAGATA 1560
1580 CTTCAGCAAAATATCATGATCCCATGAGACAGGAGGAAAGCCCTGGCTCTTAAGATA 1639
1561 TCCATCTCTCTCTGAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
1640 TCCATCTCTCTCTGAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1699
1621 ATATATGTGGGTTCAGAGAACCCGATAGCCCGTTTATTTGGTCTCTTACAACTAAGAG 1680
1700 ATATATGTGGGTTCAGAGAACCCGATAGCCCGTTTATTTGGTCTCTTACAACTAAGAG 1759
1681 AAATCTCAAGAAACAAACCAAGATGAAATTTTGAAGCAATGTTGTTTTTGGCTGC 1740
1760 AAATCTCAAGAAACAAACCAAGATGAAATTTTGAAGCAATGTTGTTTTTGGCTGC 1819
1741 AGGCATAGAGATAGGATTAATCTTACAGAAAGAGCTCAGATTTCTTAAAGATGG 1800
1820 AGGCATAGAGATAGGATTAATCTTACAGAAAGAGCTCAGATTTCTTAAAGATGG 1879
1801 ATTTTACTCATTTAAAGTTTCTTCTCAAGATGCTCTGTGTGGAGAGAGAGAGCC 1860
1880 ATTTTACTCATTTAAAGTTTCTTCTCAAGATGCTCTGTGTGGAGAGAGAGAGCC 1939
1861 CCAAGCAAGATATACAGACCAATCCAGCTTCAATGAGGACAGAGGAGGAGAAATCTTC 1920
1940 CCAAGCAAGATATACAGACCAATCCAGCTTCAATGAGGACAGAGGAGGAGAAATCTTC 1999
1921 CTTCAGAGAACCGCATATTTATGTGTGTGAGATGCAAGAAATATGCGCAAGATGTA 1980
2000 CTTCAGAGAACCGCATATTTATGTGTGTGAGATGCAAGAAATATGCGCAAGATGTA 2059
1981 CATGATGCTTGTGCAATATATATAGCAAGAGGTTGAGTTGAAAACTAAGAGCAATG 2040
2060 CATGATGCTTGTGCAATATATATAGCAAGAGGTTGAGTTGAAAACTAAGAGCAATG 2119
2041 AAAACCTGGCACTTTAAAGAAAGAAAGCGTACCTTCAAGATTTTGTGATATA 2097

DB 2120 AAAACCTGGCACTTTAAAGAAAGAAAGAAAGCGTACCTTCAAGATATTTGTATATA 2176
RESULT 5
ADM43208
ID ADM43208 standard; cDNA; 2094 BP.
XX
AC ADM43208;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human wild-type methionine synthase reductase CDS.
XX
KW Human; ss; Methionine synthase reductase polypeptide; HsMTRR; cancer;
KW cardiovascular disease; neural tube defect; hyperhomocysteinemia;
KW chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2094
FT /tag= a
FT /product= "HsMTRR"
FT /partial
FT /note= "No stop codon shown"
FT variation replace(66,A)
FT /tag= b
FT /standard_name= "Single_nucleotide_polymorphism"
FT variation replace(110,A)
FT /tag= c
FT /standard_name= "Single_nucleotide_polymorphism"
XX
EN US2003082676-A1.
XX
PD 01-MAY-2003.
XX
PF 10-AUG-1999; 99US-00371347.
XX
PR 16-JAN-1998; 98US-00716222.
PR 15-JAN-1999; 99US-00232028.
XX
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLEERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
XX
PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX
DR WPI, 2003-576610/54.
DR P-PSDB; ADM43207.
XX
PT New substantially pure nucleic acid encoding a mammalian methionine
PT synthase reductase polypeptide, useful for diagnosing, preventing or
PT treating conditions associated with altered methionine synthase activity,
PT e.g. cancer.
XX
PS Claim 3; SEQ ID NO 1; 26pp; English.
XX
XX The invention relates to a substantially pure nucleic acid that encodes a
CC mammalian methionine synthase reductase polypeptide, HsMTRR, or that
CC hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
CC ADM43209. Also included are a non-human animal where one or both genetic
CC alleles encoding the methionine synthase reductase polypeptide are
CC mutated, an antibody that specifically binds the above methionine
CC synthase reductase polypeptide, a method of detecting the presence of the
CC above polypeptide, a method for detecting sequence variants for
CC methionine synthase reductase in a mammal, methods of treating or
CC preventing cancer (or cardiovascular disease or neural tube defects) in a
CC subject, methods of screening for a compound that modulates methionine
CC synthase reductase biological activity and a method for detecting an
CC increased risk of developing a neural tube defect in a mammalian embryo
CC or foetus. The nucleic acid is useful in diagnosing, preventing or

CC treatin conditions associated with altered methionine synthase activity
CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are
CC also associated with hyperhomocysteinemia. The gene for hMTFR is
CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
CC sequence of the wild-type human hMTFR cDNA.

SQ Sequence 2094 BP; 591 A; 489 C; 481 G; 533 T; 0 U; 0 Other;

Query Match	97.4%	Score 2043	DB 11	Length 2094
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2093	Conservative 0	Mismatches 1	Indels 0	Gaps 0

QY	1	TTGAGAGAGTTCTCTGTACTATATATCTTACACAGCAGAGGGACAGGCAAAAGGCATATGCAGAA	60
Db	1	ATGAGAGAGTTCTCTTACTATATCTTACACAGCAGGAGCAGGCAAAAGGCATATGCAGAA	60
QY	61	GAAATGTGTGAGCAAGCTGTGGTACATGATTTTCTGCAGATCTTCACTAATTAAGTGA	120
Db	61	GAAATGTGTGAGCAAGCTGTGGTACATGATTTTCTGCAGATCTTCACTATTAAGTGA	120
QY	121	TCCGATATGATATGACCTTAATAAACGAAACAGTCCCTCTGTGTGTGTGTCTTACACAG	180
Db	121	TCCGATATGATATGACCTTAATAAACGAAACAGTCCCTCTGTGTGTGTGTCTTACACAG	180
QY	181	GGCACCAGGAGACCCACCCGACACAGCCCGCAGTTTGTTAAGAAATACAGAACCAACA	240
Db	181	GGCACCAGGAGACCCACCCGACACAGCCCGCAGTTTGTTAAGAAATACAGAACCAACA	240
QY	241	CTGCGCGGTGATTTCTTTGTCTCACCTGTGGGTATAGGTTATCTGGGTCTCGGTATTCAGAA	300
Db	241	CTGCGCGGTGATTTCTTTGTCTCACCTGTGGGTATAGGTTATCTGGGTCTCGGTATTCAGAA	300
QY	301	TACACCTTACTTTTGCAATGGGGGAGAAATATGATTAACGACTTCAAGAGCTTGGAGCC	360
Db	301	TACACCTTACTTTTGCAATGGGGGAGAAATATGATTAACGACTTCAAGAGCTTGGAGCC	360
QY	361	CGGCATTTCTATGACACTGAGCATGACAGATGACTGTGTAGTTTGAACCTTGTGTGAG	420
Db	361	CGGCATTTCTATGACACTGAGCATGAGATGACTGTGTAGTTTGAACCTTGTGTGAG	420
QY	421	CCGTGATTTGCTGAGCTCTGGCCAGCCCTCAGAAAAGCAATTTTAGTCAAGCAGAGACAA	480
Db	421	CCGTGATTTGCTGAGCTCTGGCCAGCCCTCAGAAAAGCAATTTTAGTCAAGCAGAGACAA	480
QY	481	GAGAGATTAAGTGGCGCACTCCCGGTGGCATCCTGCATCTTGTAGACAGACCTTGTG	540
Db	481	GAGAGATTAAGTGGCGCACTCCCGGTGGCATCCTGCATCTTGTAGACAGACCTTGTG	540
QY	541	AAGTACAGCTGTACATTTGAATCTCAAGTGCAGCTTCTAGANTTCATGATTCAGGA	600
Db	541	AAGTACAGCTGTACATTTGAATCTCAAGTGCAGCTTCTAGANTTCATGATTCAGGA	600
QY	601	AGAAAGATTTCTGAGGTTTTTGAAGCAAAATGACAGTGAACAGAACCAATCCATGTTGTA	660
Db	601	AGAAAGATTTCTGAGGTTTTTGAAGCAAAATGACAGTGAACAGAACCAATCCATGTTGTA	660
QY	661	ATTGAAAGCTTTGAGTCTCTCACTTACCCGTTGGGTACCCCCACTCTCACAGGCTCTCG	720
Db	661	ATTGAAAGCTTTGAGTCTCTCACTTACCCGTTGGGTACCCCCACTCTCACAGGCTCTCG	720
QY	721	AATATTTCTGTGTTTACCCCCAGAAATTTTACAGGTATCTGACAGGAGTCTTGTGCCAG	780
Db	721	AATATTTCTGTGTTTACCCCCAGAAATTTTACAGGTATCTGACAGGAGTCTTGTGCCAG	780
QY	781	GAGGAAGCCAGTATCTGTGACCTTACAGCAGATCCAGTTTTTCAAGTCCCAATTTCAAG	840
Db	781	GAGGAAGCCAGTATCTGTGACCTTACAGCAGATCCAGTTTTTCAAGTCCCAATTTCAAG	840
QY	841	GCAGTTCAACTATACGAATGATGCAATAAAACAATCTGTGTGATAATTTGCACATT	900
Db	841	GCAGTTCAACTATACGAATGATGCAATAAAACAATCTGTGTGATAATTTGCACATT	900

QY	901	TCGAAATACACACTTTTCTCTATCGCCGAGGAGTGCCTTCAAGCGGATCTGACCTTAAAGT	960
. Db	901	TCGAAATACAGACTTTTCTCTATCGAGCTGGAGATGCTTCAAGCTGATCTGCTTAACGT	960
QY	961	GATTCCTGAGGTACAAAGCCTACTTCCAAAGA CTGCA GCTTGAAGATMAAGAGCACTGC	1020
Db	961	GATTCCTGAGGTACAAAGCCTACTTCCAAAGA CTGCA GCTTGAAGATMAAGAGCACTGC	1020
QY	1021	GTCCTTTTGGAAAATTAAGGCGACACAAAGAAAAGACCTACCTTAACCCCGACATATA	1080
Db	1021	GTCCTTTTGGAAAATTAAGGCGACACAAAGAAAAGACCTACCTTAACCCCGACATATA	1080
QY	1081	CCTGCGGAGATGTCCTCCAGTTCATTTTAACTGAGTGCTTGGAAATCCGAGCAATTCCT	1140
Db	1081	CCTGCGGAGATGTCCTCCAGTTCATTTTAACTGAGTGCTTGGAAATCCGAGCAATTCCT	1140
QY	1141	AAAAAGCAATTTTTCGAGCGCTTGTGGACTATACAGTGA CAGTGTGMAAAGCGCAGG	1200
Db	1141	AAAAAGCAATTTTTCGAGCGCTTGTGGACTATACAGTGA CAGTGTGMAAAGCGCAGG	1200
QY	1201	CTACAGAGAGCTGTCAGTAAACAAAGGGGAGCGCAATATAGCCGCTTTGTACAGAGATGCC	1260
Db	1201	CTACAGAGAGCTGTCAGTAAACAAAGGGGAGCGCAATATAGCCGCTTTGTACAGAGATGCC	1260
QY	1261	TGTCCTGCTTGTGTGATCTCTTCCTGCTTCCCTTCTTGCACAGCCACCACTCA GTCCTC	1320
Db	1261	TGTCCTGCTTGTGTGATCTCTTCCTGCTTCCCTTCTTGCACAGCCACCACTCA GTCCTC	1320
QY	1321	CTGCTGCAACATCTTCCCTTAAACCTTCAACCCAGACATATTCGTGTGCAAGCTCAAGTTTA	1380
Db	1321	CTGCTGCAACATCTTCCCTTAAACCTTCAACCCAGACATATTCGTGTGCAAGCTCAAGTTTA	1380
QY	1381	TTTTCACCCAGGAAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTCTGTCTACCTGCACA	1440
Db	1381	TTTTCACCCAGGAAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTCTGTCTACCTGCACA	1440
QY	1441	ACAGAGGTTCTGCGGAAGGAGATGTATACAGGCTGGCTGGCTTGTGTTGCTTCA GTT	1500
Db	1441	ACAGAGGTTCTGCGGAAGGAGATGTATACAGGCTGGCTGGCTTGTGTTGCTTCA GTT	1500
QY	1501	CTTCAAGCCAAACATACATGCAATCCCATGAAAGACAGCGGAGAAAGCCCTGGCTCTTAAGATA	1560
Db	1501	CTTCAAGCCAAACATACATGCAATCCCATGAAAGACAGCGGAGAAAGCCCTGGCTCTTAAGATA	1560
QY	1561	TCGATCTCTCTCGAACAACAATTCCTTCCACTTACCAAGATGACCCCTCAATCCCATC	1620
Db	1561	TCGATCTCTCTCGAACAACAATTCCTTCCACTTACCAAGATGACCCCTCAATCCCATC	1620
QY	1621	ATAATGTGTGGGTCCAGGAACCGGATAGCCCGCTTATTTGGGTTCTTAACAACATAGAGAG	1680
Db	1621	ATAATGTGTGGGTCCAGGAACCGGATAGCCCGCTTATTTGGGTTCTTAACAACATAGAGAG	1680
QY	1681	AAACTCCAAAGAACAAACCCAGATGAGAAATTTTGGACAAATGTGGTGTGTTTTGGCTGC	1740
Db	1681	AAACTCCAAAGAACAAACCCAGATGAGAAATTTTGGACAAATGTGGTGTGTTTTGGCTGC	1740
QY	1741	AGGCAATAGAGATAGGAGATATCTATTTAGAAAAAAGCTCAGACATTTCTTAAAGCATAGGG	1800
Db	1741	AGGCAATAGAGATAGGAGATATCTATTTAGAAAAAAGCTCAGACATTTCTTAAAGCATAGGG	1800
QY	1801	ATCTTAACTCATCTTAAAGGTTTCTTCTCAAGAGATCTCCTGTGTGGGAGAGAGAAAGCC	1860
Db	1801	ATCTTAACTCATCTTAAAGGTTTCTTCTCAAGAGATCTCCTGTGTGGGAGAGAGAAAGCC	1860
QY	1861	CCAGCAAAAGTATGTACAGAACACATCAGCTTCA TGGCCAGCAGCGTGGCGAGATCTCTC	1920
Db	1861	CCAGCAAAAGTATGTACAGAACACATCAGCTTCA TGGCCAGCAGCGTGGCGAGATCTCTC	1920
QY	1921	CTTCAAGAGAAACGGCCATATTTATGTGTGTGAGATCCAAAGAAATATATGAGCCAAAGATGTA	1980
Db	1921	CTTCAAGAGAAACGGCCATATTTATGTGTGTGAGATCCAAAGAAATATATGAGCCAAAGATGTA	1980

Qy	1981	CATATGCCCTTGGCAATTAATTAAGCAAGAAGGTGGAGTTGAAAACTAGAGCATG	2040
Db	1981	CATGATGCCCTTGTGCAAATATATAGCAAGAGGCTTGAGTTGAAAACTAGAGCATG <td>2040</td>	2040
Oy	2041	AAAACCCCTGGCCACTTTAAAGAGAAAAAGCTACTCTCAGATATTTGGTCA	2094
Db	2041	AAAACCCCTGGCCACTTTAAAGAGAAAAAGCTACTCTCAGATATTTGGTCA	2094
RESULT 6			
ID	ADM43209	standard; cDNA; 2094 BP.	
AC	ADM43209;		
XX			
XX	03-JUN-2004	(first entry)	
XX			
DE	Human methionine synthase reductase CDS G66A variant.		
XX			
KW	Human; 88; Methionine synthase reductase polypeptide; HsMTRR; cancer;		
KW	cardiovascular disease; neural tube defect; hyperhomocysteinemia;		
KW	chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.		
XX			
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
FT	1..2094		
FT	/tag= a		
FT	/product= "hsMTRR"		
FT	/partial		
FT	/note= "No stop codon shown"		
FT	/replace(66,G)		
FT	/*tag= b		
FT	/standard_name= "Single_nucleotide_polymorphism"		
FT	/replace(110,A)		
FT	/*tag= c		
FT	/standard_name= "Single_nucleotide_polymorphism"		
XX			
XX	US2003082676-A1.		
XX			
PD	01-MAY-2003.		
XX			
XX	10-AUG-1999;	99US-00371347.	
XX			
PR	16-JAN-1998;	98US-0071622P.	
PR	15-JAN-1999;	98US-00232028.	
XX			
PA	(GRAV/) GRAVEL R A.		
PA	(ROZE/) ROZEN R.		
PA	(LECL/) LECLEERC D.		
PA	(WILS/) WILSON A.		
PA	(ROSE/) ROSENBLATT D.		
XX			
PI	Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;		
XX			
XX	WPI; 2003-576610/54.		
DR	P-PSDB; ADM43211.		
XX			
PT	New substantially pure nucleic acid encoding a mammalian methionine		
PT	synthase reductase polypeptide, useful for diagnosing, preventing or		
PT	treating conditions associated with altered methionine synthase activity,		
PT	e.g. cancer.		
XX			
XX			
PS	Claim 3; SEQ ID NO 41; 26pp; English.		
XX			
CC	The invention relates to a substantially pure nucleic acid that encodes a		
CC	mammalian methionine synthase reductase polypeptide, HsMTRR, or that		
CC	hybridises at high stringency to a nucleic acid appearing as ADM43208 or		
CC	ADM43209. Also included are a non-human animal where one or both genetic		
CC	alleles encoding the methionine synthase reductase polypeptide are		
CC	mutated, an antibody that specifically binds the above methionine		
CC	synthase reductase polypeptide, a method of detecting the presence of the		
CC	above polypeptide, a method for detecting sequence variants for		

[illegible]

Matches 2094; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
Qy	1	ATGAGGAGGTTCTGTACTATATGCTACAGCAGGAGGACAGGCAAAAGGCATCGAGAA	60	
Db	80	ATGAGGAGGTTCTGTACTATATGCTACAGCAGGAGGACAGGCAAAAGGCATCGAGAA	139	
Qy	61	GAATGTGTAGACAGCTGTGTACATGATTTCTGCAGATCTTCACTATATTAGTAA	120	
Db	140	GAATGTGTAGACAGCTGTGTACATGATTTCTGCAGATCTTCACTATATTAGTAA	199	
Qy	121	TCGGATAGTATGACCTTAAACCGAAACAGCTCTCTTGTGTGTGTGTCTACACG	180	
Db	200	TCGGATAGTATGACCTTAAACCGAAACAGCTCTCTTGTGTGTGTGTCTACACG	259	
Qy	181	GGCACCAGGAGCCACCCGACACAGCCCGCAAGTTGTTAAGAAATPACGAACCAACA	240	
Db	260	GGCACCAGGAGCCACCCGACACAGCCCGCAAGTTGTTAAGAAATPACGAACCAACA	319	
Qy	241	CTGCCGATGATTTCTTGTCTCAGCTGCGGATGAGTTACTGGGTCTCGGTATTCAGAA	300	
Db	320	CTGCCGATGATTTCTTGTCTCAGCTGCGGATGAGTTACTGGGTCTCGGTATTCAGAA	379	
Qy	301	TACACCTACTTTTGAATGAGGAGGAAATATTTGATTAACGACTTCAAGAGCTTGAGCC	360	
Db	380	TACACCTACTTTTGAATGAGGAGGAAATATTTGATTAACGACTTCAAGAGCTTGAGCC	439	
Qy	361	CGGCAATTTCTATGACCTGGAACATGCAATGATGTGTGTGTGTAAACCTTGTGTGTAG	420	
Db	440	CGGCAATTTCTATGACCTGGAACATGCAATGATGTGTGTGTGTAAACCTTGTGTGTAG	499	
Qy	421	CGTGTGATTTGTGACCTGTGCGCAGCCCTCAGAAACATTTTATGATCAAGACAGACAA	480	
Db	500	CGTGTGATTTGTGACCTGTGCGCAGCCCTCAGAAACATTTTATGATCAAGACAGACAA	559	
Qy	481	GAGGAGATTAAGTGGGCACTCCCGGTGGCATCCTGTACCTTGTAGAGACAGCCTTGTG	540	
Db	560	GAGGAGATTAAGTGGGCACTCCCGGTGGCATCCTGTACCTTGTAGAGACAGCCTTGTG	619	
Qy	541	AAGTCAGAGCTGTACACATTTGAACTTCAAGTGTGAGCTTGTGATTTCCATGATTTCAAGA	600	
Db	620	AAGTCAGAGCTGTACACATTTGAACTTCAAGTGTGAGCTTGTGATTTCCATGATTTCAAGA	679	
Qy	601	AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAGTGACAGCAACCAATCCATGTTGTA	660	
Db	680	AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAGTGACAGCAACCAATCCATGTTGTA	739	
Qy	661	ATTGAAGACTTTGAGTCTCACTTACCCGTTCCGTAACCCCACTCTCACAGGCTCTGTG	720	
Db	740	ATTGAAGACTTTGAGTCTCACTTACCCGTTCCGTAACCCCACTCTCACAGGCTCTGTG	799	
Qy	721	AATATTCCTGTGTACCCCAAGAAATTTTACAGGTACATGTGAGAGTCTTGTGGCAG	780	
Db	800	AATATTCCTGTGTACCCCAAGAAATTTTACAGGTACATGTGAGAGTCTTGTGGCAG	859	
Qy	781	GAGGAAAGCAAGTATCTGTGACCTTCAAGCAGATCCAGTTTCAAGTGCATTTCAAG	840	
Db	860	GAGGAAAGCAAGTATCTGTGACCTTCAAGCAGATCCAGTTTCAAGTGCATTTCAAG	919	
Qy	841	GCAGTTCAACTTATCTACGATGTGCATTAACCACTCTGTGTGTGTGTGTGTGTGTGT	900	
Db	920	GCAGTTCAACTTATCTACGATGTGCATTAACCACTCTGTGTGTGTGTGTGTGTGTGT	979	
Qy	901	TCAATATCAGACTTTTCTATCAGCTGTGAGATGCTTCAAGGTATCTGCTTAAACAT	960	
Db	980	TCAATATCAGACTTTTCTATCAGCTGTGAGATGCTTCAAGGTATCTGCTTAAACAT	1039	
Qy	961	GATTTGAGGTACAAAGCTTCTCAAGAGCTGAGCTTGAAGATTAAGAGAGACCTGC	1020	
Db	1040	GATTTGAGGTACAAAGCTTCTCAAGAGCTGAGCTTGAAGATTAAGAGAGACCTGC	1099	
Qy	1021	GTCCTTTTGAATTAAGGACGACACAAAGAAAGAGAGCTTACCCGACATATA	1080	
Db	1100	GTCCTTTTGAATTAAGGACGACACAAAGAAAGAGAGCTTACCCGACATATA	1159	

Qy	1081	CTGCGGAGATGTTCTCTCAGTTCAATTTTACCTGTGTCTTGAATCCGAGCAATTCCT	1140	
Db	1160	CTGCGGAGATGTTCTCTCAGTTCAATTTTACCTGTGTCTTGAATCCGAGCAATTCCT	1219	
Qy	1141	AAAAAGCAATTTTGTGAGCCCTTGTGACATATACAGTACAGTCTGAAAGCCGACG	1200	
Db	1220	AAAAAGCAATTTTGTGAGCCCTTGTGACATATACAGTACAGTCTGAAAGCCGACG	1279	
Qy	1201	CTACAGAGCTGTGACATTAACAGGAGGACGATTAAGCGCTTGTGTGTGTGTGTGTGT	1260	
Db	1280	CTACAGAGCTGTGACATTAACAGGAGGACGATTAAGCGCTTGTGTGTGTGTGTGTGT	1339	
Qy	1261	TGTGCTGT	1320	
Db	1340	TGTGCTGT	1399	
Qy	1321	CTGCTGAAACATCTTCTTAACTTCAACCCAGACATATTCGTGTGCAAGCTTCAAGTTA	1380	
Db	1400	CTGCTGAAACATCTTCTTAACTTCAACCCAGACATATTCGTGTGCAAGCTTCAAGTTA	1459	
Qy	1381	TTTCAACCCAGAAAGCTCATTGTCTTCAACATTTGTGAAATTTCTGTCTACGTGACAA	1440	
Db	1460	TTTCAACCCAGAAAGCTCATTGTCTTCAACATTTGTGAAATTTCTGTCTACGTGACAA	1519	
Qy	1441	ACAGAGGTTCTGCGAGAGGAGATGTACAGGCTGTGAGCCCTTGTGTGTGTGTGTGTGT	1500	
Db	1520	ACAGAGGTTCTGCGAGAGGAGATGTACAGGCTGTGAGCCCTTGTGTGTGTGTGTGTGT	1579	
Qy	1501	CTTCAGCCAAACATACATGATCCCATGAAAGACAGGAGAAAGCCCTGTGCTCTTAAGATA	1560	
Db	1580	CTTCAGCCAAACATACATGATCCCATGAAAGACAGGAGAAAGCCCTGTGCTCTTAAGATA	1639	
Qy	1561	TGCATTTCTCTGTGAAACAAATTTTCTTCACTTACAGATGACCCCTCAATCCCATTC	1620	
Db	1640	TGCATTTCTCTGTGAAACAAATTTTCTTCACTTACAGATGACCCCTCAATCCCATTC	1699	
Qy	1621	ATTAATGTGGGTTCAGGAACCCGCAATAGCCCGTTAATTTGGGTTCTTACAACTAGAGAG	1680	
Db	1700	ATTAATGTGGGTTCAGGAACCCGCAATAGCCCGTTAATTTGGGTTCTTACAACTAGAGAG	1759	
Qy	1681	AAACTCAGAAACAACCCAGATGAAATTTTGTGAGCAATGTGTGTGTGTGTGTGTGTGT	1740	
Db	1760	AAACTCAGAAACAACCCAGATGAAATTTTGTGAGCAATGTGTGTGTGTGTGTGTGTGT	1819	
Qy	1741	AGGCATTAAGATGAGATTAATCTATTCAGAAAGAGCTCAGACATTTCTTAAAGCATGGG	1800	
Db	1820	AGGCATTAAGATGAGATTAATCTATTCAGAAAGAGCTCAGACATTTCTTAAAGCATGGG	1879	
Qy	1801	ATCTTAATCTATCTAAAGGTTTCTTCTCAAGAGATGCTCTGTGTGGGAGAGAGGCC	1860	
Db	1880	ATCTTAATCTATCTAAAGGTTTCTTCTCAAGAGATGCTCTGTGTGGGAGAGAGGCC	1939	
Qy	1861	CCAGCAAGATATGTACAGACAAACATCAGCTTCAATGCGCAGAGGTGTGAGAAATCTTC	1920	
Db	1940	CCAGCAAGATATGTACAGACAAACATCAGCTTCAATGCGCAGAGGTGTGAGAAATCTTC	1999	
Qy	1921	CTTCAGAGAAAGGCAATTTATGTGTGTGAGATGCAAGAAATTTGCGCAAGATGTGA	1980	
Db	2000	CTTCAGAGAAAGGCAATTTATGTGTGTGAGATGCAAGAAATTTGCGCAAGATGTGA	2059	
Qy	1981	CATGATGCCCTTGTGAAATTAATTAAGCAAGAGGTTGTGAAATTAAGCAAGCAATG	2040	
Db	2060	CATGATGCCCTTGTGAAATTAATTAAGCAAGAGGTTGTGAAATTAAGCAAGCAATG	2119	
Qy	2041	AAAAACCTGCGCACTTTAAAGAGAAAGAAAGCTTACAGGATTTTGTGTATATA	2097	
Db	2120	AAAAACCTGCGCACTTTAAAGAGAAAGAAAGCTTACAGGATTTTGTGTATATA	2176	

RESULT 8
AD087538
ID AD087538 standard; cDNA; 3270 BP.

XX ADQ87538;
 AC 07-OCT-2004 (first entry)
 DT
 XX
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #4416.
 XX
 KM human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
 KW cancer; cell proliferative disorder; gene; ss.
 OS Homo sapiens.
 XX
 PN M02004060270-A2.
 XX
 PD 22-JUL-2004.
 XX
 PF 15-OCT-2003; 2003MO-US029126.
 XX
 PR 18-OCT-2002; 2002US-0418988P.
 XX
 PA (BETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 XX
 PI Wu TD, Zhou Y;
 XX
 DR WPI; 2004-534300/51.
 XX
 PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
 PT preventing or treating cell proliferative disorders such as cancer.
 XX
 PS Claim 1; SEQ ID NO 4416; 5504bp; English.

The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identity to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potential effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

Sequence 3270 BP; 934 A; 702 C; 680 G; 954 T; 0 U; 0 Other;

Query Match	90.3%;	Score 1893;	DB 13;	Length 3270;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 2093;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	ATGAGAGGTTTCTGTTACTATATGCTACACAGCAGGACAGCCAAAGCCATCGCAGAA	60	
Db	112	ATGAGAGGTTTCTGTTACTATATGCTACACAGCAGGACAGCCAAAGCCATCGCAGAA	171	
Qy	61	GAATGTGTGAGCACTGTGTACATGATTTTCTGAGATCTTCACTATATTAGTAA	120	
Db	172	GAATATGTGAGCACTGTGTACATGATTTTCTGAGATCTTCACTATATTAGTAA	231	
Qy	121	TCCGATTAAGTATGACTTAAACCGAAGAGCTCTCTTGTGTGTGTTTCTACACG	180	
Db	232	TCCGATTAAGTATGACTTAAACCGAAGAGCTCTCTTGTGTGTGTTTCTACACG	291	
Qy	181	GGCAGCCGAGACCCAGCCAGCAGCCGCAAGTTGTTAAGAAATPACAGAACAAACA	240	
Db	292	GGCAGCCGAGACCCAGCCAGCAGCCGCAAGTTGTTAAGAAATPACAGAACAAACA	351	
Qy	241	CTGCCGTTGATTTCTTGTCTCAGCTGCGGTATGAGTTACTGGGTCTCGGTGATTCAGAA	300	
Db	352	CTGCCGTTGATTTCTTGTCTCAGCTGCGGTATGAGTTACTGGGTCTCGGTGATTCAGAA	411	
Qy	301	TACACCTACTTTTGCATGAGGGGGGAAAGATTAATTAACGACTTCAGAGCTTGAGCC	360	
Db	412	TACACCTACTTTTGCATGAGGGGGGAAAGATTAATTAACGACTTCAGAGCTTGAGCC	471	
Qy	361	CGGCAATTTCTATGACACTGACATGACATGATGATGATGATTAACCTTGGTGTGAG	420	
Db	472	CGGCAATTTCTATGACACTGACATGACATGATGATGATGATTAACCTTGGTGTGAG	531	
Qy	421	CCGTGATTTCTGAGCTTGGCCAGCCCTCAGAAACATTTTATGATCAAGCAGAGCAAA	480	
Db	532	CCGTGATTTCTGAGCTTGGCCAGCCCTCAGAAACATTTTATGATCAAGCAGAGCAAA	541	
Qy	481	GAGAGATTAAGTGGGCACTCCGGTGGCATCCTGATCTTGAAGAGACCTTTG	540	
Db	592	GAGAGATTAAGTGGGCACTCCGGTGGCATCCTGATCTTGAAGAGACCTTTG	601	
Qy	541	AACTCAGAGCTGTACATGAAATCTCAAGTCAAGTCTGATTCAGATTCAGAG	600	
Db	652	AACTCAGAGCTGTACATGAAATCTCAAGTCAAGTCTGATTCAGATTCAGAG	711	
Qy	601	AGAAAGATTTCTGAGGTTTGAAGCAAAATGACGTAACAGCAACCAATCCATGTTGA	660	
Db	712	AGAAAGATTTCTGAGGTTTGAAGCAAAATGACGTAACAGCAACCAATCCATGTTGA	771	
Qy	661	ATTGAAGACTTGAATCTCTACCTTACCCGTTGGGTACCCCACTCTCACAAGCCTCTG	720	
Db	772	ATTGAAGACTTGAATCTCTACCTTACCCGTTGGGTACCCCACTCTCACAAGCCTCTG	831	
Qy	721	AAATATCTGTTTACCCCAAGAAATTTTACAGGTACATCTGAGAGAGTCTCTGGCCAG	780	
Db	832	AAATATCTGTTTACCCCAAGAAATTTTACAGGTACATCTGAGAGAGTCTCTGGCCAG	891	
Qy	781	GAGAAAGCAAGTATCTGTGACTTACAGAGATCCAGTTTTCAGTGCATATTTCAAG	840	
Db	892	GAGAAAGCAAGTATCTGTGACTTACAGAGATCCAGTTTTCAGTGCATATTTCAAG	951	
Qy	841	GCAATTCACCTTACGAAATGATGCTATTAACCAACCACTCTGCTGTGATGATTCAGAT	900	
Db	952	GCAATTCACCTTACGAAATGATGCTATTAACCAACCACTCTGCTGTGATGATTCAGAT	1011	
Qy	901	TCAAAATACAGACTTTTCTATACGCTTGAAGATGCTTCAAGCTATCTGCTTACAGT	960	
Db	1012	TCAAAATACAGACTTTTCTATACGCTTGAAGATGCTTCAAGCTATCTGCTTACAGT	1071	
Qy	961	GATTTGAGGTACAAAGCTTCCAAAGACTGACAGCTTGAAGATTAAGAGAGCACTGC	1020	
Db	1072	GATTTGAGGTACAAAGCTTCCAAAGACTGACAGCTTGAAGATTAAGAGAGCACTGC	1131	

QY 1021 GTCTTTGAAATAAAGCAGACCAAAAGAGAGCTTACCTTACCCGACATATA 1080
 DB 1132 GTCTTTGAAATAAAGCAGACCAAAAGAGAGCTTACCTTACCCGACATATA 1191
 QY 1081 CTTGGGGGATGTTCTCTCAGATTCAATTTTACCTGGTGTCTTGAATCCGAGCAATTCCT 1140
 DB 1192 CTTGGGGGATGTTCTCTCAGATTCAATTTTACCTGGTGTCTTGAATCCGAGCAATTCCT 1251
 QY 1141 AAAAAGGCAATTTTGGAGCCCTGTGAGCTATACAGAGAGAGCTGAGAAAGGAGCAGG 1200
 DB 1252 AAAAAGGCAATTTTGGAGCCCTGTGAGCTATACAGAGAGAGCTGAGAAAGGAGCAGG 1311
 QY 1201 CTACAGAGCTGTGAGTAACAAGAGGAGCGAGTATATAGCCGCTTTGTATGAGATGCGC 1260
 DB 1312 CTACAGAGCTGTGAGTAACAAGAGGAGCGAGTATATAGCCGCTTTGTATGAGATGCGC 1371
 QY 1261 TGTGCTGCTTGTGGATCTCTCTCGCTTTCCTTCTTGGCAGGCACTCAAGTCTC 1320
 DB 1372 TGTGCTGCTTGTGGATCTCTCTCGCTTTCCTTCTTGGCAGGCACTCAAGTCTC 1431
 QY 1321 CTGCTGGAACATCTTCTTAACTGCAACGAGCAATATGAGTGCAGAGCTCAAGTTA 1380
 DB 1432 CTGCTGGAACATCTTCTTAACTGCAACGAGCAATATGAGTGCAGAGCTCAAGTTA 1491
 QY 1381 TTTCAACCCAGAAAGCTCATTCTTCAACATTTGTGAATTTCTGTCTACTGCGACA 1440
 DB 1492 TTTCAACCCAGAAAGCTCATTCTTCAACATTTGTGAATTTCTGTCTACTGCGACA 1551
 QY 1441 ACAGAGGTTCTGCGAAGGAGTATGATACAGGCTGCGCTGTTGTGGTTCCTTCAAGTT 1500
 DB 1552 ACAGAGGTTCTGCGAAGGAGTATGATACAGGCTGCGCTGTTGTGGTTCCTTCAAGTT 1611
 QY 1501 CTTGAGCCAAATATCATGCAATCCCATGAGACAGGAGGAAAGCCCTGCTCTTAAGATA 1560
 DB 1612 CTTGAGCCAAATATCATGCAATCCCATGAGACAGGAGGAAAGCCCTGCTCTTAAGATA 1671
 QY 1561 TCCATCTCTCTCTGAAACAATAATCTTCTCACTTACAGATGACCCCTCAATCCCATC 1620
 DB 1672 TCCATCTCTCTCTGAAACAATAATCTTCTCACTTACAGATGACCCCTCAATCCCATC 1731
 QY 1621 ATTAATGTTGGTTCAGAAACCGGCAATAGCCCGTTTATTTGGTTCCTTCAACATAGAG 1680
 DB 1732 ATTAATGTTGGTTCAGAAACCGGCAATAGCCCGTTTATTTGGTTCCTTCAACATAGAG 1791
 QY 1681 AAACCTCCAAAGAACACCAACCATGGAATTTTGGAGCAATGTGTTGTTTTGGCTGC 1740
 DB 1792 AAACCTCCAAAGAACACCAACCATGGAATTTTGGAGCAATGTGTTGTTTTGGCTGC 1851
 QY 1741 AGGCAATAGGAGATATCTATTCAGAAAAAGAGCTCAGACATTTCTTAAAGCATGGG 1800
 DB 1852 AGGCAATAGGAGATATCTATTCAGAAAAAGAGCTCAGACATTTCTTAAAGCATGGG 1911
 QY 1801 ATCTTAATCTCTTAAAGGTTTCTTCTGAGAGATGCTCTGTTGGGAGAGAGAGGCC 1860
 DB 1912 ATCTTAATCTCTTAAAGGTTTCTTCTGAGAGATGCTCTGTTGGGAGAGAGAGGCC 1971
 QY 1861 CAGCAAAATATGTACAAACAACATCCAGCTTCATGGCAGAGAGGTCGAGAAATCTTC 1920
 DB 1972 CAGCAAAATATGTACAAACAACATCCAGCTTCATGGCAGAGAGGTCGAGAAATCTTC 2031
 QY 1921 CTCAGAGAGAGGAGCATATTTATGTGTGAGAGATGAGAAATATGGCAGAGATGTA 1980
 DB 2032 CTCAGAGAGAGGAGCATATTTATGTGTGAGAGATGAGAAATATGGCAGAGATGTA 2091
 QY 1981 CATGATGCCCTTGTGCAATTAATAGCAAAAGGTTGAGTTGAAAAACTAGAGCAATG 2040
 DB 2092 CATGATGCCCTTGTGCAATTAATAGCAAAAGGTTGAGTTGAAAAACTAGAGCAATG 2151
 QY 2041 AAAACCTTGGCCACTTTAAAAAGAAAGAAAGCTTACCTTCAAGATATTTGGTCAATA 2097
 DB 2152 AAAACCTTGGCCACTTTAAAAAGAAAGAAAGCTTACCTTCAAGATATTTGGTCAATA 2208

RESULT 9
 ADM43216
 ID ADM43216 standard; cDNA; 2091 BP.
 XX
 AC ADM43216;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human methionine synthase reductase CDS del 1726-1728 variant.
 XX
 KW Human; ss; Methionine synthase reductase polypeptide; HsmTRR; cancer;
 KW cardiovascular disease; neural tube defect; hyperhomocysteinemia;
 XX chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..2091
 FT /tag= a
 FT /product= "hsmTRdelR559"
 FT /partial
 FT /note= "No stop codon shown"
 FT replace(66,A)
 FT variation
 FT /tag= b
 FT /standard_name= "Single_nucleotide_polymorphism"
 FT replace(110,A)
 FT /tag= c
 FT /standard_name= "Single_nucleotide_polymorphism"
 FT replace(1726,TTGT)
 FT /tag= d
 PN US2003082676-A1.
 PD 01-MAY-2003.
 XX
 XX 10-AUG-1999; 99US-00371347.
 PF 16-JAN-1998; 98US-0071622P.
 PR 15-JAN-1999; 99US-00232028.
 PR
 XX
 PA (GRAV/) GRAVEL R A.
 PA (ROZE/) ROZEN R.
 PA (LECL/) LECLERC D.
 PA (WILS/) WILSON A.
 PA (ROSE/) ROSENBLATT D.
 XX
 PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
 DR MPI; 2003-576610/54.
 DR P-PSDB; ADM43217.
 XX
 XX New substantially pure nucleic acid encoding a mammalian methionine
 PT synthase reductase polypeptide, useful for diagnosing, preventing or
 PT treating conditions associated with altered methionine synthase activity,
 PT e.g. cancer.
 PT
 XX
 PS Disclosure; SEQ ID NO 45; 26pp; English.
 XX
 XX The invention relates to a substantially pure nucleic acid that encodes a
 CC mammalian methionine synthase reductase polypeptide, HsmTRR, or that
 CC hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
 CC ADM43209. Also included are a non-human animal where one or both genetic
 CC alleles encoding the methionine synthase reductase polypeptide are
 CC mutated, an antibody that specifically binds the above methionine
 CC synthase reductase polypeptide, a method of detecting the presence of the
 CC above polypeptide, a method for detecting sequence variants for
 CC methionine synthase reductase in a mammal, methods of treating or
 CC preventing cancer (or cardiovascular disease or neural tube defects) in a
 CC subject, methods of screening for a compound that modulates methionine
 CC synthase reductase biological activity and a method for detecting an
 CC increased risk of developing a neural tube defect in a mammalian embryo
 CC or foetus. The nucleic acid is useful in diagnosing, preventing or
 CC treating conditions associated with altered methionine synthase activity,

CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are
CC also associated with hyperhomocysteinemia. The gene for HmTR is
CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
CC sequence of a variant human hsmTR cDNA.

XX Sequence 2091 BP; 591 A; 489 C; 480 G; 531 T; 0 U; 0 Other;

Query Match 85.8%; Score 1800; DB 11; Length 2091;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2090; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 ATGAGAGGTTTCTGTTACTATATGCTACACAGAGGACAGGCAAGGCCATCGAGAA 60
DB 1 ATGAGAGGTTTCTGTTACTATATGCTACACAGAGGACAGGCAAGGCCATCGAGAA 60
QY 61 GAAATGTGAGCAAGCTGTGTACATGTGATTTTTCGCAGATCTTCACTATATTAGGAA 120
DB 61 GAAATGTGAGCAAGCTGTGTACATGTGATTTTTCGCAGATCTTCACTATATTAGGAA 120
QY 121 TCCGATTAAGTATGACCTTAAACCGAAACAGCTCTCTGTGTGTGTGTTCTACACG 180
DB 121 TCCGATTAAGTATGACCTTAAACCGAAACAGCTCTCTGTGTGTGTGTTCTACACG 180
QY 181 GGCACCGGAGACCCACCGACACAGCCCGAAGTTTGTAAAGAAATACAAACAA 240
DB 181 GGCACCGGAGACCCACCGACACAGCCCGAAGTTTGTAAAGAAATACAAACAA 240
QY 241 CTGCGGTTATTTCTTGTGTCACTGCGGTATGCGGTATGCGGTCTCGGTGATTGAG 300
DB 241 CTGCGGTTATTTCTTGTGTCACTGCGGTATGCGGTATGCGGTCTCGGTGATTGAG 300
QY 301 TACACCTACTTTTGCATGCGGGGAGATATTTGATTAACGACTTCAAGACTTGGAGC 360
DB 301 TACACCTACTTTTGCATGCGGGGAGATATTTGATTAACGACTTCAAGACTTGGAGC 360
QY 361 CGGCATTCTATGACACTGTGACATGTGATGATCTGTGTAGAACTTGTGTGAG 420
DB 361 CGGCATTCTATGACACTGTGACATGTGATGATCTGTGTAGAACTTGTGTGAG 420
QY 421 CCGTGATTTGCTGTGACCTGTGCGCAGCCCTGAGAAAGATTTTGTGTCAACAGAGCA 480
DB 421 CCGTGATTTGCTGTGACCTGTGCGCAGCCCTGAGAAAGATTTTGTGTCAACAGAGCA 480
QY 481 GAGAGATTAAGTGTGCGCACTCCCGGTGCACTGTGATCTTGTAGAGACAGACTTGTG 540
DB 481 GAGAGATTAAGTGTGCGCACTCCCGGTGCACTGTGATCTTGTAGAGACAGACTTGTG 540
QY 541 AAGTCAGAGCTGTCAACATTTGATTCGAGTGTGAGTTTGTGATTCGATTCAGGA 600
DB 541 AAGTCAGAGCTGTCAACATTTGATTCGAGTGTGAGTTTGTGATTCGATTCAGGA 600
QY 601 AGAAGGATCTGAGTTTGAAGCAAAATGCAGTGAACAGCAACCAATCCANTGTGTA 660
DB 601 AGAAGGATCTGAGTTTGAAGCAAAATGCAGTGAACAGCAACCAATCCANTGTGTA 660
QY 661 ATTGAAGACTTGTAGTCTCACTTACCCGTTCCGTGACCCCACTCTCAAGGCTCTCTG 720
DB 661 ATTGAAGACTTGTAGTCTCACTTACCCGTTCCGTGACCCCACTCTCAAGGCTCTCTG 720
QY 721 AATATTCCTGTGTTACCCCGAATATTTACAGGTATCATCTGACGAGGTCTCTTGGCAG 780
DB 721 AATATTCCTGTGTTACCCCGAATATTTACAGGTATCATCTGACGAGGTCTCTTGGCAG 780
QY 781 GAGGAAAGCAAGATCTGTGACTTCAGCAAGTCCATTTTTCAGAGCAATTTCAAG 840
DB 781 GAGGAAAGCAAGATCTGTGACTTCAGCAAGTCCATTTTTCAGAGCAATTTCAAG 840
QY 841 GCATTTCACTTACTAGATGATGCAATTAACCACTCTGCTGTGATTTGACATT 900
DB 841 GCATTTCACTTACTAGATGATGCAATTAACCACTCTGCTGTGATTTGACATT 900

QY 901 TCMAATACAGACTTTTCTTATCAGCCTGAGATGCTTTCAGGATGATCTGCCCTAACGT 960
DB 901 TCMAATACAGACTTTTCTTATCAGCCTGAGATGCTTTCAGGATGATCTGCCCTAACGT 960
QY 961 GATTCGAGGTAACAAAGCTTCTCCAAAGATGAGCTTGAAGATTAAGAGAGCACTGC 1020
DB 961 GATTCGAGGTAACAAAGCTTCTCCAAAGATGAGCTTGAAGATTAAGAGAGCACTGC 1020
QY 1021 GTCTTTTGAATAAAGGACAGACAAAGAAAGAGCTACCTTACCCAGCATATA 1080
DB 1021 GTCTTTTGAATAAAGGACAGACAAAGAAAGAGCTACCTTACCCAGCATATA 1080
QY 1081 CCTGCGGATGTTCTCTCCAGTTCACTTTTACTGTGTCTTGAATCCGAGAAATTCCT 1140
DB 1081 CCTGCGGATGTTCTCTCCAGTTCACTTTTACTGTGTCTTGAATCCGAGAAATTCCT 1140
QY 1141 AAAAAGCAATTTTGGAGCCCTTGTGAGCTATACAGAGACAGTCTGAAAAAGCCAG 1200
DB 1141 AAAAAGCAATTTTGGAGCCCTTGTGAGCTATACAGAGACAGTCTGAAAAAGCCAG 1200
QY 1201 CTACAGAGCTGTGAGTAACAAAGGAGGACCGATTAATAGCCGTTGTACGAGATGCC 1260
DB 1201 CTACAGAGCTGTGAGTAACAAAGGAGGACCGATTAATAGCCGTTGTACGAGATGCC 1260
QY 1261 TGTGCTGCTGTGTGATCTCTCTGCTTCCCTTCTTCCGACGACCACTCAATTC 1320
DB 1261 TGTGCTGCTGTGTGATCTCTCTGCTTCCCTTCTTCCGACGACCACTCAATTC 1320
QY 1321 CTGCTGAAATCTTCTTAACTTCAACCCAGACATATTTGTTGTCAGAGCTCAAGTTTA 1380
DB 1321 CTGCTGAAATCTTCTTAACTTCAACCCAGACATATTTGTTGTCAGAGCTCAAGTTTA 1380
QY 1381 TTTCAACCAAGAAAGCTTCATTTTGTCTTCAACATTTGTGAAATTTGTCTACTGCGACA 1440
DB 1381 TTTCAACCAAGAAAGCTTCATTTTGTCTTCAACATTTGTGAAATTTGTCTACTGCGACA 1440
QY 1441 ACAGAGTTCTGTGGAAGGAGATATGACAGGTGCTGCTGTTGTGTGTTGATTT 1500
DB 1441 ACAGAGTTCTGTGGAAGGAGATATGACAGGTGCTGCTGTTGTGTGTTGATTT 1500
QY 1501 CTTGACGCAAACTACATGATCCCATGAAAGACAGGAGGAAAGCCCTGAGCTCTAAGATA 1560
DB 1501 CTTGACGCAAACTACATGATCCCATGAAAGACAGGAGGAAAGCCCTGAGCTCTAAGATA 1560
QY 1561 TCCATCTCTCTGGAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
DB 1561 TCCATCTCTCTGGAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
QY 1621 ATATATGTGATGACAGAAACCGGATAGCCGTTTATTTGGTTCCTTACAACTAGAG 1680
DB 1621 ATATATGTGATGACAGAAACCGGATAGCCGTTTATTTGGTTCCTTACAACTAGAG 1680
QY 1681 AAATCTCAAGAAACAAACCCAGATGAAATTTTGAAGCAATGTGTGTTTGTGCTGC 1740
DB 1681 AAATCTCAAGAAACAAACCCAGATGAAATTTTGAAGCAATGTGTGTTTGTGCTGC 1740
QY 1741 AGGCATTAAGATTAAGATTAATCTATTCAAGAAAGCTCAGACATTTCTTAAGATGG 1800
DB 1741 AGGCATTAAGATTAAGATTAATCTATTCAAGAAAGCTCAGACATTTCTTAAGATGG 1800
QY 1738 AGGCATTAAGATTAAGATTAATCTATTCAAGAAAGCTCAGACATTTCTTAAGATGG 1797
DB 1738 AGGCATTAAGATTAAGATTAATCTATTCAAGAAAGCTCAGACATTTCTTAAGATGG 1797
QY 1801 ATCTTAATCATTAAGGTTTCTTCTCAAGAGATGCTCTCTGTGGAGAGAGAAAGCC 1860
DB 1801 ATCTTAATCATTAAGGTTTCTTCTCAAGAGATGCTCTCTGTGGAGAGAGAAAGCC 1860
QY 1798 ATCTTAATCATTAAGGTTTCTTCTCAAGAGATGCTCTCTGTGGAGAGAGAAAGCC 1857
DB 1798 ATCTTAATCATTAAGGTTTCTTCTCAAGAGATGCTCTCTGTGGAGAGAGAAAGCC 1857
QY 1861 CCAGCAAGATTAAGATTAAGATTAATCTATTCAAGAAAGCTCAGACATTTCTTAAGATGG 1920
DB 1861 CCAGCAAGATTAAGATTAAGATTAATCTATTCAAGAAAGCTCAGACATTTCTTAAGATGG 1920
QY 1858 CCAGCAAGATTAAGATTAAGATTAATCTATTCAAGAAAGCTCAGACATTTCTTAAGATGG 1917
DB 1858 CCAGCAAGATTAAGATTAAGATTAATCTATTCAAGAAAGCTCAGACATTTCTTAAGATGG 1917
QY 1921 CTCACAGAGAACGGCAATTTATGTGTGTGAGATGCAAGAAATATGCAAGATGTA 1980
DB 1921 CTCACAGAGAACGGCAATTTATGTGTGTGAGATGCAAGAAATATGCAAGATGTA 1980
QY 1918 CTCACAGAGAACGGCAATTTATGTGTGTGAGATGCAAGAAATATGCAAGATGTA 1977
DB 1918 CTCACAGAGAACGGCAATTTATGTGTGTGAGATGCAAGAAATATGCAAGATGTA 1977
QY 1981 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGGTTGAGTTGAAAACTAAGAACATG 2040

|||||
DB 1978 CATGATGCCCTTGCAATAATATACCAAGAGTTGAGTTGAAAACTAGAACGAATG 2037
QY 2041 AAAACCCCTGGCCACTTTAAAAAGAAAGAAACCGTACTTACAGATATTTGGTCA 2094
DB 2038 AAAACCTGGCCACTTTAAAAAGAAAGAAACCGTACTTACAGATATTTGGTCA 2091
RESULT 10
ADM43214
ID ADM43214 standard; cDNA; 2091 BP.
AC ADM43214;
XX
DT 03-JUN-2004 (first entry)
DE Human methionine synthase reductase CDS del 1675-1678 variant.
XX
XX Human; ss; Methionine synthase reductase polypeptide; hsmtrr; cancer;
KM cardiovascular disease; neural tube defect; hyperhomocysteinemia;
KM chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 1..2091
FT /tag= a
FT /product= "hsmtrrdelR559"
FT /partial
FT /note= "No stop codon shown"
FT /replace(66,A)
FT /tag= b
FT /standard name= "single_nucleotide polymorphism"
FT /replace(110,A)
FT /tag= c
FT /standard name= "single_nucleotide polymorphism"
FT /replace(1675,AGAG)
FT /tag= d
PN US2003082676-A1.
XX
XX 01-MAY-2003.
XX
XX 10-AUG-1999; 99US-00371347.
XX
XX 16-JAN-1998; 98US-0071622P.
XX 15-JAN-1999; 99US-00232028.
XX
XX (GRAV/) GRAVEL R. A.
XX (ROZE/) ROZEN R.
XX (LECL/) LECLEERC D.
XX (WILS/) WILSON A.
XX (ROSE/) ROSENBLATT D.
PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX WPI; 2003-576610/54.
XX P-PSDB; ADM43215.
XX
XX New substantially pure nucleic acid encoding a mammalian methionine
PT synthase reductase polypeptide, useful for diagnosing, preventing or
PT treating conditions associated with altered methionine synthase activity,
PT e.g. cancer.
PS Disclosure; SEQ ID NO 47; 26pp; English.
XX
XX The invention relates to a substantially pure nucleic acid that encodes a
CC mammalian methionine synthase reductase polypeptide. hsmtrr, or that
CC hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
CC ADM43209. Also included are a non-human animal where one or both genetic
CC alleles encoding the methionine synthase reductase polypeptide are
CC mutated, an antibody that specifically binds the above methionine
CC synthase reductase polypeptide, a method of detecting the presence of the

CC above polypeptide, a method for detecting sequence variants for
CC methionine synthase reductase in a mammal, methods of treating or
CC preventing cancer (or cardiovascular disease or neural tube defects) in a
CC subject, methods of screening for a compound that modulates methionine
CC synthase reductase biological activity and a method for detecting an
CC increased risk of developing a neural tube defect in a mammalian embryo
CC or fetus. The nucleic acid is useful in diagnosing, preventing or
CC treating conditions associated with altered methionine synthase activity,
CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are
CC also associated with hyperhomocysteinemia. The gene for hsmtrr is
CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
CC sequence of a variant human hsmtrr cDNA.
XX
SQ Sequence 2091 BP; 589 A; 489 C; 480 G; 533 T; 0 U; 0 Other;

Query Match 85.8%; Score 1800; DB 11; Length 2091;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2090; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 ATGAGAGGTTCTGTACTATATATGCTACACAGAGGACAGGCAAGGCCATCGAGAA 60
DB 1 ATGAGAGGTTCTGTACTATATATGCTACACAGAGGACAGGCAAGGCCATCGAGAA 60
QY 61 GAAATGTGAGACAGCTGTGTAATGATTTCTGAGATCTTCACTATATTAGTAA 120
DB 61 GAAATGTGAGACAGCTGTGTAATGATTTCTGAGATCTTCACTATATTAGTAA 120
QY 121 TCGATATAGTATGACTTAAACCGAAACAGCTCTTGTGTGTGTGTTCTACACG 180
DB 121 TCGATATAGTATGACTTAAACCGAAACAGCTCTTGTGTGTGTGTTCTACACG 180
QY 121 TCGATATAGTATGACTTAAACCGAAACAGCTCTTGTGTGTGTGTTCTACACG 180
DB 121 TCGATATAGTATGACTTAAACCGAAACAGCTCTTGTGTGTGTGTTCTACACG 180
QY 181 GGCACCGGAGACCCACCCACACAGCCGCAAGTTGTTAAGAAATACGAACCAACA 240
DB 181 GGCACCGGAGACCCACCCACACAGCCGCAAGTTGTTAAGAAATACGAACCAACA 240
QY 241 CTGCCGTTGATTTCTTGTCTCACTGCGGTATGAGTTCTGAGTTCTGAGTTTCA 300
DB 241 CTGCCGTTGATTTCTTGTCTCACTGCGGTATGAGTTCTGAGTTCTGAGTTTCA 300
QY 301 TACACCTACTTTTGCATATGAGGAGGAAATATATGATTAACGATTCAGAGCTTGAGCC 360
DB 301 TACACCTACTTTTGCATATGAGGAGGAAATATATGATTAACGATTCAGAGCTTGAGCC 360
QY 361 CGCATTTTATGACACTGCAATGCAATGACTGTGTGTTTGAACCTTGTGTTGAG 420
DB 361 CGCATTTTATGACACTGCAATGCAATGACTGTGTGTTTGAACCTTGTGTTGAG 420
QY 421 CCGTGATTTGCTGCACTCGGCGACGCCCTCAAGAACATTTTAGAGTCAAGAGACAA 480
DB 421 CCGTGATTTGCTGCACTCGGCGACGCCCTCAAGAACATTTTAGAGTCAAGAGACAA 480
QY 481 GAGAGATATAGTGCGCACTCCCGTGCGATCACTGATCTTGAAGACAGACTTGTG 540
DB 481 GAGAGATATAGTGCGCACTCCCGTGCGATCACTGATCTTGAAGACAGACTTGTG 540
QY 541 AAGTCAGAGCTGCTACACTTGAATTCAGATGAGCTTCTGAGATTCATGATTCAGGA 600
DB 541 AAGTCAGAGCTGCTACACTTGAATTCAGATGAGCTTCTGAGATTCATGATTCAGGA 600
QY 601 AGAAGGATTCGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCAATGTTGA 660
DB 601 AGAAGGATTCGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCAATGTTGA 660
QY 661 ATTGAAGACTTTGAGTCTCACTTACCCGTTGAGTACCCCACTTCACAAGCTTCTG 720
DB 661 ATTGAAGACTTTGAGTCTCACTTACCCGTTGAGTACCCCACTTCACAAGCTTCTG 720
QY 721 AATATTCCTGTTTACCCCAAGATTTTACAGTATCTGACAGAGTCTTGTGCGCAG 780
DB 721 AATATTCCTGTTTACCCCAAGATTTTACAGTATCTGACAGAGTCTTGTGCGCAG 780

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QY 781 GAGGAAAGCCAGATCTGTGACTTCAGCAGATCCAGTCTTTTCAAGTGGCAATTTCAAG 840
DB 781 GAGGAAAGCCAGATCTGTGACTTCAGCAGATCCAGTCTTTTCAAGTGGCAATTTCAAG 840
QY 841 GCGATTCAGATTTCTGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 900
DB 841 GCGATTCAGATTTCTGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 900
QY 901 TCAATTCAGATTTCTGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 960
DB 901 TCAATTCAGATTTCTGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 960
QY 961 GATTTCGAGTACAAAGCTTACCTCAAGAGCTGAGCTTGAAGATTAAGAGAGAGCTGC 1020
DB 961 GATTTCGAGTACAAAGCTTACCTCAAGAGCTGAGCTTGAAGATTAAGAGAGAGAGCTGC 1020
QY 1021 GTGCTTTGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 GTGCTTTGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 CTTGCGGAGATTTCTCTCAGATTTTAACTGATTTGATTTGATTTGATTTGATTTGATTTG 1140
DB 1081 CTTGCGGAGATTTCTCTCAGATTTTAACTGATTTGATTTGATTTGATTTGATTTGATTTG 1140
QY 1141 AAAAGGCAATTTTTCGAGAGCTTTGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1200
DB 1141 AAAAGGCAATTTTTCGAGAGCTTTGAGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1200
QY 1201 CTACAGAGAGCTTTCAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1260
DB 1201 CTACAGAGAGCTTTCAGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1260
QY 1261 TGTGCTGCTGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1320
DB 1261 TGTGCTGCTGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1320
QY 1321 CTGCTGCAATCTTCTCTAACTTCAACCAAGCAGATTTGATTTGATTTGATTTGATTTGATTTG 1380
DB 1321 CTGCTGCAATCTTCTCTAACTTCAACCAAGCAGATTTGATTTGATTTGATTTGATTTGATTTG 1380
QY 1381 TTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1381 TTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 ACAAGAGTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1441 ACAAGAGTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1501 CTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
DB 1501 CTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1561 TTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
DB 1561 TTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 1621 ATTAATGTTGGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
DB 1621 ATTAATGTTGGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
QY 1677 ATTAATGTTGGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1677
DB 1677 ATTAATGTTGGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1677
QY 1681 AAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
DB 1681 AAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1737 AAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1737
DB 1737 AAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1737
QY 1741 AGGATTAAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
DB 1741 AGGATTAAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1797 AGGATTAAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1797
DB 1797 AGGATTAAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1797
QY 1801 ATCTTAATCTCATCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
DB 1798 ATCTTAATCTCATCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1857
QY 1861 CAGGCAAAAGATTTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920

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DB 1858 CAGGCAAAAGATTTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1917
QY 1921 CTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
DB 1918 CTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1977
QY 1981 CATGATGCCCTTGTGCAATTAATTAAGCAAAAGAGTTGAGATTGAAAACTAGAGCAATG 2040
DB 1978 CATGATGCCCTTGTGCAATTAATTAAGCAAAAGAGTTGAGATTGAAAACTAGAGCAATG 2037
QY 2041 AAAACCTTGGCCACTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2094
DB 2038 AAAACCTTGGCCACTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2091

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RESULT 11

AA58977 standard; DNM; 3256 BP.

AA58977;

07-NOV-2000 (first entry)

A human methionine synthase reductase DNA sequence with polymorphism.

Human; methionine synthase reductase; MTRR; cancer;

cardiovascular disease; Down's Syndrome; neural tube defect;

premature coronary artery disease; ss.

Homo sapiens.

MO200042196-A2.

20-JUL-2000.

14-JAN-2000; 2000NC-IB000209.

15-JAN-1999; 99US-00232028.

10-AUG-1999; 99US-00371347.

(UIMC-) UNIV MCGILL.

Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;

WPI; 2000-466131/40.

Mammalian methionine synthase reductase nucleic acid used for detecting

an increased risk of developing a neural tube defect, Down's Syndrome or

cardiovascular disease in a mammalian embryo or fetus.

Claim 8; Page; 85pp; English.

The present sequence represents a human methionine synthase reductase

(MTRR) DNA sequence, with a polymorphism comprising of a deletion of

nucleotides 1726-1728. Inhibitors of MTRR polypeptide and polynucleotide

are used for treating or preventing cancer, cardiovascular disease,

Down's Syndrome or neural tube defects in a subject. The cardiovascular

disease is premature coronary artery disease. The compounds are detected

by methods which screen for modulators of MTRR biological activity. MTRR

polypeptide or nucleic acid is examined for the presence of a

polymorphism in the parents or embryo or foetus, and the information

used for detecting an increased risk of an embryo or foetus developing

cancer, cardiovascular disease, Down's Syndrome or neural tube defects.

note: the present sequence does not appear in the specification; it was

created using information provided

Sequence 3256 BP; 943 A; 705 C; 662 G; 946 T; 0 U; 0 Other;

Query Match 81.1%; Score 1701; DB 3; Length 3256;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2091; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

1 ATGAGGAGGTTTCTGTAATGCTATGCTACAGACAGGAGGACGAGCAAAAGCCATCGAGAA 60
80 ATGAGGAGGTTTCTGTAATGCTATGCTACAGACAGGAGGACGAGCAAAAGCCATCGAGAA 139
61 GAAATGTGAGCAAGCTGTGTACATGATGATTTTCTGAGATCTTCAATATTAATGAA 120
140 GAAATGTGAGCAAGCTGTGTACATGATGATTTTCTGAGATCTTCAATATTAATGAA 199
121 TCCGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 180
200 TCCGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTA 259
181 GGCACCGAGAGACCCACCGACAGCCGCAAGTTGTTAAGGAATTAAGAACCAACA 240
260 GGCACCGAGAGACCCACCGACAGCCGCAAGTTGTTAAGGAATTAAGAACCAACA 319
241 CTGCGGTTGATTTCTTTGCTCACTGCGGTATGAGTTAAGTTGCTGCGTATGAGAA 300
320 CTGCGGTTGATTTCTTTGCTCACTGCGGTATGAGTTAAGTTGCTGCGTATGAGAA 379
301 TAGACCTACTTTTGTGCAATGAGGAGGAAATTAATGATTAATGATTAATGATTAATG 360
380 TAGACCTACTTTTGTGCAATGAGGAGGAAATTAATGATTAATGATTAATGATTAATG 439
361 CGGCACTTTCTATGACATGAGCAATGAGATGATGATGATGATTAAGTTGATGATG 420
440 CGGCACTTTCTATGACATGAGCAATGAGATGATGATGATGATTAAGTTGATGATG 499
421 CGGTTGATTTGCTGAGATCTGCGGAGCCCTCAGAAAGCATTTTATGATCAAGAGACA 480
500 CGGTTGATTTGCTGAGATCTGCGGAGCCCTCAGAAAGCATTTTATGATCAAGAGACA 559
481 GAGGAGATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
560 GAGGAGATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 619
541 AAGTCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
620 AAGTCAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 679
601 AGAAGGATTTCTGAGGTTTGAAGCAAAATGAGTGAACAGCAACCAATGATGATG 660
680 AGAAGGATTTCTGAGGTTTGAAGCAAAATGAGTGAACAGCAACCAATGATGATG 739
661 ATTGAAGATTTGAGTCTCACTTACCGTTGCGTACCCCACTCTCAAGGCTCTCTG 720
740 ATTGAAGATTTGAGTCTCACTTACCGTTGCGTACCCCACTCTCAAGGCTCTCTG 799
721 AATATTCGAGTTTACCCCGAATATTTAAGGATGATGATGATGATGATGATGATG 780
800 AATATTCGAGTTTACCCCGAATATTTAAGGATGATGATGATGATGATGATGATG 859
781 GAGGAGGAGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 840
860 GAGGAGGAGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 919
841 GAGGATCACTTACCTAAGATGATGATGATGATGATGATGATGATGATGATGATG 900
920 GAGGATCACTTACCTAAGATGATGATGATGATGATGATGATGATGATGATGATG 979
901 TCAAAATCAAGATTTTCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
980 TCAAAATCAAGATTTTCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1039
961 GATTTGAGGAGTCAAGGCTACTCAAGAGCTGAGCTTGAAGATTAAGAGAGAGAG 1020
1040 GATTTGAGGAGTCAAGGCTACTCAAGAGCTGAGCTTGAAGATTAAGAGAGAGAG 1099
1021 GTCTTTTGAATTAAG 1080
1100 GTCTTTTGAATTAAG 1159
1081 CTGCGGAGATGTTCTCTCAAGTTCACTTTTACCTGATGATGATGATGATGATGATG 1140

1160 CCGGCGGAGTGTCTCTCAAGTTCACTTTTACCTGATGATGATGATGATGATGATG 1219
1141 AAAAAAGCATTTTGTGAGAGCCCTTGTGAGCTTATCAAGAGAGAGAGAGAGAGAG 1200
1220 AAAAAAGCATTTTGTGAGAGCCCTTGTGAGCTTATCAAGAGAGAGAGAGAGAGAG 1279
1201 CTACAGAGCTGTGAGAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
1280 CTACAGAGCTGTGAGAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1339
1261 TGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
1340 TGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1399
1321 CTGCTGAAATCTTCTTAACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
1400 CTGCTGAAATCTTCTTAACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1459
1381 TTTCACCGAGAGAGGCTCACTTTTGTCTCAATGATGATGATGATGATGATGATG 1440
1460 TTTCACCGAGAGAGGCTCACTTTTGTCTCAATGATGATGATGATGATGATGATG 1519
1441 ACAGAGGTTCTGCGAGAGAGAGATGATGATGATGATGATGATGATGATGATG 1500
1520 ACAGAGGTTCTGCGAGAGAGAGATGATGATGATGATGATGATGATGATGATG 1579
1501 CTTCAGCGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
1580 CTTCAGCGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1639
1561 TCCATCTCTCTGAG 1620
1640 TCCATCTCTCTGAG 1699
1621 ATTAATGAGGATCTGAG 1680
1700 ATTAATGAGGATCTGAG 1756
1681 AATCTCAAG 1740
1757 AATCTCAAG 1816
1741 AGGATTAAG 1800
1817 AGGATTAAG 1876
1801 ATCTTAATCACTTAAG 1860
1877 ATCTTAATCACTTAAG 1936
1861 CAG 1920
1937 CAG 1996
1921 CTTCAG 1980
1997 CTTCAG 2056
1981 CATGATGAGGCTGTGAG 2040
2057 CATGATGAGGCTGTGAG 2116
2041 AAAACCTGCGCATTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2097
2117 AAAACCTGCGCATTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2173

RESULT 12
ID AAAS8976
XX AAAS8976 standard; DNA; 3255 BP.
AC AAAS8976;

Db 1460 TTTCACCCGAGAAAGCTCCATTGTCCTTCAACATGTGGAATTTCTGTCTACTGCCACA 1519
 QY 1441 ACAGAGTTCTGCGGAGGAGATGTACAGGCTGGCTGGCTGTGTGCTTCAGTT 1500
 Db 1520 ACAGAGTTCTGCGGAGGAGATGTACAGGCTGGCTGGCTGTGTGCTTCAGTT 1579
 QY 1501 CTTGACGCAACATACATCATCCATGGAAGACAGCGGGAAGCCCTGGCTCTAGATA 1560
 Db 1580 CTTGACGCAACATACATCATCCATGGAAGACAGCGGGAAGCCCTGGCTCTAGATA 1639
 QY 1561 TCCATCTCTCTGCAACAACAATTTCTTCCATTAACAGATGACCCCTCAATCCCATC 1620
 Db 1640 TCCATCTCTCTGCAACAACAATTTCTTCCATTAACAGATGACCCCTCAATCCCATC 1695
 QY 1621 ATATAGTGGGTCCAGAACCGGCAATAGCCCGTTATTTGGTCTTACACATAGAGAG 1680
 Db 1696 ATATAGTGGGTCCAGAACCGGCAATAGCCCGTTATTTGGTCTTACACATAGAGAG 1755
 QY 1681 AAATCTCAGAACCAACCCAGATGGAATTTTGGAGCATGTGTTGTTTTTGGCTGC 1740
 Db 1756 AAATCTCAGAACCAACCCAGATGGAATTTTGGAGCATGTGTTGTTTTTGGCTGC 1815
 QY 1741 AGGCATTAAGATAGGATTTATCTTATTCAGAAAAAGCTCAGACATTTCTTAAGCATGCG 1800
 Db 1816 AGGCATTAAGATAGGATTTATCTTATTCAGAAAAAGCTCAGACATTTCTTAAGCATGCG 1875
 QY 1801 ATCTTAACATCTTAAGATTTCTTCTCAGAGATGCTCCTGTTGGAGAGAGAGAGCC 1860
 Db 1876 ATCTTAACATCTTAAGATTTCTTCTCAGAGATGCTCCTGTTGGAGAGAGAGAGCC 1935
 QY 1861 CCAGCAAAATATGTACAGAACATCCAGCTTCATGCGCAGCAGAGTGGCGAATCTCTC 1920
 Db 1936 CCAGCAAAATATGTACAGAACATCCAGCTTCATGCGCAGCAGAGTGGCGAATCTCTC 1995
 QY 1921 CTCACAGAGAACGGCCATTTATGTGTGTGAGATGACAAAGATTTGSCCAAGATGTA 1980
 Db 1996 CTCACAGAGAACGGCCATTTATGTGTGTGAGATGACAAAGATTTGSCCAAGATGTA 2055
 QY 1981 CATGATGCCCTTGTGCAATTAATAGCAAGAGTGTGAGTTGAAAAACTTAAGCAATG 2040
 Db 2056 CATGATGCCCTTGTGCAATTAATAGCAAGAGTGTGAGTTGAAAAACTTAAGCAATG 2115
 QY 2041 AAAACCTGGCCACTTTAAAGAAAGAAAAAGCTACCTTCAGAGATTTTGGTCATTA 2097
 Db 2116 AAAACCTGGCCACTTTAAAGAAAGAAAAAGCTACCTTCAGAGATTTTGGTCATTA 2172

RESULT 13

ADQ39029
ID ADQ39029 standard; DNA; 3256 BP.

XX ADQ39029;

XX 18-NOV-2004 (first entry)

XX Human SNP containing myocardial infarction-associated gene, SEQ ID 692.

XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KW cardiant; gene therapy; human; gene; ds.

XX Homo sapiens.

XX WO2004058052-A2.

XX 15-JUL-2004.

XX 22-DEC-2003; 2003WO-US040978.

XX 20-DEC-2002; 2002US-0434778P.

XX 10-MAR-2003; 2003US-0453135P.

XX 30-APR-2003; 2003US-0466412P.

XX 23-SEP-2003; 2003US-0504955P.

PA (APPL-) APPLERA CORP.
 XX
 PI Cargill M, Devlin J, Iakoubova O;
 XX
 DR WPI, 2004-533949/51.
 DR P-PSDB; ADQ39857.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX
 PS Claim 7; SEQ ID NO 692; 145bp; English.
 XX
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC polynucleotide sequence represents a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 XX
 SQ Sequence 3256 BP; 927 A; 691 C; 669 G; 940 T; 0 U; 29 Other;
 Query Match 48.5%; Score 1018; DB 13; Length 3256;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 1968; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 111 TATTAGTGAATCCGATTAAGTATGACTTAATAAACCGAAACAGCTCCTGTGTGTGTGT 170
 Db 204 TATTAGTGAATCCGATTAAGTATGACTTAATAAACCGAAACAGCTCCTGTGTGTGTGT 263
 QY 171 TTCTACACGGGACCGGAGACCCACCGACACAGCCCGCAAGTTTGTAAAGAAATACA 230
 Db 264 TTCTACACGGGACCGGAGACCCACCGACACAGCCCGCAAGTTTGTAAAGAAATACA 323
 QY 231 GAACCAACACGCGGTTGATTTCTTGTGCTACCTGCGGATTTGGTTTCTGGGTCTGG 290
 Db 324 GAACCAACACGCGGTTGATTTCTTGTGCTACCTGCGGATTTGGTTTCTGGGTCTGG 383
 QY 291 TGAATTCAGATACACCTACTTTTGGCAATGGGGGAAGATTAATGTAACGACTTCAAGA 350
 Db 384 TGAATTCAGATACACCTACTTTTGGCAATGGGGGAAGATTAATGTAACGACTTCAAGA 443
 QY 351 GCTTGAAGCCCGGCAATTTCTATGACACTGAGACATGACATGCTGTGTAGTAACT 410
 Db 444 GCTTGAAGCCCGGCAATTTCTATGACACTGAGACATGACATGCTGTGTAGTAACT 503
 QY 411 TGTGTTGAGCGGTGATTTGCTGAGCTGTGCGCACCGCTCAGAAAGCATTTAGGTCAG 470
 Db 504 TGTGTTGAGCGGTGATTTGCTGAGCTGTGCGCACCGCTCAGAAAGCATTTAGGTCAG 563
 QY 471 CAGAGACAAAGAGATTAAGTGGCGCACTCCCGGTGGCATGCTGCAATCCTTGAAGAC 530

Db 564 CAGAGCAAGAGAGATAGTGGCCGACCTCCGGTGGCATCACTGATCTCTTGAAGAC 623
 Qy 531 AGACCTTGTGAAGTCAAGAGTCTTACACATTAATCTCAAGTGAAGTTTGAAGTTCGA 590
 Db 624 AGACCTTGTGAAGTCAAGAGTCTTACACATTAATCTCAAGTGAAGTTTGAAGTTCGA 683
 Qy 591 TGAATTCAGAGAAAGAAAGATTTCTGAGTTTGAAGCAAAAATGCAATGAAACCAATTC 650
 Db 684 TGAATTCAGAGAAAGAAAGATTTCTGAGTTTGAAGCAAAAATGCAATGAAACCAATTC 743
 Qy 651 CAATGTTGTAATGAAGACTTTGAGTCTCACTTACCCGTTGGTACCCCACTCTCA 710
 Db 744 CAATGTTGTAATGAAGACTTTGAGTCTCACTTACCCGTTGGTACCCCACTCTCA 803
 Qy 711 AGCCTCTCTGAATATTTCTGTTTACCCCAAGATTTTACAGTATCATCTGACAGAGTC 770
 Db 804 AGCCTCTCTGAATATTTCTGTTTACCCCAAGATTTTACAGTATCATCTGACAGAGTC 863
 Qy 771 TCTTGGCAGAGAAAGCAAGATCTGTGACTTCAGCAGATTCAGTCTTCAAGTGGC 830
 Db 864 TCTTGGCAGAGAAAGCAAGATCTGTGACTTCAGCAGATTCAGTCTTCAAGTGGC 923
 Qy 831 AATTTCAGAGCACTTCACTTACAGATGATGCAATTAACCACTCTGCTGTGAGA 890
 Db 924 AATTTCAGAGCACTTCACTTACAGATGATGCAATTAACCACTCTGCTGTGAGA 983
 Qy 891 AATTGCAATTTCAATACAGACTTTTCTATCAGCTGAGATGCTTCAAGCTGTATCTG 950
 Db 984 AATTGCAATTTCAATACAGACTTTTCTATCAGCTGAGATGCTTCAAGCTGTATCTG 1043
 Qy 951 CCTTACAGATGATTTCTGAGTACAAAGCTTCTCAAGATGCTGAGTTTGAAGTAAAG 1010
 Db 1044 CCTTACAGATGATTTCTGAGTACAAAGCTTCTCAAGATGCTGAGTTTGAAGTAAAG 1103
 Qy 1011 AGAGCACTGCTCTTTTGAATAAAGCAGACACAAGAAAGAAAGAAAGCTTACCTTACC 1070
 Db 1104 AGAGCACTGCTCTTTTGAATAAAGCAGACACAAGAAAGAAAGAAAGCTTACCTTACC 1163
 Qy 1071 CAGACATATACCTGCGGAGATGTTCTCTCAGATTCATTTTACCTGATGCTTGAATCCG 1130
 Db 1164 CAGACATATACCTGCGGAGATGTTCTCTCAGATTCATTTTACCTGATGCTTGAATCCG 1223
 Qy 1131 AGCAATTCCTTAAAAAGCAATTTTGGCAGGCCCTTGTGACTATACAGTGAAGTGTGTA 1190
 Db 1224 AGCAATTCCTTAAAAAGCAATTTTGGCAGGCCCTTGTGACTATACAGTGAAGTGTGTA 1283
 Qy 1191 AAAGCGCAGGCTACAGAGGCTGTGAGTAAACAAAGGGGACGCAATATAGCCCTTTGT 1250
 Db 1284 AAAGCGCAGGCTACAGAGGCTGTGAGTAAACAAAGGGGACGCAATATAGCCCTTTGT 1343
 Qy 1251 ACGAGATGCTGCTGCTGCTTGTGATCTCTGCTGCTTCTTCCCTTCTTGCAGCCACC 1310
 Db 1344 ACGAGATGCTGCTGCTGCTTGTGATCTCTGCTGCTTCTTCCCTTCTTGCAGCCACC 1403
 Qy 1311 ACTCAGTCTCTGCTGCAACATCTTCTTAACTTCAACCCAGACCAATTCGTGTGAAG 1370
 Db 1404 ACTCAGTCTCTGCTGCAACATCTTCTTAACTTCAACCCAGACCAATTCGTGTGAAG 1463
 Qy 1371 CTCAGATTTATTTCAACCCAGAAAGCTCAATTTTGTCTTCAACCTTGTGAATTTCTGTC 1430
 Db 1464 CTCAGATTTATTTCAACCCAGAAAGCTTCAATTTTGTCTTCAACCTTGTGAATTTCTGTC 1523
 Qy 1431 TACTGCAACAACAGAGGTTCTGCGAAAGGAGTATGTAACAGGCTGAGCTGTGTTGGT 1490
 Db 1524 TACTGCAACAACAGAGGTTCTGCGAAAGGAGTATGTAACAGGCTGAGCTGTGTTGGT 1583
 Qy 1491 TGCTTCAGTTCTTCAAGCCAAACATACATGATCCCAAGAAAGACGCGGAAAGCCCTGGC 1550
 Db 1584 TGCTTCAGTTCTTCAAGCCAAACATACATGATCCCAAGAAAGACGCGGAAAGCCCTGGC 1643
 Qy 1551 TCCTAAGATATTCATCTCTCTCGAACAACAAATTTTCTTCACTTACAGATGACCCCTC 1610
 Db 1644 TCCTAAGATATTCATCTCTCTCGAACAACAAATTTTCTTCACTTACAGATGACCCCTC 1703

Qy 1611 AATCCCATCATATATGTTGGTTCAGAAACCGGATAGCCCGGTTTATTTGGTCTCTACA 1670
 Db 1704 AATCCCATCATATATGTTGGTTCAGAAACCGGATAGCCCGGTTTATTTGGTCTCTACA 1763
 Qy 1671 ACATAGAGAAAGCTCCAGAAACAACCCAGATGGAATTTTGGCAATGTTGTTT 1730
 Db 1764 ACATAGAGAAAGCTCCAGAAACAACCCAGATGGAATTTTGGCAATGTTGTTT 1823
 Qy 1731 TTTTGGCTCAGGCAATAGATAGGATTTATCTATTCAGAAAAGAGCTCAGATTTCTCT 1790
 Db 1824 TTTTGGCTCAGGCAATAGATAGGATTTATCTATTCAGAAAAGAGCTCAGATTTCTCT 1883
 Qy 1791 TTAAGCATGGGATCTTAACTCATCTTAAAGTTTCTTCTCAAGAGATCTCTGTTGGGA 1850
 Db 1884 TTAAGCATGGGATCTTAACTCATCTTAAAGTTTCTTCTCAAGAGATCTCTGTTGGGA 1943
 Qy 1851 GGAGGAAGCCCGCAGCAAGATATGTAACAACAATCCAGCTTCATGGCAGAGGTTGGC 1910
 Db 1944 GGAGGAAGCCCGCAGCAAGATATGTAACAACAATCCAGCTTCATGGCAGAGGTTGGC 2003
 Qy 1911 GGAATCTCTCTCCAGAGAAAGCCCATATTTATGTTGTGAGATGCAAGAATATGCG 1970
 Db 2004 GGAATCTCTCTCCAGAGAAAGCCCATATTTATGTTGTGAGATGCAAGAATATGCG 2063
 Qy 1971 CAAGATGTAATGATGCTCTTGTGCAATATATAGCAAAAGAGTTGGAGTTGAAAACCT 2030
 Db 2064 CAAGATGTAATGATGCTCTTGTGCAATATATAGCAAAAGAGTTGGAGTTGAAAACCT 2123
 Qy 2031 AGAAGCAATGAAGAAAGCTGCGCACTTTAAAGAAAGAAAGAGTACCTTCAGAGTATTTG 2090
 Db 2124 AGAAGCAATGAAGAAAGCTGCGCACTTTAAAGAAAGAAAGAGTACCTTCAGAGTATTTG 2183
 Qy 2091 GTCATTA 2097
 Db 2184 GTCATTA 2190

RESULT 14
 ADQ39030
 ID ADQ39030 standard; DNA; 3274 BP.
 AC ADQ39030;
 AC 18-NOV-2004 (first entry)
 XX
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 693.
 XX
 KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KW cardiant; gene therapy; human; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN W02004058052-A2.
 PD 15-JUL-2004.
 XX
 PF 22-DEC-2003; 2003MO-US040978.
 PR 20-DEC-2002; 2002US-0434778P.
 PR 10-MAR-2003; 2003US-0453135P.
 PR 30-APR-2003; 2003US-046412P.
 PR 23-SEP-2003; 2003US-0504955P.
 XX
 PA (APPL-) APPLERA CORP.
 PI Cargill M, Devlin JT, Iakoubova O;
 XX
 DR WPI; 2004-533949/51.
 DR P-PSDB; ADQ39858.
 XX
 PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in

QY 1731 TTTTGGCTGAGGATAGAGATAGAGATATCTATTGAGAAAAGCTGACATTTTCT 1790
DB 1842 TTTTGGCTGAGGATAGAGATAGAGATATCTATTGAGAAAAGCTGAGATTTTCT 1901
QY 1791 TAAGCATGGATCTTAATCATCTAAAGATTTCTCTCAAGAGATCTCTGTGGGGA 1850
DB 1902 TAAGCATGGATCTTAATCATCTAAAGATTTCTCTCAAGAGATCTCTGTGGGGA 1961
QY 1851 GAGAGAAAGCCCGAGCAAAAGTATGTATCAAGACATCAGCTTCAGTGGCAGAGTGGC 1910
DB 1962 GAGAGAAAGCCCGAGCAAAAGTATGTATCAAGACATCAGCTTCAGTGGCAGAGTGGC 2021
QY 1911 GAGATCTCTCTCCAGAGAAAGCGCATTTATTTATGTGTGGAGATGCAAAAGATTTGGC 1970
DB 2022 TAGATCTCTCTCCAGAGAAAGCGCATTTATTTATGTGTGGAGATGCAAAAGATTTGGC 2081
QY 1971 CAAGATGTATCATGATGCTCTGTGTGCAAAATATATAGCAAAAGAGTTGAGTTGAAAAC 2030
DB 2082 CAAGATGTATCATGATGCTCTGTGTGCAAAATATATAGCAAAAGAGTTGAGTTGAAAAC 2141
QY 2031 AGAAGCAATGAAAACCTGTGCGCACTTTAAAGAAAGAAAAGCTACCTTCAGAGATTTTG 2090
DB 2142 AGAAGCAATGAAAACCTGTGCGCACTTTAAAGAAAGAAAAGCTACCTTCAGAGATTTTG 2201
QY 2091 GTCATTA 2097
DB 2202 GTCATTA 2208

RESULT 15
ID ACN42470 standard; cDNA; 3189 BP.
AC ACN42470;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1345.
XX
KW se; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
XX dltbp.
XX
OS Homo sapiens.
XX
PN MO2004023973-A2.
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Hartshorne TA, Suchorolski MT, Altus CM, Plets SD, Elder LV;
PI Mooney EM, Delemane AM, Panesar IS, Banville SC, Reddy TP;
PI Sevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LI;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vite UA, Kitron BS;
PI Xu Y, Kong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
DR P-PSDB; ABM83818.
XX
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
PS Claim 1; Page; 190pp; English.

XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dltbp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorder,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dltbp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dltbp polynucleotide of
CC the invention. Note: The sequence data for this patent is not represented
CC in the printed specification, but was obtained in electronic format
CC directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 3189 BP; 916 A; 679 C; 665 G; 929 T; 0 U; 0 Other;

Query Match 43.2%; Score 905; DB 13; Length 3189;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1055; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ANAGAGAGGTTTCTGTACTATATGCTATACAGCAGGAGCAGGCAAGGCAATGCGAGAA 60
DB 112 ATGAGAGAGGTTTCTGTACTATATGCTATACAGCAGGAGCAGGCAAGGCAATGCGAGAA 171

QY 61 GAAATGTGAGCAAGCTGTGATCATGATTTTCTGAGATCTTCAATATATTAGAA 120
DB 172 GAAATGTGAGCAAGCTGTGATCATGATTTTCTGAGATCTTCAATATATTAGAA 231

QY 121 TCCGATAGATGACCTTAAACCGAAGACGCTCTTGTGTGTGTGTTTCTACACG 180
DB 232 TCCGATAGATGACCTTAAACCGAAGACGCTCTTGTGTGTGTGTTTCTACACG 291

QY 181 GGCACCGGAGACCCAGCCGACAGCCGCAAGTTTGAAGAAATACAGAACCAACA 240
DB 292 GGCACCGGAGACCCAGCCGACAGCCGCAAGTTTGAAGAAATACAGAACCAACA 351

QY 241 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGAGTTCTGAGTTCTGAGTTTGA 300
DB 352 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGAGTTCTGAGTTCTGAGTTTGA 411

QY 301 TACACCTACTTTTGAATGAGGAGGAAATATGATTAACGACTTCAAGGCTTGAAGC 360
DB 412 TACACCTACTTTTGAATGAGGAGGAAATATGATTAACGACTTCAAGGCTTGAAGC 471

QY 361 CGGCAATTTCTAGACACTGACATGAGATGACTGTGATGTTTAAACCTTGTGTTGAG 420
DB 472 CGGCAATTTCTAGACACTGACATGAGATGACTGTGATGTTTAAACCTTGTGTTGAG 531

QY 421 CCGTGATTTCTGAGCTGTGCGCAGCCCTCAGAAACATTTTATGATCAAGAGAGCAA 480
DB 532 CCGTGATTTCTGAGCTGTGCGCAGCCCTCAGAAACATTTTATGATCAAGAGAGCAA 591

QY 481 GAGAGATTAAGTGGCAGCTCCGTTGGCATCCTGCAATCTTGAAGACAGCTTTG 540
DB 592 GAGAGATTAAGTGGCAGCTCCGTTGGCATCCTGCAATCTTGAAGACAGCTTTG 651

QY 541 AATTCAGAGTGTATACATGAAATCTCAAGTGCAGCTTCTGAGATTTGAGTTTGA 600
DB 652 AATTCAGAGTGTATACATGAAATCTCAAGTGCAGCTTCTGAGATTTGAGTTTGA 711

QY 601 AGAAGGATTTCTGAGTTTGAAGCAAAATGAGTGAAGCAAGCAACCAATGATTTG 660
DB 712 AGAAGGATTTCTGAGTTTGAAGCAAAATGAGTGAAGCAAGCAACCAATGATTTG 771

QY 661 ATTGAAGACTTTGAGTCTTCACTTACCCGTTGGTACCCCACTTCAAGGCTTCTG 720
DB 772 ATTGAAGACTTTGAGTCTTCACTTACCCGTTGGTACCCCACTTCAAGGCTTCTG 831

QY 721 AATTTCTGTTTACCCCAAGAAATTTTACAGGTATCTGAGAGAGTCTTGGCCAG 780

Db	832	AATATTCCTGATTTAAACCCCAAGATATTTACAGGTACATCTGCAAGAGATCTCTTGCCAG	891
Qy	781	GAGGAAAGCCAAAGTATCTGTGACTTCAGCAGATCCAGTTTTCAGTGCCAATTTCAAAG	840
Db	892	GAGGAAAGCCAAAGTATCTGTGACTTCAGCAGATCCAGTTTTCAGTGCCAATTTCAAAG	951
Qy	841	GCAGTTCAACTTACTAGCAAGATGATGCCATAAAACACTGCGCTGTGATGATTTGGACATT	900
Db	952	GCAGTTCAACTTACTAGCAAGATGATGCCATAAAACACTGCGCTGTGATGATTTGGACATT	1011
Qy	901	TCAATAACAGACTTTTCTTATCAGCGTGGAGATGCTTCAGCGATCTGCCCTAACAGT	960
Db	1012	TCAATAACAGACTTTTCTTATCAGCGTGGAGATGCTTCAGCGATCTGCCCTAACAGT	1071
Qy	961	GATTCTGAGGTACAAAGCTTACTCCAAAGACTGCAGCTTGAAGATTAAGAAGACACTGC	1020
Db	1072	GATTCTGAGGTACAAAGCTTACTCCAAAGACTGCAGCTTGAAGATTAAGAAGACACTGC	1131
Qy	1021	GTCCTTTGAAAATTAAGGACAGACCAAGAAGAAAG	1058
Db	1132	GTCCTTTGAAAATTAAGGACAGACCAAGAAGAAAG	1169

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Job time : 738.49 secs

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OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 23:30:25 ; Search time 235.757 Seconds
(without alignments)
14554.251 Million cell updates/sec

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Perfect score: 2097
Sequence: 1 atgagagagcttcgtact.....ttcagatattgtcctaa 2097

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*

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- 6: /cgn2_6/prodata/1/ina/6D_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2046	97.6	3259	3 US-09-318-448-23	Sequence 23, App1
2	1893	90.3	3242	4 US-09-949-016-4215	Sequence 4215, App1
3	386	18.4	390	3 US-08-905-223-71	Sequence 71, App1
4	330	15.7	601	4 US-09-949-016-150019	Sequence 150019, App1
5	330	15.7	35916	4 US-09-949-016-15857	Sequence 15857, A
6	279	13.3	601	4 US-09-949-016-150020	Sequence 150020, A
7	189	9.0	601	4 US-09-949-016-150037	Sequence 150037, A
8	158	7.5	2475	4 US-09-566-921-88	Sequence 88, App1
9	155	7.4	601	4 US-09-949-016-150030	Sequence 150030, A
10	145	6.9	601	4 US-09-949-016-150031	Sequence 150031, A
11	137	6.5	601	4 US-09-949-016-150046	Sequence 150046, A
12	137	6.5	601	4 US-09-949-016-150047	Sequence 150047, A
13	125	6.0	601	4 US-09-949-016-150029	Sequence 150029, A
14	121	5.8	601	4 US-09-949-016-150041	Sequence 150041, A
15	121	5.8	601	4 US-09-949-016-150042	Sequence 150042, A
16	119	5.7	601	4 US-09-949-016-150008	Sequence 150008, A
17	119	5.7	601	4 US-09-949-016-150055	Sequence 150055, A
18	110	5.2	601	4 US-09-949-016-150048	Sequence 150048, A
19	96	4.5	601	4 US-09-949-016-150032	Sequence 150032, A
20	74	3.6	601	4 US-09-949-016-150018	Sequence 150018, A
21	65	3.3	244	4 US-09-471-276-495	Sequence 495, App
22	65	3.3	601	4 US-09-949-016-150007	Sequence 150007, A
23	30	1.4	1681	4 US-09-023-655-453	Sequence 453, App
24	20	1.0	273	4 US-09-513-995C-14761	Sequence 14761, A
25	20	1.0	440	4 US-09-397-787-305	Sequence 305, App
26	20	1.0	444	4 US-09-621-976-14139	Sequence 14139, A
27	20	1.0	445	3 US-09-397-787-274	Sequence 274, App

C	28	20	1.0	174259	4 US-09-949-016-11968	Sequence 11968, A
C	29	20	1.0	174262	4 US-09-949-016-14259	Sequence 14259, A
C	30	19	0.9	169	1 US-08-166-346A-8	Sequence 8, App1
C	31	19	0.9	459	4 US-09-621-976-8324	Sequence 8324, App
C	32	19	0.9	3969	3 US-09-518-386B-4	Sequence 4, App1
C	33	19	0.9	4396	3 US-09-821-736-1	Sequence 1, App1
C	34	19	0.9	14721	4 US-09-949-016-11507	Sequence 13507, A
C	35	19	0.9	25199	4 US-09-949-016-13361	Sequence 13361, A
C	36	19	0.9	129658	4 US-09-949-016-17195	Sequence 17195, A
C	37	19	0.9	186734	4 US-09-949-016-14870	Sequence 14870, A
C	38	19	0.9	193689	4 US-09-949-016-12350	Sequence 12350, A
C	39	19	0.9	193689	4 US-09-949-016-13088	Sequence 13088, A
C	40	19	0.9	200663	4 US-09-949-016-12569	Sequence 12569, A
C	41	19	0.9	203093	4 US-09-949-016-14445	Sequence 14445, A
C	42	18	0.9	78	2 US-08-749-852-56	Sequence 56, App1
C	43	18	0.9	78	2 US-08-749-852-58	Sequence 58, App1
C	44	18	0.9	531	4 US-09-252-991A-2223	Sequence 2223, App
C	45	18	0.9	601	4 US-09-949-016-49781	Sequence 49781, A

ALIGNMENTS

RESULT 1									
US-09-318-448-23									
; Sequence 23, Application US/09318448									
; Patent No. 6210950									
; GENERAL INFORMATION:									
; APPLICANT: Johnson, William G.									
; APPLICANT: Stenroos, Edward S.									
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING									
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS									
; FILE REFERENCE: 601-1-057									
; CURRENT APPLICATION NUMBER: US/09/318,448									
; CURRENT FILING DATE: 1999-05-25									
; NUMBER OF SEQ ID NOS: 46									
; SOFTWARE: Patentin Ver. 2.0									
; SEQ ID NO 23									
; LENGTH: 3259									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-09-318-448-23									
Query Match									
Best Local Similarity 97.6%; Score 2046; DB 3; Length 3259;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	1	ATGAGAGGTTTCTGTTACTATATGCTACAGCAGGAGGAGCAAGCAAGGCGATCGAGAA	60						
DB	80	ATGAGAGGTTTCTGTTACTATATGCTACAGCAGGAGGAGCAAGCAAGGCGATCGAGAA	139						
QY	61	GAATGTGTGAGCAGCTGTGTACATGATTTTTCGAGATCTTCACTATATAGTGA	120						
DB	140	GAATGTGTGAGCAGCTGTGTACATGATTTTTCGAGATCTTCACTATATAGTGA	199						
QY	121	TCGGATATGATGACCTAAACCGAAGAGCTCTTGTTGTTGTTTACACAG	180						
DB	200	TCGGATATGATGACCTAAACCGAAGAGCTCTTGTTGTTGTTTACACAG	259						
QY	181	GGCAGCGAGACCCAGCAGCCGCAAGTTTGAAGAAATACAGCAACA	240						
DB	260	GGCAGCGAGACCCAGCAGCCGCAAGTTTGAAGAAATACAGCAACA	319						
QY	241	CTGCGGTTGATTTCTTGTCTACCTGCGGTATGAGTTTCTCGTATTCAGAA	300						
DB	320	CTGCGGTTGATTTCTTGTCTACCTGCGGTATGAGTTTCTCGTATTCAGAA	379						
QY	301	TACACCTATTTGCAATGGGGGAATATGATTAACGACTTCAAGAGCTTGAGCC	360						
DB	380	TACACCTATTTGCAATGGGGGAATATGATTAACGACTTCAAGAGCTTGAGCC	439						
QY	361	CGGATTTATGACATGAGCATGAGTGTGTGATTTAGAACTTGTTGTTGAG	420						

Db 440 CGGCAATTTCTATGACACTGACATGACATGACTGTGTAGGTTTAAACAATTGGTTGAG 439
Qy 421 CCGTGATGCTGAGACTCTGAGCCAGCCCTCAGAAAGCAATTTAGTCAAGCAGAGACA 480
Db 500 CCGTGATGCTGAGACTCTGAGCCAGCCCTCAGAAAGCAATTTAGTCAAGCAGAGACA 559
Qy 481 GAGGAGATTAAGTGGCGCATCTCCGGTGGCATCACCTGCATCTTGAAGACAGACCTTGG 540
Db 560 GAGGAGATTAAGTGGCGCATCTCCGGTGGCATCACCTGCATCTTGAAGACAGACCTTGG 619
Qy 541 AAGTCAGAGCTGACACATTTGAATCTCAAGTGGAGCTTGAAGATTTCAGATTCAGGA 600
Db 620 AAGTCAGAGCTGACACATTTGAATCTCAAGTGGAGCTTGAAGATTTCAGATTCAGGA 679
Qy 601 AGAAGAGATCTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCCAAATGTGTA 660
Db 680 AGAAGAGATCTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCCAAATGTGTA 739
Qy 661 ATTGAAGACTTTGAGTCTCTCACTTACCCGTTCCGTAACCCCACTCTCAAGCCTCTG 720
Db 740 ATTGAAGACTTTGAGTCTCTCACTTACCCGTTCCGTAACCCCACTCTCAAGCCTCTG 739
Qy 721 AATATTCCTGGTTTACCCCAAGATATTTTACAGGTATCATGACAGAGAGTCTCTTGGCAG 780
Db 800 AATATTCCTGGTTTACCCCAAGATATTTTACAGGTATCATGACAGAGAGTCTCTTGGCAG 859
Qy 781 GAGGAAAGCCAGATATCTGATCTTCAAGAGATCCAGTCTTTCAGAGTCCAAATTTCAAG 840
Db 860 GAGGAAAGCCAGATATCTGATCTTCAAGAGATCCAGTCTTTCAGAGTCCAAATTTCAAG 919
Qy 841 GCAGTTCAACTTACTAGAAATGATGCAATTAACCACTCTGCTGGTGAATTTGACATT 900
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Qy 901 TCAATATCAGACTTTTCTATCAGCCTGAGATGCTTCAAGCAGTCTGCTCCCTAACAT 960
Db 980 TCAATATCAGACTTTTCTATCAGCCTGAGATGCTTCAAGCAGTCTGCTCCCTAACAT 1039
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Db 1100 GTCTTTTGAATTAAGGACAGACACAAAGAAAGAGCTTACCCACGACATATA 1159
Qy 1081 CCGCGGAGATGTTCTCCAGATTCATTTTACCGTGTGCTGTAATCCGAGCAATTCCT 1140
Db 1160 CCGCGGAGATGTTCTCCAGATTCATTTTACCGTGTGCTGTAATCCGAGCAATTCCT 1219
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Qy 1201 CTACAGAGAGCTGTGACATTAACAAGGGGACGCGATTAATAGCGCTTTGTAACAGATGCC 1260
Db 1280 CTACAGAGAGCTGTGACATTAACAAGGGGACGCGATTAATAGCGCTTTGTAACAGATGCC 1339
Qy 1261 TGGAGCCTGCTTGTGATCTCTCCTGCTTCCCTTCCGTCAGGACCAACATCAAGTCTC 1320
Db 1340 TGGAGCCTGCTTGTGATCTCTCCTGCTTCCCTTCCGTCAGGACCAACATCAAGTCTC 1399
Qy 1321 CTGCTCGAACAATCTTCTTAAACTTCAACCCAGACCATATTCGTGTGACAGCTCAAGTTTA 1380
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Qy 1381 TTTCACCCAGAAAGCTTCATTTTGTCTTCAACATTTGATTAATTTCTGTCTACTGCCACA 1440
Db 1460 TTTCACCCAGAAAGCTTCATTTTGTCTTCAACATTTGATTAATTTCTGTCTACTGCCACA 1519
Qy 1441 ACAGAGGTTCTGCGGAGAGAGATATGTAACAGGCTGAGCTTGGTGGTGGTCTCAAGTT 1500
Db 1520 ACAGAGGTTCTGCGGAGAGAGATATGTAACAGGCTGAGCTTGGTGGTGGTCTCAAGTT 1579

Qy 1501 CTTACGCAAAACATACATGATCATCCATGAAAGACGCGGAAAAAGCCCTGGCTCTTAAGATA 1560
Db 1580 CTTACGCAAAACATACATGATCATCCATGAAAGACGCGGAAAAAGCCCTGGCTCTTAAGATA 1639
Qy 1561 TCGATCTCTCTCGAACAACAAATTTTCCACTTACAGATTAACCCCTCAATCCCCATC 1620
Db 1640 TCGATCTCTCTCGAACAACAAATTTTCCACTTACAGATTAACCCCTCAATCCCCATC 1699
Qy 1621 ATATAGTGGGTTCAGAAACCGGACATAGCCCGTATTATGGTTTCTTACACATAGAGAG 1680
Db 1700 ATATAGTGGGTTCAGAAACCGGACATAGCCCGTATTATGGTTTCTTACACATAGAGAG 1759
Qy 1681 AAATCTCAAGAACACACCCAGATGAGAAATTTTGAAGCAATGTGTTTGTGGCTGC 1740
Db 1760 AAATCTCAAGAACACACCCAGATGAGAAATTTTGAAGCAATGTGTTTGTGGCTGC 1819
Qy 1741 AGGCAATTAAGATTAAGGATTTATCTTTCAGAAAAAGACTCAGACATTTCTTAAGCATGG 1800
Db 1820 AGGCAATTAAGATTAAGGATTTATCTTTCAGAAAAAGACTCAGACATTTCTTAAGCATGG 1879
Qy 1801 ATCTTAATCATCTAAAGGTTTCTCTCAGAGATGCTCTGTGGGAGAGAGAGCC 1860
Db 1880 ATCTTAATCATCTAAAGGTTTCTCTCAGAGATGCTCTGTGGGAGAGAGAGCC 1939
Qy 1861 CCAGCAAGATATGTACAGAACACATCCAGCTTCATGCGCAGAGGTGGCAGAAATCTTC 1920
Db 1940 CCAGCAAGATATGTACAGAACACATCCAGCTTCATGCGCAGAGGTGGCAGAAATCTTC 1999
Qy 1921 CTCACAGAGAACGCGCATTTTATGTGTGAGATGCAAAAGATATGCGCAAGATGTA 1980
Db 2000 CTCACAGAGAACGCGCATTTTATGTGTGAGATGCAAAAGATATGCGCAAGATGTA 2059
Qy 1981 CATGATGCCCTTGTGCAAAATTAATTAAGAGAGTTGAGTTGAAACCTAGAACATG 2040
Db 2060 CATGATGCCCTTGTGCAAAATTAATTAAGAGAGTTGAGTTGAAACCTAGAACATG 2119
Qy 2041 AAAACCTGGCCACTTTAAAGAAAGAAAAAGCTTACAGATATTTGTGATATA 2097
Db 2120 AAAACCTGGCCACTTTAAAGAAAGAAAAAGCTTACAGATATTTGTGATATA 2176

RESULT 2
US-09-949-016-4215
; Sequence 4215, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4215
; LENGTH: 3242
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4215

Query Match 90.3%; Score 1893; DB 4; Length 3242;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ATGAGAGGTTTGTGTTACTATATGCTACACAGACAGGACAAAGGCATCGCAGAA 60
|||||

Db 80 ATGAGAGGTTTCTGTATATATGCTACACAGCAGGAGCAGCAAAAGCCATCCGAGA 139
Qy 61 GAAATGTGAGCAAGCTGTGTACATGATTTTCTGCGATCTTCACTATATATGTA 120
Db 140 GAAATATGACCAAGCTGTGTACATGATTTTCTGCGATCTTCACTATATGTA 199
Qy 121 TCCGATTAAGTATGACCTTAAACCCGAAAGAGCTCTCTGTGTGTGTGTCTACAG 180
Db 200 TCCGATTAAGTATGACCTTAAACCCGAAAGAGCTCTCTGTGTGTGTGTCTACAG 259
Qy 181 GGCACCGAGAGCCCAACCGACACAGCCGCAAGTTTGTAAAGAAATACAAACCA 240
Db 260 GGCACCGAGAGCCCAACCGACACAGCCGCAAGTTTGTAAAGAAATACAAACCA 319
Qy 241 CTGCGGTGATTTCTTGTCTACCTGCGGTATGAGTTACTGGGTCTGGGTATTTAGAA 300
Db 320 CTGCGGTGATTTCTTGTCTACCTGCGGTATGAGTTACTGGGTCTGGGTATTTAGAA 379
Qy 301 TACACCTACTTTTGAATGGGGGAGATTAATTGATTAACGACTTCAAGAGCTTGAGCC 360
Db 380 TACACCTACTTTTGAATGGGGGAGATTAATTGATTAACGACTTCAAGAGCTTGAGCC 439
Qy 361 CGGCAATTTCTATGACACTGACACATGACATGACTGTAGTTTAAAGCTTGTTGAG 420
Db 440 CGGCAATTTCTATGACACTGACACATGACATGACTGTAGTTTAAAGCTTGTTGAG 499
Qy 421 CCGTGGATTTGCTGACCTTGGCCAGCCCTCAGAAAGATTTTATGTTAGCAGAGAGCA 480
Db 500 CCGTGGATTTGCTGACCTTGGCCAGCCCTCAGAAAGATTTTATGTTAGCAGAGAGCA 559
Qy 481 GAGGAGATTAAGTGGGAGCACTCCCGGTGGATACCTGACCTCTGAGAGCAGACTTGTG 540
Db 560 GAGGAGATTAAGTGGGAGCACTCCCGGTGGATACCTGACCTCTGAGAGAGCCTTGTG 619
Qy 541 AAGTCAGAGCTGTACATATGATCTCAAGTCGAGCTTCTGAGATTCATGATTCAGGA 600
Db 620 AAGTCAGAGCTGTACATATGATCTCAAGTCGAGCTTCTGAGATTCATGATTCAGGA 679
Qy 601 AGAAGGATTTCTGAGTTTGAAGCAAAATGACATGACAGCAACCAATCCAAATGTTGTA 660
Db 680 AGAAGGATTTCTGAGTTTGAAGCAAAATGACATGACAGCAACCAATCCAAATGTTGTA 739
Qy 661 ATTTGAAGCTTTGAGTCTCACTTACCCGTTGGTACCCCACTCTCAAGGCTCTG 720
Db 740 ATTTGAAGCTTTGAGTCTCACTTACCCGTTGGTACCCCACTCTCAAGGCTCTG 799
Qy 721 AATATCTGTGTTTACCCCAAGATATTTACAGTACATCTGAGAGTCTCTTGCCAG 780
Db 800 AATATCTGTGTTTACCCCAAGATATTTACAGTACATCTGAGAGTCTCTTGCCAG 859
Qy 781 GAGGAAAGCCAAATCTGTGACTTACAGCATCCAGTTTCAAGTCCAAATTTCAAG 840
Db 860 GAGGAAAGCCAAATCTGTGACTTACAGCATCCAGTTTCAAGTCCAAATTTCAAG 919
Qy 841 GCGATTCATTTCTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 920 GCGATTCATTTCTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 979
Qy 901 TCAATATACAGACTTTCTGATCAGCTGAGATGCTTCAAGCTGATCTGCTTAAAGT 960
Db 980 TCAATATACAGACTTTCTGATCAGCTGAGATGCTTCAAGCTGATCTGCTTAAAGT 1039
Qy 961 GATTTGAGGTACAAAGCTTCTCAAGAGCTGAGCTGAGTGAAGATTAAGAGAGCAG 1020
Db 1040 GATTTGAGGTACAAAGCTTCTCAAGAGCTGAGCTGAGTGAAGATTAAGAGAGCAG 1099
Qy 1021 GTCTTTTGAATTAAGAGAGAGCAAAAGAGAGAGCTTCAAGCTTCAAGCTTCAAG 1080
Db 1100 GTCTTTTGAATTAAGAGAGAGCAAAAGAGAGAGCTTCAAGCTTCAAGCTTCAAG 1159
Qy 1081 CTGCGGAGATTTCTCTCAGATTCATTTTATCTGTGTCTTGAATTCAGAGCAATTCCT 1140
Db 1160 CTGCGGAGATTTCTCTCAGATTCATTTTATCTGTGTCTTGAATTCAGAGCAATTCCT 1219

Qy 1141 AAAAGGCAATTTTTCGAGCCCTTGTGACCTATACAGTACAGTGTCTGAAAAAGCGCAG 1200
Db 1220 AAAAGGCAATTTTTCGAGCCCTTGTGACCTATACAGTACAGTGTCTGAAAAAGCGCAG 1279
Qy 1201 CTACAGAGCTGTGAGATTAACAGAGGAGCGAGATTAATAGCCGCTTGTACAGATGCC 1260
Db 1280 CTACAGAGCTGTGAGATTAACAGAGGAGCGAGATTAATAGCCGCTTGTACAGATGCC 1339
Qy 1261 TGTGCTGT 1320
Db 1340 TGTGCTGT 1399
Qy 1321 CTGCTGAAATCTTCTTAACTTCAACCCAGACATATATGCTGTGAGCTCAAGTTTA 1380
Db 1400 CTGCTGAAATCTTCTTAACTTCAACCCAGACATATATGCTGTGAGCTCAAGTTTA 1459
Qy 1381 TTTCAACCGAGAAAGCTCAATTTGTCTTCAATTTGTGAAATTTCTGTCTACTGACCA 1440
Db 1460 TTTCAACCGAGAAAGCTCAATTTGTCTTCAATTTGTGAAATTTCTGTCTACTGACCA 1519
Qy 1441 ACGAGGTTCTGCGAGAGGAGATGATGACGCTGCTGCTGTGTGTGTGTGTGTGT 1500
Db 1520 ACGAGGTTCTGCGAGAGGAGATGATGACGCTGCTGCTGTGTGTGTGTGTGTGT 1579
Qy 1501 CTTCAGCCAAATATCATGCAATCCATGAAAGCAGGAGGAAAGCCCTGCTCTTAAGATA 1560
Db 1580 CTTCAGCCAAATATCATGCAATCCATGAAAGCAGGAGGAAAGCCCTGCTCTTAAGATA 1639
Qy 1561 TCCATCTCTCTCTGAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
Db 1640 TCCATCTCTCTCTGAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1699
Qy 1621 ATATATGT 1680
Db 1700 ATATATGT 1759
Qy 1681 AAACTCCAAAGCAACACCCAGATGAAATTTTGAAGCAATGCTGTGTGTGTGTGTGT 1740
Db 1760 AAACTCCAAAGCAACACCCAGATGAAATTTTGAAGCAATGCTGTGTGTGTGTGTGT 1819
Qy 1741 AGGCAATTAAGATGAGATTAATCTATTCAGAAAAAGCTCAGACATTTCTTAAGCATGG 1800
Db 1820 AGGCAATTAAGATGAGATTAATCTATTCAGAAAAAGCTCAGACATTTCTTAAGCATGG 1879
Qy 1801 ATCTTAATCTATTAAGGTTTCTTCTCAAGATGCTCTGTTGGGAGAGAGAGCC 1860
Db 1880 ATCTTAATCTATTAAGGTTTCTTCTCAAGATGCTCTGTTGGGAGAGAGAGCC 1939
Qy 1861 CCAAGCAATTAATGACAAACAAATCCAGCTTCAATGAGCAGAGGTGGAGAAATCTTC 1920
Db 1940 CCAAGCAATTAATGACAAACAAATCCAGCTTCAATGAGCAGAGGTGGAGAAATCTTC 1999
Qy 1921 CTTCAGAGAGAGGAGCAATTTATGATGTGTGAGATGCAAGATTAATGAGCAAGATGA 1980
Db 2000 CTTCAGAGAGAGGAGCAATTTATGATGTGTGAGATGCAAGATTAATGAGCAAGATGA 2059
Qy 1981 CATGATGCCCTTGTGCAATTAATGAGCAAAAGGTTGAGTTGAAAACTGAGAGCAATG 2040
Db 2060 CATGATGCCCTTGTGCAATTAATGAGCAAAAGGTTGAGTTGAAAACTGAGAGCAATG 2119
Qy 2041 AAAAGCTGTGCACTTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2097
Db 2120 AAAAGCTGTGCACTTAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2176

RESULT 3

US-08-905-223-71
; Sequence 71, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric

APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
TISSUE TYPE: Brain
FEATURE:
NAME/KEY: s19_peptide
LOCATION: 289..357
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 6.9
OTHER INFORMATION: seq SLSLASHSVSC/SN
US-08-905-223-71

Query Match 18.4%; Score 386; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 3.1e-188;
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 970 GTCAAAAGCCTACTCCCAAGACCTGGAAGATTAAGAGAGCACTGCGTCTTTTG 1029
DB 3 GTCAAAAGCCTACTCCCAAGACCTGGAAGATTAAGAGAGCACTGCGTCTTTTG 62
QY 1030 AAATAAAGGACAGCAAAAGAAAGAGAGCTACCTTACCCCGCATATACCTGGGGA 1089
DB 63 AAATAAAGGACAGCAAAAGAAAGAGAGCTACCTTACCCCGCATATACCTGGGGA 122
QY 1090 TGTCTCTCAGTTCATTTTAACTGCTGTGTTGAAATCCGAGCAATTCCTAAAAAGCA 1149
DB 123 TGTCTCTCAGTTCATTTTAACTGCTGTGTTGAAATCCGAGCAATTCCTAAAAAGCA 182
QY 1150 TTTTGGAGAGCCCTTGAGACTATACAGTGAAGCTGCTGAAAAAGCCAGGCTACAGAG 1209
DB 183 TTTTGGAGAGCCCTTGAGACTATACAGTGAAGCTGCTGAAAAAGCCAGGCTACAGAG 242
QY 1210 CTGTCAGTAAACAAGGGGAGCGGATTAAGCCGCTTTGAGAGATGCTGTGCTGC 1269
DB 243 CTGTCAGTAAACAAGGGGAGCGGATTAAGCCGCTTTGAGAGATGCTGTGCTGC 302
QY 1270 TTGTTGATCTCTCTCTGCTTTCCCTTTCCAGGACACCTCACTGCTCTGCTGAA 1329
DB 303 TTGTTGATCTCTCTCTGCTTTCCCTTTCCAGGACACCTCACTGCTCTGCTGAA 362
QY 1330 CATCTTCTTAACTCAACCCAGACC 1355

DB 363 CATCTTCTTAACTCAACCCAGACC 368

RESULT 4
US-09-949-016-150019
Sequence 150019, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 150019
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-150019

Query Match 15.7%; Score 330; DB 4; Length 601;
Best Local Similarity 99.7%; Pred. No. 2.2e-159;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGTTGAGCCGTGATGCTGGACTCTGCGCCAGCCCTCAGAAACATT 460
DB 178 GTTTAGAACTTGTGTTGAGCCGTGATGCTGGACTCTGCGCCAGCCCTCAGAAACATT 237
QY 461 TTAGTCAAGCAGAGACAGAGAGATTAAGTGGCGCACTCCGGTGGCATCCTGCAT 520
DB 238 TTAGTCAAGCAGAGACAGAGAGATTAAGTGGCGCACTCCGGTGGCATCCTGCAT 297
QY 521 CCTTGAGGACAGCCTTGGAAGTCAAGCTGTGTAACATTAATCAAGTGAAGTTC 580
DB 298 CCTTGAGGACAGCCTTGGAAGTCAAGCTGTGTAACATTAATCAAGTGAAGTTC 357
QY 581 TGAGATTCATGATTCAGAGAAAGAGATTCGAGGTTTGAAGCAAAATGACGTGACA 640
DB 358 TGAGATTCATGATTCAGAGAAAGAGATTCGAGGTTTGAAGCAAAATGACGTGACA 417
QY 641 GCAACCAATTCATGTTGTAATTGAAGACTTTGAGTCTCACTTACCCGTTCCGTACCCC 700
DB 418 GCAACCAATTCATGTTGTAATTGAAGACTTTGAGTCTCACTTACCCGTTCCGTACCCC 477
QY 701 CACTTCAGAGGCTCTGGAATATTCCTGTTTACCCCGAGAAATTTTACAGGTACATC 760
DB 478 CACTTCAGAGGCTCTGGAATATTCCTGTTTACCCCGAGAAATTTTACAGGTACATC 537
QY 761 TGCAGAGTCTCTTGCCAGG 781
DB 538 TGCAGAGTCTCTTGCCAGG 558

RESULT 5
US-09-949-016-15957
Sequence 15957, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15957
LENGTH: 35916
TYPE: DNA
ORGANISM: Human
US-09-949-016-15957

Query Match 15.7%; Score 330; DB 4; Length 35916;
Best Local Similarity 99.7%; Pred. No. 2.8e-159;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGTTGAGCCGTGATGCTGGAAGCTTGGCCAGCCCTCAGAAAGCATT 460
DB 10781 GTTTAGAACTTGTGTTGAGCCGTGATGCTGGAAGCTTGGCCAGCCCTCAGAAAGCATT 10840
QY 461 TTAGTCAAGCAGAGACAAGAGAGATTAAGTGGCCGCACTCCCGTGGCATCACTGCAT 520
DB 10841 TTAGTCAAGCAGAGACAAGAGAGATTAAGTGGCCGCACTCCCGTGGCATCACTGCAT 10900
QY 521 CCTTGAAGCAGACCTTGTGAAGTCAAGCTGCTACATTTGAATCTCAAGTGAAGCTTC 580
DB 10901 CCTTGAAGCAGACCTTGTGAAGTCAAGCTGCTACATTTGAATCTCAAGTGAAGCTTC 10960
QY 581 TGAGATTCATGATTAAGAGAAAGAGATTCAGAGTTTGAAGCAAAATGCAGTAAACA 640
DB 10961 TGAGATTCATGATTAAGAGAAAGAGATTCAGAGTTTGAAGCAAAATGCAGTAAACA 11020
QY 641 GCACCAATCCAAATGTTTAATTGAAGACTTTGATCTCTCACTTACCCGTTGGTACCCC 700
DB 11021 GCACCAATCCAAATGTTTAATTGAAGACTTTGATCTCTCACTTACCCGTTGGTACCCC 11080
QY 701 CACTCTCACAAGCTCTGTAATATTCCTGTTTACCCCAAGAAATTTTACAGTACATC 760
DB 11081 CACTCTCACAAGCTCTGTAATATTCCTGTTTACCCCAAGAAATTTTACAGTACATC 11140
QY 761 TGCAGAGTCTCTTGGCCAGG 781
DB 11141 TGCAGAGTCTCTTGGCCAGG 11161

RESULT 6

US-09-949-016-150020
Sequence 150020, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 150020
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-150020

Query Match 13.3%; Score 279; DB 4; Length 601;

Best Local Similarity 99.5%; Pred. No. 4.2e-133;
Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGTTGAGCCGTGATGCTGGAAGCTTGGCCAGCCCTCAGAAAGCATT 460
DB 165 GTTTAGAACTTGTGTTGAGCCGTGATGCTGGAAGCTTGGCCAGCCCTCAGAAAGCATT 224
QY 461 TTAGTCAAGCAGAGACAAGAGAGATTAAGTGGCCGCACTCCCGTGGCATCACTGCAT 520
DB 225 TTAGTCAAGCAGAGACAAGAGAGATTAAGTGGCCGCACTCCCGTGGCATCACTGCAT 284
QY 521 CCTTGAAGCAGACCTTGTGAAGTCAAGCTGCTACATTTGAATCTCAAGTGAAGCTTC 580
DB 285 CCTTGAAGCAGACCTTGTGAAGTCAAGCTGCTACATTTGAATCTCAAGTGAAGCTTC 344
QY 581 TGAGATTCATGATTAAGAGAAAGAGATTCAGAGTTTGAAGCAAAATGCAGTAAACA 640
DB 345 TGAGATTCATGATTAAGAGAAAGAGATTCAGAGTTTGAAGCAAAATGCAGTAAACA 404
QY 641 GCACCAATCCAAATGTTTAATTGAAGACTTTGATCTCTCACTTACCCGTTGGTACCCC 700
DB 405 GCACCAATCCAAATGTTTAATTGAAGACTTTGATCTCTCACTTACCCGTTGGTACCCC 464
QY 701 CACTCTCACAAGCTCTGTAATATTCCTGTTTACCCCAAGAAATTTTACAGTACATC 760
DB 465 CACTCTCACAAGCTCTGTAATATTCCTGTTTACCCCAAGAAATTTTACAGTACATC 524
QY 761 TGCAGAGTCTCTTGGCCAGG 781
DB 525 TGCAGAGTCTCTTGGCCAGG 545

RESULT 7

US-09-949-016-150037
Sequence 150037, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 150037
TYPE: DNA
ORGANISM: Human
US-09-949-016-150037

Query Match 9.0%; Score 189; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 9.8e-87;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1369 AGCTCAAGTTTATTTTACCAGGAAGCTCAATTTGTCTTCAACATTTGTAATTTCTG 1428
DB 18 AGCTCAAGTTTATTTTACCAGGAAGCTCAATTTGTCTTCAACATTTGTAATTTCTG 77
QY 1429 TCTACTGCCACAACAGAGTTCTGCGAAGGAGATATGTAAGGCTGCGCTTGTG 1488
DB 78 TCTACTGCCACAACAGAGTTCTGCGAAGGAGATATGTAAGGCTGCGCTTGTG 137
QY 1489 GTTGCTTCAAGTTCTTGAAGCAACATATGATCCATGAAAGACGCGGAAAGCCCTG 1548
DB 138 GTTGCTTCAAGTTCTTGAAGCAACATATGATCCATGAAAGACGCGGAAAGCCCTG 197

Oy	1549	GCTCCTAAG	1557
Db	198	GCTCCTAAG	206

RESULT 8
US-09-566-921-88
; Sequence 88, Application US/09566921

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; GENERAL INFORMATION:
;
; APPLICANT: Loring, Jeanne F.
;
; APPLICANT: Tingley, Debora W.
;
; ADDRESSES: Edwards, Carol W.

```

QY	522	GAGGACAGACCTTTGGAATCAGAGCTGTCACTGAATCTCAAGTCAGCTTCGAG	584
	16	GAGGACAGACCTTTGGAATCAGAGCTGTCACTGAATCTCAAGTCAGCTTCGAG	75
Db			
QY	585	ATTCCATGATTCAGGAAGGAAGGATTCGAGCTTTTGAAGCAAAATGCACTGAACGCA	644
	76	ATTCCATGATTCAGGAAGGAAGGATTCGAGCTTTTGAAGCAAAATGCACTGAACGCA	135

RESULT 9
US-09-949-016-150030
; Sequence 150030, Application US/09949016

Query Match	7.4%	Score 155;	DB 4;	length 601;
Best Local Similarity	100.0%;	Pred. No. 3.2e-69;		
Matches 155; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	904	320	964	380	QY	1024	440
QY	AAATACAGACTTTTCTATCAGCCCTGGAGATGCCCTTCACCGCGTAATCGCCCTTAACAGTAT	AAATACAGACTTTTCTATCAGCCCTGGAGATGCCCTTCACCGCGTAATCGCCCTTAACAGTAT	TCGAGAGTCAAAAGCCTAATCCAAAGACTGAGCTTGAAGATTAAGTAAGAGACATGCGCTC	TCGAGAGTCAAAAGCCTAATCCAAAGACTGAGCTTGAAGATTAAGTAAGAGACATGCGCTC	QY	CTTTGAAAATTAAGGACAGACAAATAAAGAAAGS	CTTTGAAAATTAAGGACAGACAAATAAAGAAAGS
Db					Db		

RESULT 10
US-09-949-016-150031
Sequence 150031, Application US/09949016

Query Match	6.9%	Score 145	DB 4	Length 601
Best Local Similarity	100.0%	Pred. No. 4.6e-64		
Matches 145	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Accession	Sequence	Position
Qy	AATACACATCTTTCCTATCAGCCCTGGAGATGCTCTACACGGATCTGCGCTTAACAGTAT	963
Db	156 AATACACATCTTTCCTATCAGCCCTGGAGATGCTCTACACGGATCTGCGCTTAACAGTAT	215
Qy	964 TCTGAGGTACAAAGCCCTACCTCCAAAGCTGAGCTTGAAAGTAAAGAGACACATGCGTC	1022
Db	216 TCTGAGGTACAAAGCCCTACCTCCAAAGCTGAGCTTGAAAGTAAAGAGACACATGCGTC	275
Qy	1024 CTTTGGAAAATTAAGGCAGACACAA	1048
Db	276 CTTTGGAAAATTAAGGCAGACACAA	300

RESULT 11
US-09-949-016-150046
; Sequence 150046; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

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?
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: FASTSEQ for Windows Version 4.0.
? SEQ ID NO 150046
? LENGTH: 601
? TYPE: DNA
? ORGANISM: Human
? US-09-949-016-150046

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Query Match	6.5%	Score 137;	DB 4;	Length 601;	-
Best Local Similarity	99.5%;	Pred. No. 6e-60;			
Matches 187;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1765	TTTCAGAAAAGAGCTCAGACATTTCTCTTAAGATGGATCTTAACTCACTCTAAAGGTTTCC	1824
Db	413	TTTCAGAAAAGAGCTCAGACATTTCTCTTAAGATGGATCTTAACTCACTCTAAAGGTTTCC	472
QY	1825	TTTCTCAAGAGATGCTCTCTGTTGGGAGGAGGAAGCCCCAGCAAGATATGTACAAGACAAC	1884
Db	473	TTTCTCAAGAGATGCTCTCTGTTGGGAGGAGGAAGCCCCAGCAAGATATGTACAAGACAAC	532
QY	1885	ATCCAGCTTCATGCGCCAGACAGATGGCCAGGAATCCTCTCTCCAGAGAAAGCGGCATATTAT	1944
Db	533	ATCCAGCTTCATGCGCCAGACAGATGGCCAGGAATCCTCTCTCCAGAGAAAGCGGCATATTAT	592
QY	1945	GTGTGTGTG	1952
Db	593	GTGTGTGTG	600

```

RESULT 12
US-09-949-016-150047
: Sequence 150047, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 150047
: LENGTH: 601
: TYPE: DNA
: ORGANISM: Human
: US-09-949-016-150047

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	Query Match	Similarity	6.5%	Score 137	DB 4	Length 601				
	Best Local	Similarity	99.5%	Pred. No. 6e-60						
	Matches	187	Conservative	0	Mismatches	1	Indels	0	Gaps	0
Qy	1765	TTGAGAAAAGAGCTCAGACATTTCTTAAAGCATGGATCTTAACTCATCTAAAGGTTCC					1824			
Db	191	TTGAGAAAAGAGCTCAGACATTTCTTAAAGCATGGATCTTAACTCATCTAAAGGTTCC					250			
Qy	1825	TTCTCAGAGATGCTCTGTGGGAGGAGGAGAGCCCAAGCAAGTATGTACAGACAC					1888			
Db	251	TTCTCAGAGATGCTCTGTGGGAGGAGGAGAGCCCAAGCAAGTATGTACAGACAC					310			
Qy	1885	ATTCAGCTTCATGGCCAGCAGGTGGCGAAGTCCCTCCCAAGGAGATGGGCATTTAT					1944			
Db	311	ATTCAGCTTCATGGCCAGCAGGTGGCGAAGTCCCTCCCAAGGAGATGGGCATTTAT					370			

QY	1945	GTGTGTGG	1952
Db	371	GTGTGTGG	378

RESULT 13
US-09-949-016-150029

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? Patent No.6812339
? GENERAL INFORMATION:
? APPLICANT: VENTER, J. Craig et al.
? TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
? TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
? FILE REFERENCE: C0001307
? CURRENT APPLICATION NUMBER: US/09/949,016
? CURRENT FILING DATE: 2000-04-14
? PRIOR APPLICATION NUMBER: 60/241,755
? PRIOR FILING DATE: 2000-10-20
? PRIOR APPLICATION NUMBER: 60/237,768
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 150029
? LENGTH: 601
? TYPE: DNA
? ORGANISM: Human
US-09-949-016-150029

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Query Match	6.0%	Score 125;	DB 4;	Length 601;
Best Local Similarity	100.0%	Pred. No. 9.2e-54;		
Matches 125;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	779	AGGAGGAAAGCCAGTATCTGTGACTTGACGAGATCCAGTTTTCAGAGGCCAATTTCGA	838
Db	379	AGGAGGAAAGCCAAATATCTGTGACTTTCAGCGAGATCCAGTTTTCAGAGGCCAATTTCGA	438
QY	839	AGGCGGTCAACTTACTACGAAATGATGCGCAATAAAACGCACTGCTGCTGATGAATTGGACA	898
Db	439	AGGCGATTCAACTTACTACGAAATGATGCGCAATAAAACGCACTGCTGCTGATGAATTGGACA	498
QY	899	TTTCCA	903
Db	499	TTTCCA	503

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RESULT 14
US-09-949-016-150041
: Sequence 150041: Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C0001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 150041
: LENGTH: 601
: TYPE: DNA
: ORGANISM: Human
US-09-949-016-150041

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Query Match 5.8%; Score 121; DB 4; Length 601;

Best Local Similarity 100.0%; Pred. No. 1.1e-51;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1556 AGATATTCATCTCTCTCGAACAACAATCTTTCACATTACGATGACCCCTCAATCC 1615

Db 124 AGATATTCATCTCTCTCGAACAACAATCTTTCACATTACGATGACCCCTCAATCC 183

QY 1616 CCATCATTAATGGTGGGTCCAGGAACCGGCATAGCCCGTTTATTGGGTTCTTACAACATA 1675

Db 184 CCATCATTAATGGTGGGTCCAGGAACCGGCATAGCCCGTTTATTGGGTTCTTACAACATA 243

QY 1676 G 1676

Db 244 G 244

RESULT 15

US-09-949-016-150042

/ Sequence 150042, Application US/09949016

/ Patent No. 6812339

/ GENERAL INFORMATION:

/ APPLICANT: VENTER, J. Craig et al.

/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

/ FILE REFERENCE: C1001307

/ CURRENT APPLICATION NUMBER: US/09/949,016

/ CURRENT FILING DATE: 2000-04-14

/ PRIOR APPLICATION NUMBER: 60/241,755

/ PRIOR FILING DATE: 2000-10-20

/ PRIOR APPLICATION NUMBER: 60/237,768

/ PRIOR FILING DATE: 2000-10-03

/ PRIOR APPLICATION NUMBER: 60/231,498

/ PRIOR FILING DATE: 2000-09-08

/ NUMBER OF SEQ ID NOS: 207012

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 150042

/ LENGTH: 601

/ TYPE: DNA

/ ORGANISM: Human

US-09-949-016-150042

Query Match 5.8%; Score 121; DB 4; Length 601;

Best Local Similarity 100.0%; Pred. No. 1.1e-51;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 95 AGATATTCATCTCTCTCGAACAACAATCTTTCACATTACGATGACCCCTCAATCC 154

QY 1616 CCATCATTAATGGTGGGTCCAGGAACCGGCATAGCCCGTTTATTGGGTTCTTACAACATA 1675

Db 155 CCATCATTAATGGTGGGTCCAGGAACCGGCATAGCCCGTTTATTGGGTTCTTACAACATA 214

QY 1676 G 1676

Db 215 G 215

Search completed: August 27, 2005, 16:18:18
Job time : 237.757 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 00:17:56 ; Search time 900.401 Seconds
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15238.608 Million cell updates/sec

Title: US-09-371-347A-43

Perfect score: 2097
Sequence: 1 atgagagaggttcctgtact.....ttcagagatttgcataaa 2097

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 7331713 seqs, 3271544945 residues

Word size : 0

Total number of hits satisfying chosen parameters: 14663426

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database :

Published Applications NA.*
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21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
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24: /cgn2_6/ptodata/2/pubpna/US11A_NEW_PUB.seq.*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2097	100.0	2097	10	US-09-371-347-43
2	2096	97.6	2097	10	US-09-371-347-1
3	2046	97.6	3259	10	US-09-371-347-24
4	1995	95.1	2097	10	US-09-371-347-41
5	1803	86.0	2094	10	US-09-371-347-45
6	1742	83.1	2093	10	US-09-371-347-47
7	1018	48.5	3256	21	US-10-741-600-692

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	US-10-741-600-693	US-10-029-386-6369	US-10-029-386-20100	US-10-029-386-1735	US-10-029-386-15435	US-10-741-600-17757	US-10-029-386-633	US-10-029-386-14338	US-09-909-5678-38	US-10-755-700-88	US-10-741-600-17986	US-10-741-600-15583	US-10-741-600-15584	US-10-741-600-15589	US-10-741-600-15590	US-10-741-600-15592	US-10-741-600-15593	US-10-741-600-15594	US-10-741-600-15598	US-10-741-600-15599	US-10-741-600-15602	US-10-741-600-15606	US-10-741-600-15609	US-10-741-600-15610	US-10-741-600-15612	US-10-741-600-15613	US-10-741-600-15614	US-10-741-600-15620	US-10-741-600-15621	US-10-741-600-15623	US-10-741-600-15624	US-10-741-600-15625	US-10-741-600-15629	US-10-741-600-15630	US-10-741-600-15631	US-10-741-600-15633	US-10-741-600-15637			

ALIGNMENTS

RESULT 1
US-09-371-347-43
; Sequence 43, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE;
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-371-347-43

Query Match 100.0%; Score 2097; DB 10; Length 2097;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGAGAGGTTCTGTTACTATATCTACACAGCAGGACAGGCAAGCCATCGCAGAA 60
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TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
FILE REFERENCE: 50004/003003
CURRENT APPLICATION NUMBER: US/09/371,347
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/071,622
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 09/232,028
PRIOR FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2097
TYPE: DNA
ORGANISM: Homo sapiens
US-09-371-347-1

Query Match 97.6%; Score 2046; DB 10; Length 2097;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 ATGAGAGAGTTTCTGTTACTATATGCTACACAGCAGGACAGGCAAGGCCATCGCAGAA 60
QY 61 GAAATGTGAGCAGCTGTGTGATGATGATTTTCTGAGATCTTCACTATATATGAGAA 120
DB 61 GAAATGTGAGCAGCTGTGTGATGATGATTTTCTGAGATCTTCACTATATATGAGAA 120
QY 121 TCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 121 TCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
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QY 181 GGCACCGGAGACCCACCCGACACAGCCGCGAGTTTGTATGAGAAATACAGAACCA 240
DB 181 GGCACCGGAGACCCACCCGACACAGCCGCGAGTTTGTATGAGAAATACAGAACCA 240
QY 241 CTGCGCGTGTGATTTCTTGTGTCACCTGCGGTATGAGTTTCTGCGGTGATGAGAA 300
DB 241 CTGCGCGTGTGATTTCTTGTGTCACCTGCGGTATGAGTTTCTGCGGTGATGAGAA 300
QY 301 TACACCTACTTTTGTGATGAGGAGGAGATATGATTAAGCACTTCAAGAGCTTGAGCC 360
DB 301 TACACCTACTTTTGTGATGAGGAGGAGATATGATTAAGCACTTCAAGAGCTTGAGCC 360
QY 361 CGGCAATTTCTATGACACTGACATGACATGACATGACATGACATGACATGACATGAC 420
DB 361 CGGCAATTTCTATGACACTGACATGACATGACATGACATGACATGACATGACATGAC 420
QY 421 CGGTGATGCTGAGACTCTGCGCAGCCCTCAGAAACATTTTATGATGATGATGATGAT 480
DB 421 CGGTGATGCTGAGACTCTGCGCAGCCCTCAGAAACATTTTATGATGATGATGATGAT 480
QY 481 GAGGAGATAGTGGCCCACTCCCGGTGACATCCTGACATCCTTGAAGACAGACCTTGT 540
DB 481 GAGGAGATAGTGGCCCACTCCCGGTGACATCCTGACATCCTTGAAGACAGACCTTGT 540
QY 541 AAGTCAGAGCTGTACACATTTGATCTCAAGTCACTTCTGAGATTTCAATGATGAGAA 600
DB 541 AAGTCAGAGCTGTACACATTTGATCTCAAGTCACTTCTGAGATTTCAATGATGAGAA 600
QY 601 AGAAAGATTTCTGAGGTTTGAAGCAAAATGAGTGAACAGCAACCAATCAATGATGAT 660
DB 601 AGAAAGATTTCTGAGGTTTGAAGCAAAATGAGTGAACAGCAACCAATCAATGATGAT 660
QY 661 ATTGAAGACTTTGAGTCTCACTTACCCGTTCCGTTACCCCACTCTCAAGAGCTCTCTG 720
DB 661 ATTGAAGACTTTGAGTCTCACTTACCCGTTCCGTTACCCCACTCTCTCAAGAGCTCTCTG 720
QY 721 AATATTCCTGTTTACCCCAAGATATTTTACAGATCATCTGACAGAGTCTCTTGGCCAG 780
DB 721 AATATTCCTGTTTACCCCAAGATATTTTACAGATCATCTGACAGAGTCTCTTGGCCAG 780

QY 781 GAGAAAGCCAGATATCTGTGACTTCAGCAGATCCAGTTTTCAGTGCATTTCAAG 840
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QY 841 GCAATTCATCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 GCAATTCATCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
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QY 961 GATTCAGAGTACAAAGCTTCAAGAGCTGACAGTTGAAGATTAAGAGAGCATGTC 1020
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DB 1261 TGTGCTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 CTGCTGGAACATCTTCTTAACTTCAACCCAGACATATTCGTGTCAGAGCTCAAGTTTA 1380
DB 1321 CTGCTGGAACATCTTCTTAACTTCAACCCAGACATATTCGTGTCAGAGCTCAAGTTTA 1380
QY 1381 TTTCAACCCAGAAAGCTCATTTTGTCTTCAATTTGGAATTTCTGTCTACTGCA 1440
DB 1381 TTTCAACCCAGAAAGCTCATTTTGTCTTCAATTTGGAATTTCTGTCTACTGCA 1440
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DB 1441 ACAGAGTTCTGCGAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
QY 1501 CTTGAGCCAAACATACATCATCCATGGAAGACAGGAGGAAAGCCCTGCTCTTAAGATA 1560
DB 1501 CTTGAGCCAAACATACATCATCCATGGAAGACAGGAGGAAAGCCCTGCTCTTAAGATA 1560
QY 1561 TCCATCTCTCTGGAACAAATTTTCTTCACTTACAGATGACCTTCAATCCCATC 1620
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QY 1621 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1621 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 AAATCTCAAGAACCAACCAAGTGAATTTTGAAGCATGATGATGATGATGATGATGATGAT 1740
DB 1681 AAATCTCAAGAACCAACCAAGTGAATTTTGAAGCATGATGATGATGATGATGATGATGAT 1740
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DB 1741 AGGATTAAGATTAAGATTAATCTTATGAGAAAGCTCAGACATTTCTTAAAGATGCG 1800
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QY 1861 CCAGCAAGATATGATCAAGAACATTCAGTTTCAATGCGACAGAGTGGCAGAAATCTTC 1920

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Qy 1921 CTCAGAGAAAGGCGCATATTTATGTGTGAGATCAAAAGATATAGCCAGAGATGTA 1980
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Qy 1981 CATGATGCCCTTGTGCAAAATATAGCAAGAGGTTGAGTGAATACTAGAACATG 2040
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RESULT 3
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Sequence 24, Application US/09371347
Publication No. US20030082676A1
GENERAL INFORMATION:
APPLICANT: Roy A. Gravel et al.
TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
FILE REFERENCE: 50004/003003
CURRENT APPLICATION NUMBER: US/09/371.347
CURRENT FILING DATE: 1999-08-10
PRIORITY FILING DATE: 60/071.622
PRIORITY FILING DATE: 1998-01-16
PRIORITY FILING DATE: 1999-01-15
PRIORITY FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 3259
TYPE: DNA
ORGANISM: Homo sapiens
US-09-371-347-24

Query Match 97.6%; Score 2046; DB 10; Length 3259;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2096; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 80 ATGAGAGGTTTCTGTACTATATGCTACACAGCAGGACAGGCAAGCCATCGCAGAA 139
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Qy 121 TCCGATTAAGTATGACTTAATAACCGAAACAGCTCCTGTGTGTGTGTGTTTCTAACCA 180
Db 200 TCCGATTAAGTATGACTTAATAACCGAAACAGCTCCTGTGTGTGTGTGTTTCTAACCA 259
Qy 181 GGCACCGGAGACCCACCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
Db 260 GGCACCGGAGACCCACCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 319
Qy 241 CTCGCGGTTATTTCTTTGCTCACTGCGGTATGGGTACTGCGGTCTCGGTATTCAGAA 300
Db 320 CTCGCGGTTATTTCTTTGCTCACTGCGGTATGGGTACTGCGGTCTCGGTATTCAGAA 379
Qy 301 TACACCTACTTTTGCATATGGGGGAGATATTGATTAAGCACTTCAAGAGCTTGAAGCC 360
Db 380 TACACCTACTTTTGCATATGGGGGAGATATTGATTAAGCACTTCAAGAGCTTGAAGCC 439
Qy 361 CGGCAATTTCTATGACACTGACATGACATGACTGTAGATTGAACTTGTGTGAG 420
Db 440 CGGCAATTTCTATGACACTGACATGACATGACTGTAGATTGAACTTGTGTGAG 499
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Db 500 CCGTGATTTGCTGAGCTCTGGCCAGCCCTCAAGAAAGCAATTTTGTAGGCAAGACAGCA 559
Qy 481 GAGAGATTAAGTGGCCACCTCCGATGGCATCTGCACTCTTGAAGACAGACCTTGTG 540
Db 560 GAGAGATTAAGTGGCCACCTCCGATGGCATCTGCACTCTTGAAGACAGACCTTGTG 619
Qy 541 AAGTCAGCTGTGACATTAAGTATCAAGTGAAGCTTCTGAGATTGATGATTCAGGA 600
Db 620 AAGTCAGCTGTGACATTAAGTATCAAGTGAAGCTTCTGAGATTGATGATTCAGGA 679
Qy 601 AGAAAGATTTCTGAGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATTCATTTGTA 660
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Db 740 ATTAAGACTTTGAGTCTCATCTTACCCGTTGGGTACCCCACTCTCACAGGCTCTGTG 799
Qy 721 AATATTCCTGTATACCCCGAGAAATTTTACAGGTACATCTGAGAGATCTTGGCCAG 780
Db 800 AATATTCCTGTATACCCCGAGAAATTTTACAGGTACATCTGAGAGATCTTGGCCAG 859
Qy 781 GAGGAAAGCCAGTATCTGTGACTTGAAGATCCAGTTTTCAGATTCGCAATTTGAAAG 840
Db 860 GAGGAAAGCCAGTATCTGTGACTTGAAGATCCAGTTTTCAGATTCGCAATTTGAAAG 919
Qy 841 GCAGTCAACTTACTACGATGATGCAATTAACCACTCTGTGTAGATTTGACATTT 900
Db 920 GCAGTCAACTTACTACGATGATGCAATTAACCACTCTGTGTAGATTTGACATTT 979
Qy 901 TCAATATCAGACTTTTCTATCAGCTGTGAGATGCTTCAAGCTGATCTGCCCTAACAT 960
Db 980 TCAATATCAGACTTTTCTATCAGCTGTGAGATGCTTCAAGCTGATCTGCCCTAACAT 1039
Qy 961 GATTTGAGGTACAAAGCCCTACCCAAAGACCTGACCTTGAATTAAGAGAGCACTGC 1020
Db 1040 GATTTGAGGTACAAAGCCCTACCCAAAGACCTGACCTTGAATTAAGAGAGCACTGC 1099
Qy 1021 GTCTTTTGAATAAATTAAGGACAGACAAAGAAAGAGAGCTTACCCCGACATATA 1080
Db 1100 GTCTTTTGAATAAATTAAGGACAGACAAAGAAAGAGAGCTTACCCCGACATATA 1159
Qy 1081 CTGCGGAGATTTCTCTCAAGTTCAATTTTCTGCTGTCTTGAATTCGAGCAATTCCT 1140
Db 1160 CTGCGGAGATTTCTCTCAAGTTCAATTTTCTGCTGTCTTGAATTCGAGCAATTCCT 1219
Qy 1141 AAAAAGCAATTTTGGAGCCCTTGTGACTATACAGAGACAGTCTGAAGAGCCGAGG 1200
Db 1220 AAAAAGCAATTTTGGAGCCCTTGTGACTATACAGAGACAGTCTGAAGAGCCGAGG 1279
Qy 1201 CTACAGAGCTGTGACATTAACAGAGGAGCCGATTAATGAGCCGTTTGTACAGATGCC 1260
Db 1280 CTACAGAGCTGTGACATTAACAGAGGAGCCGATTAATGAGCCGTTTGTACAGATGCC 1339
Qy 1261 TGTGCTGCTTGTGATCTCTCTGCTTCTCTTCTTTCAGACGACCACTCAAGTCTC 1320
Db 1340 TGTGCTGCTTGTGATCTCTCTGCTTCTCTTCTTTCAGACGACCACTCAAGTCTC 1399
Qy 1321 CTCGCTGAACATTTCTTAACCTTCAACCGACGACATTTGCTGAGTCAAGCTTGA 1380
Db 1400 CTCGCTGAACATTTCTTAACCTTCAACCGACGACATTTGCTGAGTCAAGCTTGA 1459
Qy 1381 TTTCAACCGAAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTCTGTACTGACACA 1440
Db 1460 TTTCAACCGAAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTCTGTACTGACACA 1519
Qy 1441 ACAGAGTTCTGCGAAGGAGATATGATGAGCTGAGCTGAGCTTGTGTGCTTCAATT 1500
Db 1520 ACAGAGTTCTGCGAAGGAGATATGATGAGCTGAGCTGAGCTTGTGTGCTTCAATT 1579
Qy 1501 CTTCAACCGAAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTCTGTACTGACATA 1560

Db 1580 CTTGACCCAAACATACATGATCCCATGAGACAGCGGAAAGCCCTGGCTCTTAAGATA 1639
Qy 1561 TCCATCTCTCCGGAACAAATCTTCCATTAACGAGATGAGCCCTCATCCCATC 1620
Db 1640 TCCATCTCTCCGGAACAAATCTTCCATTAACGAGATGAGCCCTCATCCCATC 1699
Qy 1621 ATAATGTGGTTCAGAAACCGGATAGCCCGCTTAAATGGGTTCTTAACAATAGAGAG 1680
Db 1700 ATAAATGTGGTTCAGAAACCGGATAGCCCGCTTAAATGGGTTCTTAACAATAGAGAG 1759
Qy 1661 AAATCCCAAGAACCAACCCAGATGAAATTTTGAAGCAATGTGTTTTTGGCTGC 1740
Db 1760 AAATCCCAAGAACCAACCCAGATGAAATTTTGAAGCAATGTGTTTTTGGCTGC 1819
Qy 1741 AGGCAATAGGATAGGATTAATCTATTCAGAAAAGCTAGACATTTCTTAAGCATGGG 1800
Db 1820 AGGCAATAGGATAGGATTAATCTATTCAGAAAAGCTAGACATTTCTTAAGCATGGG 1879
Qy 1801 ATCTTAATCATTAAGGTTCTCTTCAGAGATGCTCTGTTGGGAGGAGGAGCC 1860
Db 1880 ATCTTAATCATTAAGGTTCTCTTCAGAGATGCTCTGTTGGGAGGAGGAGCC 1939
Qy 1861 CCAGCAAGATATGTAACAACAACATCCAGCTTCAATGGCCAGAGTGGCGAATCTC 1920
Db 1940 CCAGCAAGATATGTAACAACAACATCCAGCTTCAATGGCCAGAGTGGCGAATCTC 1999
Qy 1921 CTCGAGAGAAAGGCAATTTTATGTGTGTGAGATGCAAAAGATTTGGCCAAAGATGTA 1980
Db 2000 CTCGAGAGAAAGGCAATTTTATGTGTGTGAGATGCAAAAGATTTGGCCAAAGATGTA 2059
Qy 1981 CATGATGCTCTGTGCAAAATTAAGCAAAAGGTTGAGTTGAAAACTAGAGCAATG 2040
Db 2060 CATGATGCTCTGTGCAAAATTAAGCAAAAGGTTGAGTTGAAAACTAGAGCAATG 2119
Qy 2041 AAACCTGCGCACTTTAAAGAGAAAAAGCTACCTTCAGATTAATTTGTCATTA 2097
Db 2120 AAACCTGCGCACTTTAAAGAGAAAAAGCTACCTTCAGATTAATTTGTCATTA 2176

RESULT 4
US-09-371-347-41
; Sequence 41, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE;
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-41

Query Match 95.1%; Score 1995; DB 10; Length 2097;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2095; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAGAGAGTTTCTGTTACTATATGCTACACAGCAGGACAGCAAAAGCCATCGAGAA 60
Db 1 ATGAGAGAGTTTCTGTTACTATATGCTACACAGCAGGACAGCAAAAGCCATCGAGAA 60
Qy 61 GAAATGTGAGCAAGCTGTGATCAATGATTTTCTGAGATCTTCACTATATTAGTAA 120
Db 61 GAAATGTGAGCAAGCTGTGATCAATGATTTTCTGAGATCTTCACTATATTAGTAA 120

Db 61 GAAATGTGAGCAAGCTGTGATCAATGATTTTCTGAGATCTTCACTATATTAGTAA 120
Qy 121 TCCGATTAAGTATGACCTTAACAAACGAAACAGCTCCCTTGTGTGTGTGTTCTACAG 180
Db 121 TCCGATTAAGTATGACCTTAACAAACGAAACAGCTCCCTTGTGTGTGTGTTCTACAG 180
Qy 181 GGCACCGAGAACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
Db 181 GGCACCGAGAACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
Qy 241 CTGCGGTTGATTTCTTTGCTCACTCGGAGTATGGGTTACTGGGTTCTCGGTATTCAGA 300
Db 241 CTGCGGTTGATTTCTTTGCTCACTCGGAGTATGGGTTACTGGGTTCTCGGTATTCAGA 300
Qy 301 TACACCTACTTTTGAATGGGGGAAATTAATGATTAACGACTCAAGAGCTGGAGCC 360
Db 301 TACACCTACTTTTGAATGGGGGAAATTAATGATTAACGACTCAAGAGCTGGAGCC 360
Qy 361 CGGCATTTCTATGACACTGAGACATGCAATGACTGTGAGTTTGAACCTGTGGTGAAG 420
Db 361 CGGCATTTCTATGACACTGAGACATGCAATGACTGTGAGTTTGAACCTGTGGTGAAG 420
Qy 421 CCGTGAATTTGCTGAATCTGGCCAGCCCTCAGAAAGCAATTTAGTCAAGAGAGACAA 480
Db 421 CCGTGAATTTGCTGAATCTGGCCAGCCCTCAGAAAGCAATTTAGTCAAGAGAGACAA 480
Qy 481 GAGAGATTAAGTGGGCACTCCCGGTGGATACCTGTGATCTTTAGAGACACACCTTGG 540
Db 481 GAGAGATTAAGTGGGCACTCCCGGTGGATACCTGTGATCTTTAGAGACACACCTTGG 540
Qy 541 AAGTCAGAGCTCTACACATTAATCTCAATCGAGCTTCTGAGATTCGATATTCAGGA 600
Db 541 AAGTCAGAGCTCTACACATTAATCTCAATCGAGCTTCTGAGATTCGATATTCAGGA 600
Qy 601 AGAAAGATTTCTGAGGTTTGAAGCAAAATGAGTAAACAGAACCAATTCATGTTGTA 660
Db 601 AGAAAGATTTCTGAGGTTTGAAGCAAAATGAGTAAACAGAACCAATTCATGTTGTA 660
Qy 661 ATTGAAGACTTTGAGTCTCTACATTAACCGTTGGTATACCCCACTCTCAAGCTCTCG 720
Db 661 ATTGAAGACTTTGAGTCTCTACATTAACCGTTGGTATACCCCACTCTCAAGCTCTCG 720
Qy 721 AATATTCCTGTTTACCCCAAGATATTTTACAGTATCATCTGAGAGTCTCTTGGCCAG 780
Db 721 AATATTCCTGTTTACCCCAAGATATTTTACAGTATCATCTGAGAGTCTCTTGGCCAG 780
Qy 781 GAGAAAGCCAGATATCTGTGACTTCAGAGATTCAGATTTTCAAGTGCATTTCAAG 840
Db 781 GAGAAAGCCAGATATCTGTGACTTCAGAGATTCAGATTTTCAAGTGCATTTCAAG 840
Qy 841 GCAATTCACATTAATCAATGATGCAATTAACCACTGTGTGTGATTAATTTGACATT 900
Db 841 GCAATTCACATTAATCAATGATGCAATTAACCACTGTGTGTGATTAATTTGACATT 900
Qy 901 TCAATATACAGACTTTTCTATCAGGCTGAGATGCTTCAGGATGATCTGCCCTAACAT 960
Db 901 TCAATATACAGACTTTTCTATCAGGCTGAGATGCTTCAGGATGATCTGCCCTAACAT 960
Qy 961 GATTCGAGGTACCAAGCTCTCAAGAGCTGACGCTTGAAGATTAAGAGAGACCTGC 1020
Db 961 GATTCGAGGTACCAAGCTCTCAAGAGCTGACGCTTGAAGATTAAGAGAGACCTGC 1020
Qy 1021 GTCTTTTGAATAATAGGAGACACAAAGAAAGAGCTTACCTTACCCAGCATTA 1080
Db 1021 GTCTTTTGAATAATAGGAGACACAAAGAAAGAGCTTACCTTACCCAGCATTA 1080
Qy 1081 CCGGCGGAGTGTCTCTCAGGTTCAATTTTACCTGAGTCTTGAATTCGAGCAATTTCT 1140
Db 1081 CCGGCGGAGTGTCTCTCAGGTTCAATTTTACCTGAGTCTTGAATTCGAGCAATTTCT 1140
Qy 1141 AAAAAGCAATTTTGGAGCCCTTGTGACTTATACAGTGAAGTGTGAAAAGCGCAGG 1200
Db 1141 AAAAAGCAATTTTGGAGCCCTTGTGACTTATACAGTGAAGTGTGAAAAGCGCAGG 1200

QY 1201 CTACAGAGCTGTGCACTAAACAAGGGGACGCCGATTATAGCCGCTTTGTACGAGATGCC 1260
DB 1201 CTACAGAGCTGTGCACTAAACAAGGGGACGCCGATTATAGCCGCTTTGTACGAGATGCC 1260
QY 1261 TGTGCGCTGTGTGATCT 1320
DB 1261 TGTGCGCTGTGTGATCT 1320
QY 1321 CTGCTGGAACATCTTCTTAACCTTCAACCCAGACATATTCGTGTGAAGCTCAAGTTTA 1380
DB 1321 CTGCTGGAACATCTTCTTAACCTTCAACCCAGACATATTCGTGTGAAGCTCAAGTTTA 1380
QY 1381 TTTTACCAGGAAAGCTCCATTTTGTCTTCAACATGTGGAATTTGTCTACTGCCACA 1440
DB 1381 TTTTACCAGGAAAGCTCCATTTTGTCTTCAACATGTGGAATTTGTCTACTGCCACA 1440
QY 1441 ACAGAGTTTGTGGGAAAGGATATGACAGGCTGTGGCTGTGTGTGTGTGTGTGTGTGT 1500
DB 1441 ACAGAGTTTGTGGGAAAGGATATGACAGGCTGTGGCTGTGTGTGTGTGTGTGTGTGT 1500
QY 1501 CTTCAGCCAAACATACATGATCCCATGAGACAGCGGAAAGCCCTGCTCTCTTAAGATA 1560
DB 1501 CTTCAGCCAAACATACATGATCCCATGAGACAGCGGAAAGCCCTGCTCTCTTAAGATA 1560
QY 1561 TCCATCTCTCTCGAACAACAAATCTTTCACCTTACAGATGACCCCTCAATCCCATC 1620
DB 1561 TCCATCTCTCTCGAACAACAAATCTTTCACCTTACAGATGACCCCTCAATCCCATC 1620
QY 1621 ATATAGTGTGGTCCAGGACCGGATAGCCCGTTTATTTGGGTTTCTTCAACATTAAGAG 1680
DB 1621 ATATAGTGTGGTCCAGGACCGGATAGCCCGTTTATTTGGGTTTCTTCAACATTAAGAG 1680
QY 1681 AAATCCAAACAACAACCCAGATGGAATTTTGAAGCAATGTGTGTGTGTGTGTGTGTGT 1740
DB 1681 AAATCCAAACAACAACCCAGATGGAATTTTGAAGCAATGTGTGTGTGTGTGTGTGTGT 1740
QY 1741 AGGATATAGATAGGATATCTATTCAGAAAAGGCTCAACATTTCTTTAAGCATGGG 1800
DB 1741 AGGATATAGATAGGATATCTATTCAGAAAAGGCTCAACATTTCTTTAAGCATGGG 1800
QY 1801 ATCTTAATCTATCTAAAGGTTTCTTCTCAAGAGATCTCTGTGTGGGAGGAGAAAGCC 1860
DB 1801 ATCTTAATCTATCTAAAGGTTTCTTCTCAAGAGATCTCTGTGTGGGAGGAGAAAGCC 1860
QY 1861 CCAGCAAGATATGACAAACAACATCAGCTTCAATGCGCAGCAGAGTGGGAGATCTC 1920
DB 1861 CCAGCAAGATATGACAAACAACATCAGCTTCAATGCGCAGCAGAGTGGGAGATCTC 1920
QY 1921 CTCGAGGAGAACGGCCATATTTATGTGTGAGATCAAAAGATATGCGCAAGATGTA 1980
DB 1921 CTCGAGGAGAACGGCCATATTTATGTGTGAGATCAAAAGATATGCGCAAGATGTA 1980
QY 1981 CAGATATCCCTTGTGCAAAATTAAGCAAGAGGTTGAGTGAATACTAAGACATG 2040
DB 1981 CAGATATCCCTTGTGCAAAATTAAGCAAGAGGTTGAGTGAATACTAAGACATG 2040
QY 2041 AAAACCTGTGCACTTTAAAGAAAGAAAGCTACCTTCAAGATATTTGTCTATA 2097
DB 2041 AAAACCTGTGCACTTTAAAGAAAGAAAGCTACCTTCAAGATATTTGTCTATA 2097

RESULT 5
US-09-371-347-45
; Sequence 45, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347

; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-45

Query Match 86.0%; Score 1803; DB 10; Length 2094;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 ATGAGAGAGTTTCTGTACTATATGCTATACAGCAGGAGCAGGCAAAAGCCATCGAGAA 60
DB 1 ATGAGAGAGTTTCTGTACTATATGCTATACAGCAGGAGCAGGCAAAAGCCATCGAGAA 60
QY 61 GAAATGTGAGCAGAGCTGTGTACATGATTTTCTGAGATCTTCACTATATTAGTGA 120
DB 61 GAAATGTGAGCAGAGCTGTGTACATGATTTTCTGAGATCTTCACTATATTAGTGA 120
QY 121 TCCGATATGATGACTTAAAAACCGAAACGCTCTTGTGTGTGTGTGTGTGTGTGTGT 180
DB 121 TCCGATATGATGACTTAAAAACCGAAACGCTCTTGTGTGTGTGTGTGTGTGTGTGT 180
QY 181 GGCACGGAGACCCACCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACAAACA 240
DB 181 GGCACGGAGACCCACCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACAAACA 240
QY 241 CTGCGCGTGAATTTCTTGTCTCACTGCGGTATGAGTTACTGGGTCTCGGTATTCAGA 300
DB 241 CTGCGCGTGAATTTCTTGTCTCACTGCGGTATGAGTTACTGGGTCTCGGTATTCAGA 300
QY 301 TACACCTACTTTTGCAATGGGGGAAAGATATGATTAACGACTTCAAGAGCTTGAAGCC 360
DB 301 TACACCTACTTTTGCAATGGGGGAAAGATATGATTAACGACTTCAAGAGCTTGAAGCC 360
QY 361 CGGCAATTTCTAGACACTGGACATGAGATGACTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB 361 CGGCAATTTCTAGACACTGGACATGAGATGACTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 421 CCGTGAATGTGTGACTGTGGCCAGCTCCGCTGAGATCACTGCACTCTTGAAGAGCACTTGTG 540
DB 421 CCGTGAATGTGTGACTGTGGCCAGCTCCGCTGAGATCACTGCACTCTTGAAGAGCACTTGTG 540
QY 481 GAGGATATAGTGGGCACTCCGCTGGCATCACTGTGATCTTGAAGAGCACTTGTGTG 540
DB 481 GAGGATATAGTGGGCACTCCGCTGGCATCACTGTGATCTTGAAGAGCACTTGTGTG 540
QY 541 AACTGAGCTGTACACATGAAATCTCAAGTGAAGTGTGATTCAGATTCAGAGTA 600
DB 541 AACTGAGCTGTACACATGAAATCTCAAGTGAAGTGTGATTCAGATTCAGAGTA 600
QY 601 AGAAGGATTTCTGAGTTTGAAGCAAAATGACGTGAACAGCAACCAATCCAATGTTGTA 660
DB 601 AGAAGGATTTCTGAGTTTGAAGCAAAATGACGTGAACAGCAACCAATCCAATGTTGTA 660
QY 661 ATTTGAAGCTTTGAGTCTTCACTTACCCGTTCCGTTACCCCACTCTCAAGCTCTCTG 720
DB 661 ATTTGAAGCTTTGAGTCTTCACTTACCCGTTCCGTTACCCCACTCTCAAGCTCTCTG 720
QY 721 AATATTCGTGTTTACCCCAAGAAATTTTACAGATTCATGAGAGTCTTGGCCAG 780
DB 721 AATATTCGTGTTTACCCCAAGAAATTTTACAGATTCATGAGAGTCTTGGCCAG 780
QY 781 GAGGAAAGCCAAATATCTGTGACTTCAAGCATCAAGTTTCAAGTCCCAATTTCAAG 840
DB 781 GAGGAAAGCCAAATATCTGTGACTTCAAGCATCAAGTTTCAAGTCCCAATTTCAAG 840


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Db      481 GAGAGGTAAGTGGCGACTCCGCGTGGCATCTGCACTTGTGAGAGACGACTGTG 540
Qy      541 AACTGAGCTGCTACATTTGATCTCAAGTGGAGCTTGTGATTCATGATTCAGAG 600
Db      541 AAGTCAGCTGCTACATTTGATCTCAAGTGGAGCTTGTGATTCATGATTCAGAG 600
Qy      601 AGAAGGATTCGAGGTTTGAACCAATGCAAGTGAACCAACCAATTCATGTTGA 660
Db      601 AGAAGGATTCGAGGTTTGAACCAATGCAAGTGAACCAACCAATTCATGTTGA 660
Qy      661 ATTGAAGATTTGAGTCTCACTTACCCGTGGTACCCCACTCTCAAGGCTCTCG 720
Db      661 ATTGAAGATTTGAGTCTCACTTACCCGTGGTACCCCACTCTCAAGGCTCTCG 720
Qy      721 AATATTCCTGTTTACCCCAAGATTTTACAGGATCATGAGAGAGTCTTGGCCAG 780
Db      721 AATATTCCTGTTTACCCCAAGATTTTACAGGATCATGAGAGAGTCTTGGCCAG 780
Qy      781 GAGGAAAGCCAGATCTGTGACTTCAGAGATCCAGTTTTCAGTGCATTTCAAG 840
Db      781 GAGGAAAGCCAGATCTGTGACTTCAGAGATCCAGTTTTCAGTGCATTTCAAG 840
Qy      841 GCGATTCATCTACTAGGATGATGCAATTAACCACTCTGCTGGTGAATTTGACAT 900
Db      841 GCGATTCATCTACTAGGATGATGCAATTAACCACTCTGCTGGTGAATTTGACAT 900
Qy      901 TCAATTCAGACTTTTCTCATAGCTGAGAGTCCCTGACGGTATCTGCCCTAACAT 960
Db      901 TCAATTCAGACTTTTCTCATAGCTGAGAGTCCCTGACGGTATCTGCCCTAACAT 960
Qy      961 GATTCGAGGTACCAAGCTTCTCAAGACTGAGAGTCTTGAAGTAAAGAGACATGC 1020
Db      961 GATTCGAGGTACCAAGCTTCTCAAGACTGAGAGTCTTGAAGTAAAGAGACATGC 1020
Qy      1021 GTCTTTTGAATTAAGGACGACACAAAGAAAGAGACTTACCTCCACGACATTA 1080
Db      1021 GTCTTTTGAATTAAGGACGACACAAAGAAAGAGACTTACCTCCACGACATTA 1080
Qy      1081 CCGCGGAGATGTTCTCCAGATCATTTTACCTGGTCTTGAATCCGAGCAATTCCT 1140
Db      1081 CCGCGGAGATGTTCTCCAGATCATTTTACCTGGTCTTGAATCCGAGCAATTCCT 1140
Qy      1141 AAAAAGCATTTTTCGAGCCCTTGTGACATTAACAGTGAACAGTGTGAAAAGCCGAG 1200
Db      1141 AAAAAGCATTTTTCGAGCCCTTGTGACATTAACAGTGAACAGTGTGAAAAGCCGAG 1200
Qy      1201 CTACAGAGCTGTGACATTAACAAAGGGGACCGATTAATAGCCGCTTGTGAACAGATGCC 1260
Db      1201 CTACAGAGCTGTGACATTAACAAAGGGGACCGATTAATAGCCGCTTGTGAACAGATGCC 1260
Qy      1261 TGTGCTGCTGTGATCTCTCTGCTCTGCTTCCCTTCTTGCCAGCAGCACTCAAGTCTC 1320
Db      1261 TGTGCTGCTGTGATCTCTCTGCTCTGCTTCCCTTCTTGCCAGCAGCACTCAAGTCTC 1320
Qy      1321 CTGCTGACATCTTCTTAACTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTA 1380
Db      1321 CTGCTGACATCTTCTTAACTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTA 1380
Qy      1381 TTTTCAACCAAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTCTGTCTACGCCACA 1440
Db      1381 TTTTCAACCAAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTCTGTCTACGCCACA 1440
Qy      1441 ACAGAGGTTCTGCGAAGGAGATGTAACAGGCTGAGGCTTGTGTTGCTTCAAGT 1500
Db      1441 ACAGAGGTTCTGCGAAGGAGATGTAACAGGCTGAGGCTTGTGTTGCTTCAAGT 1500
Qy      1501 CTTTCAAGCAACATTAATGATCCCATGAAGACAGCGGAAAGCCCTGCTCTTAAGATA 1560
Db      1501 CTTTCAAGCAACATTAATGATCCCATGAAGACAGCGGAAAGCCCTGCTCTTAAGATA 1560
Qy      1561 TCCATCTCTCTGAAACAAATTTTTCATTTACATGATGACCCCTCAATCCCATC 1620

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Db      1561 TCCATCTCTCTGAAACAAATTTCTTTCATTAACAGATGACCCCTCAATCCCATC 1620
Qy      1621 ATATGATGGGTTCAGAAACCGGACATAGCCCGGTTTATTTGGTTCTTACATAGAGAG 1680
Db      1621 ATATGATGGGTTCAGAAACCGGACATAGCCCGGTTTATTTGGTTCTTACATAGAGAG 1680
Qy      1681 AAATCTCAAGAACACACCCAGATGGAATTTTGGACATGTGTTTGTGTTTGGCTGC 1740
Db      1677 AAATCTCAAGAACACACCCAGATGGAATTTTGGACATGTGTTTGTGTTTGGCTGC 1736
Qy      1741 AGGATTAAGATTAAGGATTAATCTATTCAGAAAAGAGCTCAGACATTTCTTAAAGATGG 1800
Db      1737 AGGATTAAGATTAAGGATTAATCTATTCAGAAAAGAGCTCAGACATTTCTTAAAGATGG 1796
Qy      1801 ATCTTAATCATCTTAAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGAGAAAGCC 1860
Db      1797 ATCTTAATCATCTTAAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGAGAAAGCC 1856
Qy      1861 CCAGCAAGATTAATGTAACAAACATCCAGCTTCATGCGCAAGAGTGGCGAATCTTC 1920
Db      1857 CCAGCAAGATTAATGTAACAAACATCCAGCTTCATGCGCAAGAGTGGCGAATCTTC 1916
Qy      1921 CTCAGAGAAAGGCGCATTTTATGATGATGAGATGCAAAAGATATGGCCAAAGATGA 1980
Db      1917 CTCAGAGAAAGGCGCATTTTATGATGATGAGATGCAAAAGATATGGCCAAAGATGA 1976
Qy      1981 CATGATCCCTGTTGCAAAATTAATTAACAAAGAGTGAAGTTGAAAACTAGAACATG 2040
Db      1977 CATGATCCCTGTTGCAAAATTAATTAACAAAGAGTGAAGTTGAAAACTAGAACATG 2036
Qy      2041 AAAACCTGCGCATTTTAAAGAAAGAAACGCTACCTTCAGATATTTGGTATTA 2097
Db      2037 AAAACCTGCGCATTTTAAAGAAAGAAACGCTACCTTCAGATATTTGGTATTA 2093

RESULT 7
US-10-741-600-692
; Sequence 692, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 692
; LENGTH: 3256
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-692

Query Match      48.5%; Score 1018; DB 21; Length 3256;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1968; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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QY 351 GCTTGGAGCCCGCATTTCTATGACATGAGATGACTGCTGTTAGTAACT 410
 DB 444 GCTTGGAGCCCGCATTTCTATGACATGAGATGACTGCTGTTAGTAACT 503
 QY 411 TGTGTTGAGCCGTGATGCTGAGCTGCGCAGCCCTCAGAAAGCATTTTAACT 470
 DB 504 TGTGTTGAGCCGTGATGCTGAGCTGCGCAGCCCTCAGAAAGCATTTTAACT 563
 QY 471 CAGAGGACAAAGAGATTAAGTGGCGACTCCCGTGGCATCACTGCACTCTTGAGAC 530
 DB 564 CAGAGGACAAAGAGATTAAGTGGCGACTCCCGTGGCATCACTGCACTCTTGAGAC 623
 QY 531 AGACCTTGAAGTGAAGTGTGATCACTGAATCTCAAGTGAAGTGTGATCACT 590
 DB 624 AGACCTTGAAGTGAAGTGTGATCACTGAATCTCAAGTGAAGTGTGATCACT 683
 QY 591 TGAATCAGAGAAAGATTTCTGAGGTTTGAAGCAAAATGCAATGAAAGCAACCAATC 650
 DB 684 TGAATCAGAGAAAGATTTCTGAGGTTTGAAGCAAAATGCAATGAAAGCAACCAATC 743
 QY 651 CAATGTTGTAATGAAAGCTTGAAGTCTCACTTACCCGTTGGTACCCCACTTCA 710
 DB 744 CAATGTTGTAATGAAAGCTTGAAGTCTCACTTACCCGTTGGTACCCCACTTCA 803
 QY 711 AGCCTCTGAATATCTGCTTACCCCGAAATTTTACAGTTCATCTGAGAGATC 770
 DB 804 AGCCTCTGAATATCTGCTTACCCCGAAATTTTACAGTTCATCTGAGAGATC 863
 QY 771 TCTTGGCCAGAGAAAGCAAGATCTGATCTGATGAGATCTGATGAGATCTGATGAG 830
 DB 864 TCTTGGCCAGAGAAAGCAAGATCTGATCTGATGAGATCTGATGAGATCTGATGAG 923
 QY 831 AATTCAAAAGGCACTTCACTTCACTGATGAGATCTGATGAGATCTGATGAGATCT 890
 DB 924 AATTCAAAAGGCACTTCACTTCACTGATGAGATCTGATGAGATCTGATGAGATCT 983
 QY 891 ATTGGAATTTCAAAATGAGATCTTCTATGAGCTGAGATCTGAGATCTGAGATCT 950
 DB 984 ATTGGAATTTCAAAATGAGATCTTCTATGAGCTGAGATCTGAGATCTGAGATCT 1043
 QY 951 CCTTACAGATTTCTGAGATCAAAAGCTTCTCAAAAGCTGAGATCTGAGATCTGAG 1010
 DB 1044 CCTTACAGATTTCTGAGATCAAAAGCTTCTCAAAAGCTGAGATCTGAGATCTGAG 1103
 QY 1011 AGAGCACTGGCTCTTTTGAATAAAGGAGACACAAAGAAAGAGATCTTACC 1070
 DB 1104 AGAGCACTGGCTCTTTTGAATAAAGGAGACACAAAGAAAGAGATCTTACC 1163
 QY 1071 CCAGCATATCTGCGGAGATTTCTCCAGTTCATTTTACCTGCTGCTTGAATCCG 1130
 DB 1164 CCAGCATATCTGCGGAGATTTCTCCAGTTCATTTTACCTGCTGCTTGAATCCG 1223
 QY 1131 AGCAATTTCTTAAAGGATTTTGAAGGAGCTTGTGAGCTTATACAGATGAGATCTGA 1190
 DB 1224 AGCAATTTCTTAAAGGATTTTGAAGGAGCTTGTGAGCTTATACAGATGAGATCTGA 1283
 QY 1191 AAAGGAGGCTTCAAGAGCTGTGAGATTAACAAGGAGGAGCCGATTTATAGCCCTTGT 1250
 DB 1284 AAAGGAGGCTTCAAGAGCTGTGAGATTAACAAGGAGGAGCCGATTTATAGCCCTTGT 1343
 QY 1251 AGAGATGCTGCTGCTGCTTGTGAGATCTCTCTCTGCTTCTCTCTCTCTCTCTCT 1310
 DB 1344 AGAGATGCTGCTGCTGCTTGTGAGATCTCTCTCTGCTTCTCTCTCTCTCTCTCT 1403
 QY 1311 ACTCAGTCTCTGCTGAGATCTTCTTAAATCTCAACCAAGACATATCTGCTGAG 1370
 DB 1404 ACTCAGTCTCTGCTGAGATCTTCTTAAATCTCAACCAAGACATATCTGCTGAG 1463
 QY 1371 CTCAAGTTTATTTCAACCAAGAAAGCTCAATTTTGTCTTCAACATTTGAGATTTCTGTC 1430
 DB 1464 CTCAAGTTTATTTCAACCAAGAAAGCTCAATTTTGTCTTCAACATTTGAGATTTCTGTC 1523

QY 1431 TACTGCCAACAAGGTTCTGCGAAGGAGATATGACAGGCTGCTGCTTGTGCT 1490
 DB 1524 TACTGCCAACAAGGTTCTGCGAAGGAGATATGACAGGCTGCTGCTTGTGCT 1583
 QY 1491 TGTCTGAGTTCTTCAAGCCAAATATGATGATCTTCAATGAAAGACGCGGAAAGCCCTGCG 1550
 DB 1584 TGTCTGAGTTCTTCAAGCCAAATATGATGATCTTCAATGAAAGACGCGGAAAGCCCTGCG 1643
 QY 1551 TCTTAAGATATCATCTCTCTGAAACAAATTTTCCACTTACAGATGAGCCCTC 1610
 DB 1644 TCTTAAGATATCATCTCTCTGAAACAAATTTTCCACTTACAGATGAGCCCTC 1703
 QY 1611 AATCCCATCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1670
 DB 1704 AATCCCATCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1763
 QY 1671 ACATAGAGAAATCTCAAGAAACAAACCAAGATGAAATTTTGAAGATGATGATGAT 1730
 DB 1764 ACATAGAGAAATCTCAAGAAACAAACCAAGATGAAATTTTGAAGATGATGATGAT 1823
 QY 1731 TTTTGGCTGAGCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1790
 DB 1824 TTTTGGCTGAGCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1883
 QY 1791 TTAAGCATGAGATCTTAACTCACTAAAGGTTCTCTCAAGATGATGATGATGATGAT 1850
 DB 1884 TTAAGCATGAGATCTTAACTCACTAAAGGTTCTCTCAAGATGATGATGATGATGAT 1943
 QY 1851 GGAGAAAGCCCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1910
 DB 1944 GGAGAAAGCCCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2003
 QY 1911 GAGAAATCTCTCCAGAGAAAGGATGATGATGATGATGATGATGATGATGATGATGAT 1970
 DB 2004 GAGAAATCTCTCCAGAGAAAGGATGATGATGATGATGATGATGATGATGATGATGAT 2063
 QY 1971 CAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2030
 DB 2064 CAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2123
 QY 2031 AGAAGCAATGAAACCTTGGCCACTTAAAGAAAGAAACCTTACAGATATTTT 2090
 DB 2124 AGAAGCAATGAAACCTTGGCCACTTAAAGAAAGAAACCTTACAGATATTTT 2183
 QY 2091 GTCATTA 2097
 DB 2184 GTCATTA 2190

RESULT 8
 US-10-741-600-693
 ; Sequence 693, Application US/10741600
 ; Publication No. US20050026169A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001499
 ; CURRENT APPLICATION NUMBER: US/10/741,600
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 73997
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 693
 ; LENGTH: 3274
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-741-600-693

Query Match 48.5%; Score 1018; DB 21; Length 3274;
 Best Local Similarity 99.0%; Pred. No. 0;
 Matches 1968; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 111 TATTAGTGAATCGATTAAGTATGACTTAAACCAAGACAGCTCTCTTGTGTGTGTGT 170

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Db 222 TATTAGGAATCCGATAGATAGACTTAAACCGAAACAGCTCTCTTGTGTGGT 281
Qy 171 TTCTACACCGGGACCCGAGACCCGACACAGCCCGCAAGTTGTTAAGAAATACA 230
Db 282 TTCTACACGGGGACCGGAGACCCGACACAGCCCGCAAGTTGTTAAGAAATACA 341
Qy 231 GAACCAACACTCGCCGGTGAATTTCTTGTCTCACCTGCGGTATGGTTACTGGCTCGG 230
Db 342 GAACCAACACTCGCCGGTGAATTTCTTGTCTCACCTGCGGTATGGTTACTGGCTCGG 401
Qy 291 TGAATTGAAATACCTACTTTTGCATATGGGGGAGATAATGATTAAGATTAAGACTTCAAGA 350
Db 402 TGAATTGAAATACCTACTTTTGCATATGGGGGAGATAATGATTAAGATTAAGACTTCAAGA 461
Qy 351 GCTTGAAGCCCGCATTTCTATGACACTGACATGACATGACATGATGATGATGATGATGAT 410
Db 462 GCTTGAAGCCCGCATTTCTATGACACTGACATGACATGACATGATGATGATGATGATGAT 521
Qy 411 TGTGTTGAGCCCGGATTTGCTGAGACTGTGCGCCAGCCCTCAAGAAAGCATTTTATGATCAAG 470
Db 522 TGTGTTGAGCCCGGATTTGCTGAGACTGTGCGCCAGCCCTCAAGAAAGCATTTTATGATCAAG 581
Qy 471 CAGAGCAAGAGAGATTAAGTGGCGCACTCCGCGTGGCATCACTGATCTTGTAGAGAC 530
Db 582 CAGAGCAAGAGAGATTAAGTGGCGCACTCCGCGTGGCATCACTGATCTTGTAGAGAC 641
Qy 531 AGACTTGTGATGCTCAGAGCTGTACACATGAAATCTCAAGTGGAGCTTGTGAGATTCGA 590
Db 642 AGACTTGTGATGCTCAGAGCTGTACACATGAAATCTCAAGTGGAGCTTGTGAGATTCGA 701
Qy 591 TGAATTCAGAGAAAGATTTCTGAGTTTGAAGCAAAATGCAATGCAATGCAATGCAATGCA 650
Db 702 TGAATTCAGAGAAAGATTTCTGAGTTTGAAGCAAAATGCAATGCAATGCAATGCAATGCA 761
Qy 651 CAATGTGTATGAAAGACTTTGAGTCTCACTTACCTGCGTACCCCACTGCTGACA 710
Db 762 CAATGTGTATGAAAGACTTTGAGTCTCACTTACCTGCGTACCCCACTGCTGACA 821
Qy 711 AGCTCTCTGATATATCTCTGATTTACCCCAATATTTTACAGTACATCTGAGAGATC 770
Db 822 AGCTCTCTGATATATCTCTGATTTACCCCAATATTTTACAGTACATCTGAGAGATC 881
Qy 771 TCTTGGCAGAGAGAAAGCCAGATTTCTGAGCTTCAAGATTCAGATTTTCAAGTGGC 830
Db 882 TCTTGGCAGAGAGAAAGCCAGATTTCTGAGCTTCAAGATTCAGATTTTCAAGTGGC 941
Qy 831 AATTTCAGAGAGATTCAGATTTCTGAGCTTCAAGATTCAGATTTTCAAGTGGC 890
Db 942 AATTTCAGAGAGATTCAGATTTCTGAGCTTCAAGATTCAGATTTTCAAGTGGC 1001
Qy 891 ATTGGACATTTCAATACAGACTTTTCTATCAGCTGAGATGCTTCAAGCTGATCTG 950
Db 1002 ATTGGACATTTCAATACAGACTTTTCTATCAGCTGAGATGCTTCAAGCTGATCTG 1061
Qy 951 CCCCTAACAGATTTCTGAGTACAAAGCTTACTCAAAAGATGAGCTTGAAGTAAAG 1010
Db 1062 CCCCTAACAGATTTCTGAGTACAAAGCTTACTCAAAAGATGAGCTTGAAGTAAAG 1121
Qy 1011 AGAGCACTGGCTCTTTTGAATAATTAAGCAGACACAAAGAAAGAGACTACTTACC 1070
Db 1122 AGAGCACTGGCTCTTTTGAATAATTAAGCAGACACAAAGAAAGAGACTACTTACC 1181
Qy 1071 CAGAGATATACCTGCGGATGTTCTCAGTTCAATTTTACCTGATGCTTGAATCCG 1130
Db 1182 CAGAGATATACCTGCGGATGTTCTCAGTTCAATTTTACCTGATGCTTGAATCCG 1241
Qy 1131 AGCAATTCCTAAAGAGCATTTTTCGAGCCCTTGTGACTATACAGTGAACAGTGTGA 1190
Db 1242 AGCAATTCCTAAAGAGCATTTTTCGAGCCCTTGTGACTATACAGTGAACAGTGTGA 1301
Qy 1191 AAAGCGAGGCTACAGAGCTGTGCTAGTAAACAAGGGGAGCGCATTAATGCGCTTGT 1250
|||||

Db 1302 AAAGCGAGGCTACAGAGACTGTGCTAGTAAACAAGGGGAGCGCATTAATGCTTGT 1361
Qy 1251 AGAGATGCTGTGCTGCTTGTGTGATCTCTCTGCTTCTCTTGTGCGAGCAC 1310
Db 1362 AGAGATGCTGTGCTGCTTGTGTGATCTCTCTGCTTCTCTTGTGCGAGCAC 1421
Qy 1311 ACTGATCTCTGCTGGAACATTTCTTAACTTGAACCCAGACATTTGCTGTCAG 1370
Db 1422 ACTGATCTCTGCTGGAACATTTCTTAACTTGAACCCAGACATTTGCTGTCAG 1481
Qy 1371 CTCAGTTTATTTCAACCCAGAGAAAGCTTCATTTTGTCTTCAATTTGGAATTTGTC 1430
Db 1482 CTCAGTTTATTTCAACCCAGAGAAAGCTTCATTTTGTCTTCAATTTGGAATTTGTC 1541
Qy 1431 TACTGCAACAACAGATTTCTGCGAAGGAGATATGACAGCTGCTGCTTGTGGT 1490
Db 1542 TACTGCAACAACAGAGTTCTGCGAAGGAGATATGACAGCTGCTGCTTGTGGT 1601
Qy 1491 TGTCTGATTTCTTCAACCCAAACATATGATCTCCATGAAAGACAGGGGGAAAGCCCTGGC 1550
Db 1602 TGTCTGATTTCTTCAACCCAAACATATGATCTCCATGAAAGACAGGGGGAAAGCCCTGGC 1661
Qy 1551 TCCTAAGATATCATCTCTCTGAAACAATAATCTTCTCACTTACAGATGACCCCTC 1610
Db 1662 TCCTAAGATATCATCTCTCTGAAACAATAATCTTCTCACTTACAGATGACCCCTC 1721
Qy 1611 AATCCCATCATATATGCTGCTCAGAAACCGGATAGCCCGTTATTTGGTCTTACA 1670
Db 1722 AATCCCATCATATATGCTGCTCAGAAACCGGATAGCCCGTTATTTGGTCTTACA 1781
Qy 1671 AATTAAGAGAAACCTCAAGAACCAACCCAGATGAAATTTTGGAGCAATGCTGTT 1730
Db 1782 AATTAAGAGAAACCTCAAGAACCAACCCAGATGAAATTTTGGAGCAATGCTGTT 1841
Qy 1731 TTTTGGCTCAGGATATAGATTAAGATTAATCTTCAAGAAAGAGCTCAGATTTCT 1790
Db 1842 TTTTGGCTCAGGATATAGATTAAGATTAATCTTCAAGAAAGAGCTCAGATTTCT 1901
Qy 1791 TAAGCATGGATCTTAATCTATCTAATTAAGTTCTCTTCAAGATGCTCTGTTGGGA 1850
Db 1902 TAAGCATGGATCTTAATCTATCTAATTAAGTTCTCTTCAAGATGCTCTGTTGGGA 1961
Qy 1851 GAGAGAAAGCCCGCAAGATTAATTAAGTACAGACATCCAGCTTCAAGGAGAGTGGC 1910
Db 1962 GAGAGAAAGCCCGCAAGATTAATTAAGTACAGACATCCAGCTTCAAGGAGAGTGGC 2021
Qy 1911 GAGATCTCTCTCAGAGAAACCGCATTTTATGCTGTGAGATGCAAAAGATTTGCT 1970
Db 2022 RAGATCTCTCTCAGAGAAACCGCATTTTATGCTGTGAGATGCAAAAGATTTGCT 2081
Qy 1971 CAAGATGTAATGATGCTCTTGTGCAATTAATTAAGCAAAAGAGCTTGAATAACT 2030
Db 2082 CAAGATGTAATGATGCTCTTGTGCAATTAATTAAGCAAAAGAGCTTGAATAACT 2141
Qy 2031 AGAAGCAATGAATAACCTGCGCATTTTAAAGAAAGAAACGCTTACCTCAGGATTTTG 2090
Db 2142 AGAAGCAATGAATAACCTGCGCATTTTAAAGAAAGAAACGCTTACCTCAGGATTTTG 2201
Qy 2091 GTCATAA 2097
Db 2202 GTCATAA 2208
RESULT 9
US-10-029-386-6369
; Sequence 6369, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G;
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: A60MICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 6369
LENGTH: 591
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008727.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.45
OTHER INFORMATION: NT HIT: AF121205.1, EVALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUE 3.30e+00
OTHER INFORMATION: EST_HUMAN HIT: AUI32586.1, EVALUE 0.00e+00
US-10-029-386-6369

Query Match 15.7%; Score 330; DB 16; Length 591;
Best Local Similarity 99.7%; Pred. No. 1.3e-169;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGTGAGCCGTGATTTGCTGAGACTTGGCCAGCCCTCAGAAAGCATT 460
DB 38 GTTTAGAACTTGTGTGAGCCGTGATTTGCTGAGACTTGGCCAGCCCTCAGAAAGCATT 97
QY 461 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCCGGTGGCATCCTGCAAT 520
DB 98 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCCGGTGGCATCCTGCAAT 157
QY 521 CCTTGAAGCAGAGCCTTGTGAAGTCAAGCTGCTACATTAATCTCAAGTGAAGCTTC 580
DB 158 CCTTGAAGCAGAGCCTTGTGAAGTCAAGCTGCTACATTAATCTCAAGTGAAGCTTC 217
QY 581 TGAATTCATGATTTAGAGAGAGAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAAC 640
DB 218 TGAATTCATGATTTAGAGAGAGAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAAC 277
QY 641 GCAACCAATCCAAATGTTAATTAATGAAGACTTGAAGCTTCACTTACCCGTTGGTACCCC 700
DB 278 GCAACCAATCCAAATGTTAATTAATGAAGACTTGAAGCTTCACTTACCCGTTGGTACCCC 337
QY 701 CACTCTCAAGAGCCTCTGTAATATTCCTGTTTACCCCAAGATATTTTACAGGTACATC 760
DB 338 CACTCTCAAGAGCCTCTGTAATATTCCTGTTTACCCCAAGATATTTTACAGGTACATC 397
QY 761 TGCAGAGTCTCTTGGCCAGG 781
DB 398 TGCAGAGTCTCTTGGCCAGG 418

RESULT 10
US-10-029-386-20100
Sequence 20100, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: A60MICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20100
LENGTH: 379
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008727.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.45
OTHER INFORMATION: NT HIT: g14729757, EVALUE 0.00e+00

OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUE 1.80e+00
OTHER INFORMATION: EST_HUMAN HIT: AUI32586.1, EVALUE 0.00e+00
US-10-029-386-20100

Query Match 15.6%; Score 328; DB 16; Length 379;
Best Local Similarity 99.7%; Pred. No. 1.6e-168;
Matches 378; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 402 TTTAGAACTTGTGTGAGCCGTGATTTGCTGAGACTTGGCCAGCCCTCAGAAAGCATT 461
DB 1 TTTAGAACTTGTGTGAGCCGTGATTTGCTGAGACTTGGCCAGCCCTCAGAAAGCATT 60
QY 462 TAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCCGGTGGCATCCTGCAAT 521
DB 61 TAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCCGGTGGCATCCTGCAAT 120
QY 522 CTGTGAGCAGAGCCTTGTGAATCTAGAGCTGCTACATTAATCTCAAGTGAAGCTTC 581
DB 121 CTGTGAGCAGAGCCTTGTGAATCTAGAGCTGCTACATTAATCTCAAGTGAAGCTTC 180
QY 582 GAGATTCATGATTTAGAGAGAGAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAAC 641
DB 181 GAGATTCATGATTTAGAGAGAGAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAAC 240
QY 642 CAACCAATCCAAATGTTAATTAATGAAGACTTGAAGCTTCACTTACCCGTTGGTACCCC 701
DB 241 CAACCAATCCAAATGTTAATTAATGAAGACTTGAAGCTTCACTTACCCGTTGGTACCCC 300
QY 702 ACTCTCAAGAGCCTCTGTAATATTCCTGTTTACCCCAAGATATTTTACAGGTACATC 761
DB 301 ACTCTCAAGAGCCTCTGTAATATTCCTGTTTACCCCAAGATATTTTACAGGTACATC 360
QY 762 GCAGAGTCTCTTGGCCAG 780
DB 361 GCAGAGTCTCTTGGCCAG 379

RESULT 11
US-10-029-386-1735
Sequence 1735, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: A60MICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 1735
LENGTH: 591
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC021609.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
OTHER INFORMATION: NT HIT: AF121205.1, EVALUE 0.00e+00
OTHER INFORMATION: EST_HUMAN HIT: AUI32586.1, EVALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUE 3.30e+00
US-10-029-386-1735

Query Match 13.3%; Score 279; DB 16; Length 591;
Best Local Similarity 99.5%; Pred. No. 1.3e-141;
Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTAGAAGCTTGTGTGAGCCGTGAGTTGCTGAGACTTGGCCAGCCCTCAGAAAGCATT 460
Db 38 GTTAGAAGCTTGTGTGAGCCGTGAGTTGCTGAGACTTGGCCAGCCCTCAGAAAGCATT 97
QY 461 TTAGGTCAAGCAGAGCAGAAAGAGATTAAGTGGCGCACTCCGGTGGCATTCAGCTTCAT 520
Db 98 TTAGGTCAAGCAGAGCAGAAAGAGATTAAGTGGCGCACTCCGGTGGCATTCAGCTTCAT 157
QY 521 CCTTGAGAGCAGACTTGTGAGTCAAGGCTGTACACATTTGAATCTCAAGTCGAGCTTC 580
Db 158 CCGTAGAGCAGAGCCTGTGAGTCAAGGCTGTACACATTTGAATCTCAAGTCGAGCTTC 217
QY 581 TGAGATTGAGTATTCAGAGAAAGAGATTTCTGAGCTTTGAGCAAAATGCAAGTGAACA 640
Db 218 TGAGATTGAGTATTCAGAGAAAGAGATTTCTGAGCTTTGAGCAAAATGCAAGTGAACA 277
QY 641 GCAACCAATCCATGTTGTAATTGAAGACTTGTGAGTCTGACATTAACCGTGGTACCCC 760
Db 278 GCAACCAATCCATGTTGTAATTGAAGACTTGTGAGTCTGACATTAACCGTGGTACCCC 337
QY 701 CACTTCACAGCCTCTCTGAATATTCCTGTTTACCCCAAGATATTTACAGGTACATC 760
Db 338 CACTTCACAGCCTCTCTGAATATTCCTGTTTACCCCAAGATATTTACAGGTACATC 397
QY 761 TGCAGAGTCTCTTGGCCAGG 781
Db 398 TGCAGAGTCTCTTGGCCAGG 418

RESULT 12

US-10-029-386-15435
; Sequence 15435, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 15435
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021609.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
; OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUATE 1.80e+00
; OTHER INFORMATION: EST HUMAN HIT: AU132586.1, EVALUATE 0.00e+00
; OTHER INFORMATION: NT HIT: g14729757, EVALUATE 0.00e+00
US-10-029-386-15435

Query Match 13.2%; Score 277; DB 16; Length 379;
Best Local Similarity 99.5%; Pred. No. 1.5e-140;
Matches 377; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 402 TTATGAAGCTTGTGTGAGCCGTGAGTTGCTGAGACTTGGCCAGCCCTCAGAAAGCATT 461
Db 1 TTATGAAGCTTGTGTGAGCCGTGAGTTGCTGAGACTTGGCCAGCCCTCAGAAAGCATT 60
QY 462 TAGTCAGAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCGGTGGCATTCAGCTTCATC 521
Db 61 TAGTCAGAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCGGTGGCATTCAGCTTCATC 120

QY 522 CTTGAGAGCAGACTTGTGAGTCAAGGCTGTACACATTTGAATCTCAAGTCGAGCTTC 581
Db 121 CTTGAGAGCAGACTTGTGAGTCAAGGCTGTACACATTTGAATCTCAAGTCGAGCTTC 180
QY 582 GAGATTCGATGATTCAGAGAAAGAGATTTCTGAGCTTTGAGCAAAATGCAAGTGAACA 641
Db 181 GAGATTCGATGATTCAGAGAAAGAGATTTCTGAGCTTTGAGCAAAATGCAAGTGAACA 240
QY 642 CAACCAATCCATGTTGTAATTGAAGACTTGTGAGTCTGACATTAACCGTGGTACCCCC 701
Db 241 CAACCAATCCATGTTGTAATTGAAGACTTGTGAGTCTGACATTAACCGTGGTACCCCC 300
QY 702 ACTTCACAGCCTCTCTGAATATTCCTGTTTACCCCAAGATATTTACAGGTACATC 761
Db 301 ACTTCACAGCCTCTCTGAATATTCCTGTTTACCCCAAGATATTTACAGGTACATC 360
QY 762 GCAGAGTCTCTTGGCCAG 780
Db 361 GCAGAGTCTCTTGGCCAG 379

RESULT 13

US-10-741-600-17757
; Sequence 17757, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17757
; LENGTH: 43985
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-17757

Query Match 12.7%; Score 266; DB 21; Length 43985;
Best Local Similarity 99.5%; Pred. No. 2.1e-134;
Matches 366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTAGAAGCTTGTGTGAGCCGTGAGTTGCTGAGACTTGGCCAGCCCTCAGAAAGCATT 460
Db 14836 GTTAGAAGCTTGTGTGAGCCGTGAGTTGCTGAGACTTGGCCAGCCCTCAGAAAGCATT 14895
QY 461 TTAGGTCAAGCAGAGCAGAAAGAGATTAAGTGGCGCACTCCGGTGGCATTCAGCTTCAT 520
Db 14896 TTAGGTCAAGCAGAGCAGAAAGAGATTAAGTGGCGCACTCCGGTGGCATTCAGCTTCAT 14955
QY 521 CCTTGAGAGCAGACTTGTGAGTCAAGGCTGTACACATTTGAATCTCAAGTCGAGCTTC 580
Db 14956 CCTTGAGAGCAGACTTGTGAGTCAAGGCTGTACACATTTGAATCTCAAGTCGAGCTTC 15015
QY 581 TGAGATTGAGTATTCAGAGAAAGAGATTTCTGAGCTTTGAGCAAAATGCAAGTGAACA 640
Db 15016 TGAGATTGAGTATTCAGAGAAAGAGATTTCTGAGCTTTGAGCAAAATGCAAGTGAACA 15075
QY 641 GCAACCAATCCATGTTGTAATTGAAGACTTGTGAGTCTGACATTAACCGTGGTACCCC 700
Db 15076 GCAACCAATCCATGTTGTAATTGAAGACTTGTGAGTCTGACATTAACCGTGGTACCCC 15135
QY 701 CACTTCACAGCCTCTCTGAATATTCCTGTTTACCCCAAGATATTTACAGGTACATC 760
Db 15136 CACTTCACAGCCTCTCTGAATATTCCTGTTTACCCCAAGATATTTACAGGTACATC 15195
QY 761 TGCAGAG 768
Db 15196 TGCAGAG 15203

RESULT 14
US-10-029-386-633/c
; Sequence 633, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 633
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021609.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.48
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.58
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.52
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.57
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.79
; OTHER INFORMATION: SWISSPROT HIT: P37039, EVALU8 1.00e-06
; OTHER INFORMATION: EST HUMAN HIT: BF346446.1, EVALU8 1.00e-98
; OTHER INFORMATION: NT HIT: AF121212.1, EVALU8 0.00e+00
US-10-029-386-633

Query Match 9.0%; Score 188; DB 16; Length 525;

Best Local Similarity 100.0%; Pred. No. 1.1e-91; Mismatches 0; Indels 0; Gaps 0;

Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1765 TTCAGAAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAATCATCTAAAGTTTCC 1824
DB 234 TTCAGAAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAATCATCTAAAGTTTCC 175
QY 1825 TTCTCAAGAGATGCTCTGTTGGGAGAGAAAGCCCGCAAGATGTATCAAGACAAC 1884
DB 174 TTCTCAAGAGATGCTCTGTTGGGAGAGAAAGCCCGCAAGATGTATCAAGACAAC 115
QY 1885 ATCCAGCTTCATGCGCAGACAGTGGGAGAAATCTCTCCAGAGAAAGCCCATATTAT 1944
DB 114 ATCCAGCTTCATGCGCAGACAGTGGGAGAAATCTCTCCAGAGAAAGCCCATATTAT 55
QY 1945 GTGTGTGG 1952
DB 54 GTGTGTGG 47

RESULT 15

US-10-029-386-14338/c

; Sequence 14338, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G

; FILE REFERENCE: AEOMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 34288

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 14338

; LENGTH: 175

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO AC021609.3

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.48
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.58
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.52
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.57
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.79
; OTHER INFORMATION: SWISSPROT HIT: O61608, EVALU8 4.00e-04
; OTHER INFORMATION: EST HUMAN HIT: AA085543.1, EVALU8 7.00e-94
; OTHER INFORMATION: NT HIT: g113325067, EVALU8 5.00e-94
US-10-029-386-14338

Query Match 8.3%; Score 175; DB 16; Length 175;

Best Local Similarity 100.0%; Pred. No. 1.5e-84; Mismatches 0; Indels 0; Gaps 0;

Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1770 AAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAATCATCTAAAGTTTCC 1829
DB 175 AAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAATCATCTAAAGTTTCC 116
QY 1830 AAGAGTCTCTGTTGGGAGAGAAAGCCCGCAAGATGTATCAAGACAATCCA 1889
DB 115 AAGAGTCTCTGTTGGGAGAGAAAGCCCGCAAGATGTATCAAGACAATCCA 56
QY 1890 GCTTCATGCGCAGACAGTGGGAGAAATCTCTCCAGAGAAAGCCCATATTAT 1944
DB 55 GCTTCATGCGCAGACAGTGGGAGAAATCTCTCCAGAGAAAGCCCATATTAT 1

Search completed: August 27, 2005, 17:33:29
Job time : 904.401 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 23:18:31 ; Search time 4539.53 Seconds
(without alignments)
17558.328 Million cell updates/sec

Title: US-09-371-347A-45

Perfect score: 2094

Sequence: 1 atgaggaggttcctgtact.....ttcagatatttgcataca 2094

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_g881:*
9: gb_g882:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1349	64.4	3100	3	BC062577 Homo sapi
2	956	45.7	3143	3	BC035977 Homo sapi
3	719	34.3	908	3	BX348674 BX348674
4	689	32.9	874	4	BM801462 AGENCOURT
5	623	29.8	646	7	CN260357 170004241
6	565	27.0	565	1	AU279788 AU279788
7	533	25.9	877	1	AU124440 AU124440
8	531	25.4	1061	5	BQ218755 AGENCOURT
9	512	24.7	826	4	BI772430 60305786
10	512	24.5	776	6	CB997527 AGENCOURT
11	507	24.2	834	5	BU941078 AGENCOURT
12	485	21.7	822	1	AU132586 AU132586
13	448	21.4	591	2	AW965709 EST377782
14	446	21.3	818	6	CD559384 AGENCOURT
15	434	20.7	591	4	BI025283 RCS-MT025
16	431	20.6	974	5	BX375211 BX375211
17	406	19.4	710	5	BU570323 AGENCOURT
18	384	18.3	527	4	BI025277 RCS-MT025
19	374	17.9	579	7	CN260360 170006001
20	361	17.2	692	7	CN260359 170004706
21	360	17.1	685	4	BM049352 603626120
22	359	17.1	499	6	CD704108 EST62635
23	354	16.9	386	1	AA279726 z692d10.r
24	351	16.8	839	4	BG531787 602560355

25	343	16.4	852	5	BQ431497	BQ431497 AGENCOURT
26	341	16.3	395	4	BM838530	BM838530 K-EST0114
27	340	16.2	526	2	AW952883	AW952883 EST344953
28	337	16.1	818	7	CE995233	CE995233 AGENCOURT
29	335	16.0	413	2	BF810368	BF810368 AGENCOURT
30	335	16.0	413	2	BF810479	BF810479 RCS-C1014
31	332	15.9	366	1	AA085543	AA085543 z44h11.r
32	331	14.9	478	4	BM754488	BM754488 K-EST0031
33	302	14.4	440	4	CG877205	CG877205 OV3-HT046
34	297	14.2	416	6	CB996520	CB996520 AGENCOURT
35	292	13.9	528	2	BE301292	BE301292 B689D07.X
36	291	13.9	664	7	CR768694	CR768694 DKF2P459K
37	291	13.9	667	7	CR770923	CR770923 DKF2P469N
38	291	13.9	767	7	CR557482	CR557482 DKF2P469K
39	282	13.5	521	6	CR164340	CR164340 K-EST0225
40	276	13.2	481	7	CR549172	CR549172 DKF2P459J
41	272	13.0	301	1	AL704780	AL704780 DKF2P686M
42	264	12.6	366	6	CB298361	CB298361 z20019.te
43	257	12.3	366	2	BF808461	BF808461 CVL-C1017
44	257	12.3	368	1	AA355001	AA355001 EST63417
45	252	12.0	324	1	AA469901	AA469901 zc94D04.r

ALIGNMENTS

RESULT 1	BC062577	3100 bp	mrna	linear	HTC 25-NOV-2003
LOCUS	Homo sapiens	cdna	clone IMAGE:5189058,	containing frame-shift errors.	
DEFINITION	BC062577.1	GI:38511756			
ACCESSION	BC062577				
VERSION	BC062577.1				
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Strausberg, R., D., Mullaly, S., J., Bosak, S., A., McGowan, P., J., McKernan, K., J., Hale, S., Garcia, A., M., Gay, L., J., Hilyk, S., W., Villalón, D., K., Muzny, D., M., Sodergren, B., J., Lu, X., Gibbs, R., A., Fahney, J., Helton, B., Kettelman, M., Madan, A., C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Young, J., C., Green, E., D., Bouffard, G., G., Blakesley, R., W., Touchman, J., W., Green, E., D., Dickson, M., C., Rodriguez, A., C., Grimwood, J., Schmutz, J., Myers, R., M., Butterfield, Y., S., Krzywicki, M., I., Skalska, U., Smallus, D., E., Butcher, A., Schein, J., E., Jones, S., J., and Marra, M., A.				
AUTHORS	Strausberg, R., D., Mullaly, S., J., Bosak, S., A., McGowan, P., J., McKernan, K., J., Hale, S., Garcia, A., M., Gay, L., J., Hilyk, S., W., Villalón, D., K., Muzny, D., M., Sodergren, B., J., Lu, X., Gibbs, R., A., Fahney, J., Helton, B., Kettelman, M., Madan, A., C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Young, J., C., Green, E., D., Bouffard, G., G., Blakesley, R., W., Touchman, J., W., Green, E., D., Dickson, M., C., Rodriguez, A., C., Grimwood, J., Schmutz, J., Myers, R., M., Butterfield, Y., S., Krzywicki, M., I., Skalska, U., Smallus, D., E., Butcher, A., Schein, J., E., Jones, S., J., and Marra, M., A.				
TITLE	human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99	(26)	16899-16903	(2002)
MEDLINE	22388257				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 3100)				
AUTHORS	Strausberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (24-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,				
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov				
COMMENT	Contact: MGC help desk Email: cgabs-r@mail.nih.gov Tissue Procurement: Life Technologies, Inc.				

CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),

galtner@duburg.maryland.edu
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgrl.nih.gov
Akhter, N., Ayele, K., Beckert-Strom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooke, S.,
Dierich, N.L., Grante, S., Guan, X., Gupta, J., Hachigiri, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,
Maduro, Q.L., Masello, C., Markert, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Statistikop, S., Thomas, P.J., Touchman, J.W.,
Tsurugem, C., Vogt, J.-H., Walker, M.A., Wetherby, K.D., Wiggin, L.,
Young, A., Zhang, L., Li, and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
 Series: IRAX Plate: 135 Row: e Column: 21
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4505278
 This clone has the following problem: frame shifted.

FEATURES

Source

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1. .3100
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5189058"
/class="type=Colon, Kidney, Stomach, adult, whole pooled"
/clone_id="NH_MGC_116"
/lab_host="DH10B"
/notes="Vector: pCMV-Sport6"
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ORIGIN

Query Match	64.4%	Score 1349;	DB 3;	Length 3100;
Best Local Similarity	99.7%	Pred. No. 0;		
Matches 1809; Conservative	0;	Mismatches 2;	Indels 4;	Gaps 2;

QY	283	GGTCGGGTGATTTGCAATATACCCATCTTTTGCAATGGGGGGAAGATTAATGATTAAGCA	342
Db	172	GGCTCCGGTATTCAGAAATCACTACTTTTGCANTGGGGGAGATTAATGATTAAGCA	231
QY	343	CTTCAGAGCTTGGAGCCCGGCACTTTCTATGACATGGAACATGCAGATGACTGTGTAGT	402
Db	232	CTTCAGAGAGCTTGGAGCCCGGCACTTTCTATGACACTGGACATGCAAGATGACTGTGTAGT	291
QY	403	TTAGAACTGTGGTTGAGCCGGTGAATGCTGTGGACCTGTGGACGCCCTGAGAAAGATTTT	462
Db	292	TTAGAACTGTGGTTGAGCCGGTGAATGCTGTGGACCGCCCTGAGAAAGATTTT	351
QY	463	AGGTCAGACAGAGACAAGAGAGATTAAGTGGCGGCACTCCCGGTGGACTCACCTTGACATCC	522
Db	352	AGGTCAGACAGAGACAAGAGAGATTAAGTGGCGGCACTCCCGGTGGACTCACCTTGACATCC	411
QY	523	TTGAGGACAGACCTTTGAGTGCAGAGCGTGCTACCATTTGAATCTCAAGTGGAGCTCTG	582
Db	412	TCGAGGACAGACCTTTGAGTGCAGAGCTGCTACCATTTGAATCTCAAGTGGAGCTCTG	471
QY	583	AGATTTCAGTATTCAGAGAAAGAGATTCAGAGTTTGAAGCAAAATGCAGTGAACGC	642
Db	472	AGATTTCAGTATTCAGAGAAAGAGATTCAGAGTTTGAAGCAAAATGCAGTGAACGC	531
QY	643	AACCAATCCAAATGTTGTAATGGAACCTTGAAGTCTCACTTAACCGTTCGGTACCCCA	702
Db	532	AACCAATCCAAATGTTGTAATGGAACCTTGAAGTCTCACTTAACCGTTCGGTACCCCA	591
QY	703	CTCTCAAGGCTCTCTGAATATTTCTGTGTTTACCCCGACAGATATTTACAGTACATCTG	762
Db	592	CTCTCAAGGCTCTCTGAATATTTCTGTGTTTACCCCGACAGATATTTACAGTACATCTG	651
QY	763	CAGGAGTCTCTTGGCCAGAGAGAAAGCCCAAGTATCTGTGACTTCAGCAGATCCAGTTTTT	822
Db	652	CAGGAGTCTCTTGGCCAGAGAGAAAGCCCAAGTATCTGTGACTTCAGCAGATCCAGTTTTT	711

[illegible]

QY	1900	CAGGTGGCGGAATCCCTCCACGAGAAAGGCCCATTTATGTGTGGAGATGCAAG	1959
Db	1791	CAGGTGGCGGAATCCCTCCACGAGAAAGGCCCATTTATGTGTGGAGATGCAAG	1850
QY	1960	AATATGGCCGAAGATGTACATGATGACCTCTGTGCAATTAATTAAGCAAAAGGTGAGTT	2019
Db	1851	AATATGGCCGAAGATGTACATGATGACCTCTGTGCAATTAATTAAGCAAAAGGTGAGTT	1910
QY	2020	GAAAACTAGACGATGAAAAACCTGGCCACTTTAAAGAAGAAAAACGTTACCTTCAG	2079
Db	1911	GAAAACTAGACGATGAAAAACCTGGCCACTTTAAAGAAGAAAAACGTTACCTTCAG	1970
QY	2080	GATATTTGGTCATTA 2094	
Db	1971	GATATTTGGTCATTA 1985	
RESULT 2			
LOCUS	BC035977		
DEFINITION	BC035977	3143 bp	mRNA
ACCESSION	BC035977		linear
VERSION	BC035977.1		HTC 20-SEP-2002
KEYWORDS	HTC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 3143)		
JOURNAL	Strausberg, R.		
	Direct Submission		
	Submitted (31-JUL-2002)		National Institutes of Health, Mammalian

REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (HLN1)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-ibgc.stanford.edu>
Contact: (Dickson, Mark) mdc@pdx1.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>
 Series: IRAL Plate: 41 Row: 9 Column: 2
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4505278
 This clone has the following problem: frame shifted.

FEATURES	Location/Qualifiers
SOURCE	1. .3143

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/db_xref="taxon:9606"
/cdone="IMAGE:4611253"
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/notes="Vector: pDNR-LTB"

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ORIGIN

Query Match	45.7%	Score 956,	DB 3,	Length 3143,
Best Local Similarity	99.8%	Pred. No. 0,		
Matches 1056; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Oy 1 ATGAGAGAGGTTTCTGTACTATATGCTACACAGCAGGACAGGCAAAAGCCATCGCAGAA 60
 |||||
 Db 52 ATGAGAGAGGTTTCTGTACTATATGCTACACAGCAGGACAGGCAAAAGCCATCGCAGAA 111

Chr	Start	End	Strand	Gene	Transcript	Feature	Score
1	112	112	+	6	GAATGTGTAGAGCAAGCTGTGTGTACATGAAATTTTCTGCAATCTTCACTGTATATAGGAA	120	6
1	112	112	+	112	GAATATATGTAGCAAGCTGTGTGTACATGAAATTTTCTGCAATCTTCACTGTATATAGGAA	171	112
1	121	121	+	121	TCCGATTAAGTATGACCTTAATAAACCGAAACAGCTTCTCTGTGTGTGTGTCTTACACAG	180	121
1	172	172	+	172	TCCGATTAAGTATGACCTTAATAAACCGAAACAGCTTCTCTGTGTGTGTGTCTTACACAG	231	172
1	181	181	+	181	GGCAACCGGACACCCACCCGACACAGCCCCGAGATTTGTAAAGAAATACAAACAAACA	240	181
1	232	232	+	232	GGCAACCGGACACCCACCCGACACAGCCCCGAGATTTGTAAAGAAATACAAACAAACA	291	232
1	241	241	+	241	CTGCGCGGTGATTTCTTGTGCTCACTTGGGTATATGAGTTACTGCGGTCTCGGTATTCAGAA	300	241
1	292	292	+	292	CTGCGCGGTGATTTCTTGTGCTCACTTGGGTATATGAGTTACTGCGGTCTCGGTATTCAGAA	351	292
1	301	301	+	301	TACACCTACTTTTGGCAATGAGGAGGAGAGATTAATGATTAACGACTTCAAGAGCTTGAAGCC	360	301
1	352	352	+	352	TACACCTACTTTTGGCAATGAGGAGGAGAGATTAATGATTAACGACTTCAAGAGCTTGAAGCC	411	352
1	361	361	+	361	CGGATTTTCTATGACACTGACATGACAGATGACATGATGATTTGAACCTTGTGTGTAG	420	361
1	412	412	+	412	CGGATTTTCTATGACACTGACATGACAGATGACATGATGATTTGAACCTTGTGTGTAG	471	412
1	421	421	+	421	CCGATGATTTGCTGACACTTGGGCGAGCCCTCAGAAAGATTTTATAGTCAAGCAGAGACAA	480	421
1	472	472	+	472	CCGATGATTTGCTGACACTTGGGCGAGCCCTCAGAAAGATTTTATAGTCAAGCAGAGACAA	531	472
1	481	481	+	481	GAGAGATTAAGTGTGCGCACTCCCGGTGGCATTCACCTTGCATCTTTGAGGACAGACTTGTG	540	481
1	532	532	+	532	GAGAGATTAAGTGTGCGCACTCCCGGTGGCATTCACCTTGCATCTTCGAGGACAGACTTGTG	591	532
1	541	541	+	541	AAGTCAGAGCTGTCAACATTTGAATCTCAAGTGTGAGCTTCTGAGATTCGATGATTCAGGA	600	541
1	592	592	+	592	AAGTCAGAGCTGTCAACATTTGAATCTCAAGTGTGAGCTTCTGAGATTCGATGATTCAGGA	651	592
1	601	601	+	601	AGAAAGATTTCTGAGTTTGAAGCAAAATGACGTGAACAGCAACCAATCCAAATGTTGTA	660	601
1	652	652	+	652	AGAAAGATTTCTGAGTTTGAAGCAAAATGACGTGAACAGCAACCAATCCAAATGTTGTA	711	652
1	661	661	+	661	ATTGAAGACTTTGAGTCTTCACTTACCCGTTGCGTACCCCACTTCAACAGCTTCTGTG	720	661
1	712	712	+	712	ATTGAAGACTTTGAGTCTTCACTTACCCGTTGCGTACCCCACTTCAACAGCTTCTGTG	771	712
1	721	721	+	721	AATATTCCTGTGTTATCCCCAGAAATATTTCAAGTATATCTGACAGAGTCTCTTGGCCAG	780	721
1	772	772	+	772	AATATTCCTGTGTTATCCCCAGAAATATTTCAAGTATATCTGACAGAGTCTCTTGGCCAG	831	772
1	781	781	+	781	GAGAAAGCCCAAGATCTGTGACTTCAAGAGATCAAGTTTTCAGTGGCCAAATTTCAAG	840	781
1	832	832	+	832	GAGAAAGCCCAAGATCTGTGACTTCAAGAGATCAAGTTTTCAGTGGCCAAATTTCAAG	891	832
1	841	841	+	841	GCAAGTCAACTTACTACGATGATGATGACATTAATAACCACTGTCTGTGTGAATTTGACATT	900	841
1	892	892	+	892	GCAAGTCAACTTACTACGATGATGATGACATTAATAACCACTGTCTGTGTGAATTTGACATT	951	892
1	901	901	+	901	TCAAAATACAGACTTTTCTATCAGCCCTGTGAGATGACCTTCAAGCGTATCTGCCCTTAACGT	960	901
1	952	952	+	952	TCAAAATACAGACTTTTCTATCAGCCCTGTGAGATGACCTTCAAGCGTATCTGCCCTTAACGT	1011	952
1	961	961	+	961	GATTTCTGAGGTACAAAGCCTACTCAAAAGACTGACGCTTGAAGATTAATAAGAGACACTGC	1020	961
1	1012	1012	+	1012	GATTTCTGAGGTACAAAGCCTACTCAAAAGACTGACGCTTGAAGATTAATAAGAGACACTGC	1071	1012
1	1021	1021	+	1021	GTCCTTTTGAATTAAGGACAGACAAAGAGAAAG	1058	1021
1	1072	1072	+	1072	GTCCTTTTGAATTAAGGACAGACAAAGAGAAAG	1109	1072

RESULT 3		
BX348674		
LOCUS	908 bp	mRNA
		linear
BX348674		EST 08-APR-2004

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DEFINITION BX348674 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
ACCESSION BX348674
VERSION BX348674.1 GI:30375301
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 908)
JOURNAL Pull-length cDNA libraries and normalization
COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: sequef@genoscope.cns.fr Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3392.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0BAG0062B02_CS00490_1&c=3392.f

FEATURES
source
Location/Qualifiers
1..908
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/db_xref="taxon:9606"
/clone="CS0C010Y11"
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/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6
vector. Library was normalized."
ORIGIN
Query Match 34.3%; Score 719; DB 5; Length 908;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 674 AGTCCTCACTTACCCGTTCCGTAACCCCACTCTCACAAAGCCTCTGATATATCTGGTT 723
DB 28 AGTCCTCACTTACCCGTTCCGTAACCCCACTCTCACAAAGCCTCTGATATATCTGGTT 87
QY 734 TACCCCCGAATATTACAGTACATCTGCAGAGAGTCTTGGCCAGAGAAAGCCAG 793
DB 88 TACCCCCGAATATTACAGTACATCTGCAGAGAGTCTTGGCCAGAGAAAGCCAG 147
QY 794 TATCTGAGACTTCAGAGATCCAGTTTTCAGAGCCAAATTTCAAGAGCGAGTTCAACTTA 853
DB 148 TATCTGAGACTTCAGAGATCCAGTTTTCAGAGCCAAATTTCAAGAGCGAGTTCAACTTA 207
QY 854 CTACGATGATGCGATTAACCACTCTGCTGTAAGATTGACATTTCAATACAGACT 913
DB 208 CTACGATGATGCGATTAACCACTCTGCTGTAAGATTGACATTTCAATACAGACT 267
QY 914 TTTCTATCAGCTGAGATGCTTCAAGCTGATCTGCCCTTAACAGTGAATTCGAGGTAC 973
DB 268 TTTCTATCAGCTGAGATGCTTCAAGCTGATCTGCCCTTAACAGTGAATTCGAGGTAC 327
QY 974 AAGGCCATCTCCAAAGCTGAGCTTGAAGTAAAGAGCACTGGCTCTTTGAAA 1033
DB 328 AAGGCCATCTCCAAAGCTGAGCTTGAAGTAAAGAGCACTGGCTCTTTGAAA 387
QY 1034 TAAAGGAGACACAAAGAGAGAGACTTATACCCAGCATATCTGCGGAGATT 1093
DB 388 TAAAGGAGACACAAAGAGAGAGACTTATACCCAGCATATCTGCGGAGATT 447
QY 1094 CTCTCAGATTCAATTTTACTGCTGCTTGAATTCGAGCAATTCCTAAAGGCAATTTT 1153
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DB 448 CTCTCAGATTCAATTTTACTGCTGCTTGAATTCGAGCAATTCCTAAAGGCAATTTT 507
QY 1154 TCGAGACCCCTTGTGACATATACAGAGACAGTCTGAAAAGCGAGCTACAGAGCTGT 1213
DB 508 TCGAGACCCCTTGTGACATATACAGAGACAGTCTGAAAAGCGAGCTACAGAGCTGT 567
QY 1214 GCAGTAAACAAAGGCGAGCCGATTAATACCGCTTTGTACAGATGCTGTGCTGCTTGT 1273
DB 568 GCAGTAAACAAAGGCGAGCCGATTAATACCGCTTTGTACAGATGCTGTGCTGCTTGT 627
QY 1274 TGGATTCCTCTCTGCTTCCCTTCTTGGACGACCACTGCTCCGCTCGAATATC 1333
DB 628 TGGATTCCTCTCTGCTTCCCTTCTTGGACGACCACTGCTCCGCTCGAATATC 687
QY 1334 TTCTTAACCTTAACCCAGACCAATATTCGTGCAAGCTCAAGTTATTTCAACCCAGA 1392
DB 688 TTCTTAACCTTAACCCAGACCAATATTCGTGCAAGCTCAAGTTATTTCAACCCAGA 746

RESULT 4
BM801462 874 bp mRNA linear EST 05-MAR-2002
LOCUS BM801462
DEFINITION AGENCOURT_6459212 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5560477
5', mRNA sequence.
ACCESSION BM801462
VERSION BM801462.1 GI:19118285
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 874)
JOURNAL NIH-MGC http://mgc.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12286 row: 1 column: 14
High quality sequence stop: 710.

FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5560477"
/issue_type="duodenal adenocarcinoma, cell line"
/lab_note="NIH 88 (phage-resistant)"
/clone_lib="NIH_MGC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
ORIGIN
Query Match 32.9%; Score 689; DB 4; Length 874;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 739; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAGAGGTTCTGTACTATATGCTTACACAGAGGAGCAGCAAGGCCATGCGAGAA 60
DB 50 ATGAGAGGTTCTGTACTATATGCTTACACAGAGGAGCAGCAAGGCCATGCGAGAA 109
QY 61 GAAATGTGAGAGAGCTGTGTATGATGATTTTCTGCAAGATTTCACTGATATTAAGAA 120
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REFERENCE 1 (bases 1 to 565)
AUTHORS Imabayashi, H., Mori, T., Gojo, S., Kiyono, T., Sugiyama, T., Irie, R.,
Isogai, T., Hata, J., Tomoya, Y., and Umezawa, A.
TITLE Redifferentiation of dedifferentiated chondrocytes and
chondrogenesis of human bone marrow stromal cells via chondrosphere
formation with expression profiling by large-scale cDNA analysis
JOURNAL Exp. Cell Res. 288 (1), 35-50 (2003)
MEDLINE 22760698
PUBMED 12878157
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human CDNA Project, Sugiyama, T.; Wakamatsu, A.; Irie, R.;
Umezawa, A.; Fukuma, M.; Kusakari, S.; Hata, J.; Ishii, S.; Yamamoto, J.;
Iseno, Y.; Saito, K.; Nakamura, Y.; Masuno, Y.; Nagai, K.; Isogai, T.
HRI human CDNA project; cDNA library construction & 5'-end one
pass sequencing: Helix Research Institute.
location/Qualifiers
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/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 2.1e-298;
Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

819 TTTTCAAGTCCCAATTTCAAAAGGCACTTCACTTACGAATGATGCCATAAAACCAC 878
Db 1 TTTTCAAGTCCCAATTTCAAAAGGCACTTCACTTACGAATGATGCCATAAAACCAC 60

879 TCTGCTGGTGAATTTGGACATTTCAAAATACAGACTTTTCTATCAGCTGAGATGCTT 938
Db 61 TCTGCTGGTGAATTTGGACATTTCAAAATACAGACTTTTCTATCAGCTGAGATGCTT 120

939 CAGCTGATCTGCCCTAACAGTATCTGAGTACAAAGCTTCTCCAAAGCTGACGT 998
Db 121 CAGCTGATCTGCCCTAACAGTATCTGAGTACAAAGCTTCTCCAAAGCTGACGT 180

999 TGAAGATTAAG 1058
Db 181 TGAAGATTAAG 240

1059 AGCTACCTTACCCAGAGATTAACCTGCGGAGATGTTCTCCAGTTCAATTTTAACTG 1118
Db 241 AGCTACCTTACCCAGAGATTAACCTGCGGAGATGTTCTCCAGTTCAATTTTAACTG 300

1119 TCTTGAATCCAGAGATTTCTTAAAAAGCATTTTTCGAGCCCTTGTGACTATACAG 1178
Db 301 TCTTGAATCCAGAGATTTCTTAAAAAGCATTTTTCGAGCCCTTGTGACTATACAG 360

1179 TGAAGTGTGAAAAGCGAGAGCTACAGAGCTGTGAGTAACAGAGGCGAGCCGATTA 1238
Db 361 TGAAGTGTGAAAAGCGAGAGCTACAGAGCTGTGAGTAACAGAGGCGAGCCGATTA 420

1239 TAGCGGCTTTGTGAGATGCTGTGCTGCTGTTGGATCTCTCTGCTTCCCTTC 1298
Db 421 TAGCGGCTTTGTGAGATGCTGTGCTGCTGTTGGATCTCTCTGCTTCCCTTC 480

1299 TTGCGAGCAGCACTCAGTCTCTGCTGCAACATCTTCTAACTTCAACCCAGACATA 1358
Db 481 TTGCGAGCAGCACTCAGTCTCTGCTGCAACATCTTCTAACTTCAACCCAGACATA 540

ORIGIN
Query Match 25.9%; Score 543; DB 1; Length 877;
Best Local Similarity 100.0%; Pred. No. 2.8e-286;
Matches 543; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1143 AAAGGATTTTTCGAGCCCTTGTGACTATACAGTGAACAGTGTGAAAAGGCGAGGCT 1202
Db 192 AAAGGATTTTTCGAGCCCTTGTGACTATACAGTGAACAGTGTGAAAAGGCGAGGCT 251

1203 ACAGAGCTGTGAGTAACAGAGGCGAGCCGATTAAGCCGCTTTGTAGAGATGCTG 1262
Db 252 ACAGAGCTGTGAGTAACAGAGGCGAGCCGATTAAGCCGCTTTGTAGAGATGCTG 311

1263 TGGCTGCTTGTGAGATCTCTCTGCTTCCCTTTTGGCAGCCCACTCAGTCTCCT 1322
Db 312 TGGCTGCTTGTGAGATCTCTCTGCTTCCCTTTTGGCAGCCCACTCAGTCTCCT 371

1323 GCTCGAAGCATCTTCCATTAACCAACGAGACATATTGTGTGGAAGCTCAAGTTATT 1382
Db 372 GCTCGAAGCATCTTCCATTAACCAACGAGACATATTGTGTGGAAGCTCAAGTTATT 431

1383 TCACCGAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTACTGCGCAAC 1442
Db 432 TCACCGAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTACTGCGCAAC 491

Db		61	AAGGAGCTACCTTAACCCAGCAATATCCTGGGGATTTCTCTCAGTTCATTTTTACT	120
Oy		1115	GGTGTCTTGAAATCCGAGCAATTCCTAAAAGGATTTTTGCCAGCCCTTGGAATA	1174
Db		121	GGGTCTTTGAAATCCGAGCAATTCCTAAAAGGATTTTGCGAGCCCTTGGAATA	180
Oy		1175	CCAGTGCAGTGCAGAAAAGGCGAGGCTACAGAGCTGTGCAGATGAACAAGGCGAGCG	1234
Db		181	CCAGTGCAGTGCAGAAAAGGCGAGGCTACAGAGCTGTGCAGATGAACAAGGCGAGCG	240
Oy		1235	ATTATAGCCGCTTGTATACAGATGCTGTGCTGCTGTTGGATCTCTCTGCTTTC	1294
Db		241	ATTATAGCCGCTTGTATACAGATGCTGTGCTGCTGTTGGATCTCTCTGCTTTC	300
Oy		1295	CTTCTTGCCAGCCACCACTAGTCTCTGCTGCAACATCTTCTTAACTTAACCAGAC	1354
Db		301	CTTCTTGCCAGCCACCACTAGTCTCTGCTGCAACATCTTCTTAACTTAACCAGAC	360
Oy		1355	CATATTGGTGGCGAAGCTCAAGTTATTTACCCAGAAAGCTCATTTTGCTTCAACA	1414
Db		361	CATATTGGTGGCGAAGCTCAAGTTATTTACCCAGAAAGCTCATTTTGCTTCAACA	420
Oy		1415	TTCGGAATTTCTGTCTACTGECACAACAGAGTTTCGCGAGGATATGACAGCT	1474
Db		421	TTCGGAATTTCTGTCTACTGECACAACAGAGTTTCGCGAGGATATGACAGCT	480
Oy		1475	GGCTGGCCCTTGTGTGTGCTTCAAGTTCTTCAGCCAAATATCATGATCCC	1525
Db		481	GGCTGGCCCTTGTGTGTGCTTCAAGTTCTTCAGCCAAATATCATGATCCC	531
RESULT 9				
Bt772430				
LOCUS		826 bp	mRNA	linear EST 25-SEP-2001
DEFINITION		603055786P1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5205285 5'		
ACCESSION		Bt772430		
VERSION		Bt772430.1		GI:15764008
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE		1 (bases 1 to 826)		
JOURNAL		NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT		National Institutes of Health, Mammalian Gene Collection (MGC)		
		Unpublished (1999)		
		Contact: Robert Strausberg, Ph.D.		
		Email: cgapbs-remail.nih.gov		
		Tissue Procurement: Life Technologies, Inc.		
		cDNA Library Preparation: Life Technologies, Inc.		
		cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
		DNA Sequencing by: Incyte Genomics, Inc.		
		Clone distribution: MGC clone distribution information can be		
		found through the I.M.A.G.E. Consortium/LNL at:		
		http://image.lnl.gov		
		Plate: LHAM1514 row: 1 column: 22		
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		/clone_lib="NIH_MGC_122"		
		/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6		
		Site 1: NotI; Site 2: EcoRV (destroyed); RNA source		
		anonymous pool of 24 week female lungs; 16 week female		
		spleen, and 20-22 week male spleens. Library is oligo-dT		
		primed and directionally cloned (EcoRV site is destroyed		
		upon cloning). Average insert size 1.4 kb, insert size		

ORIGIN

range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH_MGC Library."

Query Match 24.7%; Score 517; DB 4; Length 826;
Best Local Similarity 99.7%; Pred. No. 5.7e-272;
Matches 617; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ATGAGAGGTTTCTGTTACTATATGCTACACAGAGGAGACAGCAAGCCATCGCAGAA 60
DB 53 ATGAGAGGTTTCTGTTACTATATGCTACACAGAGGAGACAGCAAGCCATCGCAGAA 112
QY 61 GAATGTTGTAGCAAGCTGTGTGATCATGATTTTCTGACATCTTCACTGTATTAGTAA 120
DB 113 GAATATGTAGCAAGCTGTGTGATCATGATTTTCTGACATCTTCACTGTATTAGTAA 172
QY 121 TCCGATTAAGTATGACCTTAAACCGAAACAGCTCTCTGTGTGTGTGTTCTACACAG 180
DB 173 TCCGATTAAGTATGACCTTAAACCGAAACAGCTCTCTGTGTGTGTGTTCTACACAG 232
QY 181 GGACCCGAGAGCCACCCGACACAGCCCGAAGTTTGTAAAGAAATACAGAACCAACA 240
DB 233 GGACCCGAGAGCCACCCGACACAGCCCGAAGTTTGTAAAGAAATACAGAACCAACA 292
QY 241 CTGCGCGTTGATTTCTTGTCTACCTGCGGTATGAGTTTCTGCGTCTCGGTATTCAGAA 300
DB 293 CTGCGCGTTGATTTCTTGTCTACCTGCGGTATGAGTTTCTGCGTCTCGGTATTCAGAA 352
QY 301 TACACCTACTTTTGCATGAGGGGAGAAATTAATGATTAAGACCTTCAAGAGCTTGGAGCC 360
DB 353 TACACCTACTTTTGCATGAGGGGAGAAATTAATGATTAAGACCTTCAAGAGCTTGGAGCC 412
QY 361 CGGCAATTTCTATGACACTGTGACATGACATGCTGTAGTGTAGAACTTGTGTGAG 420
DB 413 CGGCAATTTCTATGACACTGTGACATGACATGCTGTAGTGTAGAACTTGTGTGAG 472
QY 421 CCGTGATTTGCTGACCTGTGCGCAGCCCTCAAGAAAGATTTTAAAGTACAGACAGACAA 480
DB 473 CCGTGATTTGCTGACCTGTGCGCAGCCCTCAAGAAAGATTTTAAAGTACAGACAGACAA 532
QY 481 GAGAGATTAAGTGGCGCACTCCGGTGGACATCCCTGACCTTGAAGAGACAGACTTGTG 540
DB 533 GAGAGATTAAGTGGCGCACTCCGGTGGACATCCCTGACCTTGAAGAGACAGACTTGTG 592
QY 541 AAGTCAGAGCTGTCTACATTCATTCAGTTCAGAGCTTCTGAGATTTCATGATTTCAGGA 600
DB 593 AAGTCAGAGCTGTCTACATTCATTCAGTTCAGAGCTTCTGAGATTTCATGATTTCAGGA 652
QY 601 AGAAGAGATTCTGAGTTT 619
DB 653 AGAAGAGATTCTGAGTTT 671
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RESULT 10

CB97527

776 bp mRNA linear EST 01-MAY-2003

LOCUS CB97527
DEFINITION AGENCOURT 13620640 NIH MGC 148 Homo sapiens cDNA clone
IMAGE:30338684 5', mRNA sequence.

ACCESSION

CB97527

CB97527.1

GI:30292047

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens (human)

REFERENCE

1 (bases 1 to 776)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

COMMENT

Email: cgabbs-remail.nih.gov

Tissue Procurement: Dr. Stefan Hanson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: NDAM365 row: 1 column: 21
High quality sequence stop: 564.
Location/Qualifiers

FEATURES

source

1..776

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/clone_id="NIH_MGC_148"

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all-XhoI; Site: 2; BamH; Library is oligo-dT primed and

directionally cloned using primer

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size 2.3 kb and normalized to ROT 5. This is a primary

library enriched for full-length clones and constructed

using the Cap-trapper method (Carninci, in preparation).

Library constructed by M. Brownstein (NIH/NHGRI,

National Institutes of Health). Note: this is a NIH_MGC

Library."

ORIGIN

Query Match 24.5%; Score 512; DB 6; Length 776;
Best Local Similarity 99.7%; Pred. No. 3.2e-269;
Matches 612; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 88 ATGAGAGGTTTCTGTTACTATATGCTACACAGAGGAGACAGCAAGCCATCGCAGAA 147
QY 61 GAATGTTGTAGCAAGCTGTGTGATCATGATTTTCTGACATCTTCACTGTATTAGTAA 120
DB 148 GAATGTTGTAGCAAGCTGTGTGATCATGATTTTCTGACATCTTCACTGTATTAGTAA 207
QY 121 TCCGATTAAGTATGACCTTAAACCGAAACAGCTCTTGTGTGTGTTCTACACAG 180
DB 208 TCCGATTAAGTATGACCTTAAACCGAAACAGCTCTTGTGTGTGTTCTACACAG 267
QY 181 GGACCCGAGAGCCACCCGACACAGCCCGAAGTTTGTAAAGAAATACAGAACCAACA 240
DB 268 GGACCCGAGAGCCACCCGACACAGCCCGAAGTTTGTAAAGAAATACAGAACCAACA 327
QY 241 CTGCGCGTTGATTTCTTGTCTCACTGCGGTATGAGTTTCTGCGTCTCGGTATTCAGAA 300
DB 328 CTGCGCGTTGATTTCTTGTCTCACTGCGGTATGAGTTTCTGCGTCTCGGTATTCAGAA 387
QY 301 TACACCTACTTTTGCATGAGGGGAGAAATTAATGATTAAGACCTTCAAGAGCTTGAAGCC 360
DB 388 TACACCTACTTTTGCATGAGGGGAGAAATTAATGATTAAGACCTTCAAGAGCTTGAAGCC 447
QY 361 CGGCAATTTCTATGACACTGTGACATGACATGCTGTAGTGTAGAACTTGTGTGAG 420
DB 448 CGGCAATTTCTATGACACTGTGACATGACATGCTGTAGTGTAGAACTTGTGTGAG 507
QY 421 CCGTGATTTGCTGACCTTGGCCAGCCCTCAGAAAGATTTTAAAGTCAAGAGAGACAA 480
DB 508 CCGTGATTTGCTGACCTTGGCCAGCCCTCAGAAAGATTTTAAAGTCAAGAGAGACAA 567
QY 481 GAGAGATTAAGTGGCGCACTCCGGTGGACATCCCTGACATCTTGAAGACAGACTTGTG 540
DB 568 GAGAGATTAAGTGGCGCACTCCGGTGGACATCCCTGACATCTTGAAGACAGACTTGTG 627
QY 541 AAGTCAGAGCTGTACATTCATTCAGTTCAGAGCTTCTGAGATTTCATGATTTCAGGA 600
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Db	628	AAGTCAGAGCTGTACACATGATTCAATCTCAATCGAGCTTTGAGATTGCATGATTCAAGCA	687
Qy	601	AGAAAGATTCTGA	614
Db	688	AGAAAGATTCTGA	701
RESULT	11		
LOCUS	BU941078		
DEFINITION	BU941078	834 bp	mRNA
	AGENCOURT_10540067 NIH-MGC_128 Homo sapiens cDNA clone		linear
	IMAGE:6712893.5', mRNA sequence.		
ACCESSION	BU941078		
VERSION	BU941078.1	GI:24129897	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 834)		
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/ .		
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)		
TITLE	Unpublished (1999)		
JOURNAL	Contact: Robert Strausberg, Ph.D.		
COMMENT	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: NCI		
	CDNA Library Preparation: Michael Brownstein Laboratory		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNLN at:		
	http://image.lnl.gov		
	Plate: LNCM3022 row: e column: 21		
	High quality sequence stop: 586.		

FEATURES	Location/Qualifiers
source	1. .834

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/notes="vector: pDNR-LIB; Site_1: SfiI (ggccatcagcc);
Site_2: SfiI (ggccgcctggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AGAGCGGTGATCAACGAGATGGCATTCATTCGGCCGGG-3' and
5'-ATTCTGAGGCCGAGCGCGCGGACATC-dT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the >2 kb
size fraction (other fractions present in NIH MGC 126 and
NIH MGC 127). Library created in the laboratory of T.
Usdin, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC
library."

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	Query Match	24.2%	Score 507;	DB 5;	Length 834;		
	Best Local Similarity	99.7%	Pred. No. 1,8e+26;				
	Matches	607;	Conservative	0;	Mismatches	2;	
				Indels	0;	Gaps	0;
OY	379	GGACATGAGATGACTGTCTAGCTTTAAACCTGTGTGTGAAGCCCGTATGCTTGACATC	438				
Dd	3	GGACATGAGATGACTGTGTGTGTGTGTGAACCTGTGTGTGAACCTGTGTGTGTGCATCTC	62				
OY	439	TGGCCAGCCTTCAGAACCATTTTAGTGTCAAGCAGAGACAAGAGAGATTAATGTGGCCCA	498				
Dd	63	TGGCCAGCCTTCAGAACCATTTTAGTGTCAAGCAGAGACAAGAGAGATTAATGTGGCCCA	122				

Oy	499	CTCCCGGTGGATCACTGCATCCCTTGAGAGACAGACTTGGAAGTCAGAGCTGACAC	558
Db	123	CTCCCGGTGGATCACTGCATCCCTTGAGAGACAGACTTGGAAGTCAGAGCTGACAC	182
Oy	559	ATTGAATCTCAAGTCAGACTTCTGAGATGATGATTCAGGAGAAAGATTCGAGGTT	618
Db	183	ATTGAATCTCAAGTCAGACTTCTGAGATGATGATTCAGGAGAAAGATTCGAGGTT	242
Oy	619	TTGAGCAAAATGCAATGCAAGCAAGCAATTCCAATGTGATTTGAAGACTTTGAGTCC	678
Db	243	TTGAGCAAAATGCAATGCAAGCAAGCAATTCCAATGTGATTTGAAGACTTTGAGTCC	302
Oy	679	TCACTTACCGGTGGTACCCCACTTCACAGCCTCTCGAATATTTCTGTGGTTTACC	738
Db	303	TCACTTACCGGTGGTACCCCACTTCACAGCCTCTCGAATATTTCTGTGGTTTACC	362
Oy	739	CCAGAAATTTTACAGGTACATCTGCAGAGATCTCTGGCCAGAGGAAAGCCAGTATCT	798
Db	363	CCAGAAATTTTACAGGTACATCTGCAGAGATCTCTGGCCAGAGGAAAGCCAGTATCT	422
Oy	799	GTGACTTCAGAGAGATCCAGTTTTTCAAGTGCCAATTTCAAGGCAAGTTCAACTACTACG	858
Db	423	GTGACTTCAGAGAGATCCAGTTTTTCAAGTGCCAATTTCAAGGCAAGTTCAACTACTACG	482
Oy	859	AATGATSCCATATAAAACCACTCTGCTGGTGAATTTGACATTTCAATPACAGACTTTTCC	918
Db	483	AATGATSCCATATAAAACCACTCTGCTGGTGAATTTGACATTTCAATPACAGACTTTTCC	542
Oy	919	TATCAGCTTGAGAGATGCTTTCAGCGTGATCTGCCCTTAACAGTGAATCTGAGGTCAAAAGC	978
Db	543	TATCAGCTTGAGAGATGCTTTCAGCGTGATCTGCCCTTAACAGTGAATCTGAGGTCAAAAGC	602
Oy	979	CTACTCCAA 987	
Db	603	CTACTCCAA 611	

RESULT 12	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
AV132586	AV132586	AV132586 NT2RP4 Homo sapiens cDNA clone NT2RP4000141 5', mRNA sequence.	AV132586	AV132586.1	GI:10992940	EST.	Homo sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheta; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 822)	Oca,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,U., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuno,Y. and Isogai,T.	HRI human cDNA project (Oca,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,U., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuno,Y., Isogai,T.)	Unpublished (2000)	Contact: Takao Isogai

Helix Research Institute
1532-3 Yana, Kagarazu, Chiba 292-0812, Japan
Tel.: 81-438-52-3975
Tel.: 81-438-52-3986
Fax: 81-438-52-3986
Email: genomice@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. 822
/organism="Homo sapiens"
/mol_type="mRNA"

/db xref="taxon:9606"
/clone="NT2RP4000141"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_1ib="NT2RP4"
/note="Vector: PME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"

ORIGIN

Query Match 21.7%; Score 455; DB 1; Length 822;
Best Local Similarity 99.6%; Pred. No. 7.3e-238;
Matches 555; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 283 GGTCTGGTATTCAGAAATACCTTACTTTTGCAATGGGGGAAAGATTAATGTAACCA 342
DB 182 GGTCTGGTATTCAGAAATACCTTACTTTTGCAATGGGGGAAAGATTAATGTAACCA 241
QY 343 CTTCAGAGCTTGAAGCCGGCAATTTCTATGACACTGACATGACATGCTGTAGGT 402
DB 242 CTTCAGAGCTTGAAGCCGGCAATTTCTATGACACTGACATGACATGCTGTAGGT 301
QY 403 TTGAACTTGTGTGAGCCGTGATTTGCTGACCTGTGACAGCCCTCAGAAAGCAATTT 462
DB 302 TTGAACTTGTGTGAGCCGTGATTTGCTGACCTGTGACAGCCCTCAGAAAGCAATTT 361
QY 463 AGCTCAGAGCAGAGAGAGATTAAGTGGGCACTCCCGGTGGCATCACTGCATCC 522
DB 362 AGCTCAGAGCAGAGAGAGATTAAGTGGGCACTCCCGGTGGCATCACTGCATCC 421
QY 523 TTGAGCAGAGCCTTGTGAGTCAAGCTCTACACATTAATCTCAAGTCAAGCTTCTG 582
DB 422 TCGAGAGCAGAGCCTTGTGAGTCAAGCTCTACACATTAATCTCAAGTCAAGCTTCTG 481
QY 583 AGATTGATGATTCAGAGAGAGATTTGAGGTTTGAAGCAATGCAATGCAAGC 642
DB 482 AGATTGATGATTCAGAGAGAGATTTGAGGTTTGAAGCAATGCAATGCAAGC 541
QY 643 AACCAATCCAAATTTGAAAGCTTTGAGTCTTCACTTACCCCTTGGTACCCCA 702
DB 542 AACCAATCCAAATTTGAAAGCTTTGAGTCTTCACTTACCCCTTGGTACCCCA 601
QY 703 CTCTCAGAGCCTCTGTAATTTCTGTTTACCCCAAGATTAATTTACAGTACATCTG 762
DB 602 CTCTCAGAGCCTCTGTAATTTCTGTTTACCCCAAGATTAATTTACAGTACATCTG 661
QY 763 CAGAGTCTCTTGGCCAGAGAGAGCAAGATCTGTGACTTCAGCAATTCAGTTT 822
DB 662 CAGAGTCTCTTGGCCAGAGAGAGCAAGATCTGTGACTTCAGCAATTCAGTTT 721
QY 823 CAGTGCATTTCAAA 839
DB 722 CAGTGCATTTCAAA 738

RESULT 13
AM965709 591 bp mRNA linear EST 01-JUN-2000
LOCUS EST377782 MAGE resequences, MAGI Homo sapiens cDNA, mRNA sequence.
DEFINITION AM965709
ACCESSION AM965709.1 GI:8155545
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 591)
AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and Quackenbush, J.
TITLE Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnd@tigr.org
Plate: 218
Seq primer: Reverse.
Location/Qualifiers
1. 591
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_1ib="MAGE resequences, MAGI"
/note="Vector: pBluescriptSkm"

FEATURES

source

ORIGIN

Query Match 21.4%; Score 448; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 4.9e-234; Indels 0; Gaps 0;
Matches 448; Conservative 0; Mismatches 0;

QY 1192 AAGCGAGGCTACAGAGCTGTGACATTAACAAGGGCAGCCGATTAAGCCGTTTGT 1251
DB 1 AAGCGAGGCTACAGAGCTGTGACATTAACAAGGGCAGCCGATTAAGCCGTTTGT 60
QY 1252 CGAGATGCTGTGCTGCTGTTGATCTCTCCCTGCTTCCCTTCCGACGACCA 1311
DB 61 CGAGATGCTGTGCTGCTGTTGATCTCTCCCTGCTTCCCTTCCGACGACCA 120
QY 1312 CTCAGTCTCTGCTCGAATCTTCTTAACCTTCAACCGACATATTTGTGTCAAG 1371
DB 121 CTCAGTCTCTGCTCGAATCTTCTTAACCTTCAACCGACATATTTGTGTCAAG 180
QY 1372 TCAGATTATTTCAACCAGAGAAAGCTCAATTTGTCTTCAACTGTGAAATTTCTGTCT 1431
DB 181 TCAGATTATTTCAACCAGAGAAAGCTCAATTTGTCTTCAACTGTGAAATTTCTGTCT 240
QY 1432 ACTGCCAACAAGAGTTCTGGGGAAGAGATGATGACAGGCTGCTGCTTGTGTT 1491
DB 241 ACTGCCAACAAGAGTTCTGGGGAAGAGATGATGACAGGCTGCTGCTTGTGTT 300
QY 1492 GCTTCAGTCTTTCAGCAAAATACATGATCCATGAGAGACAGCGGAAAGCCCTGCT 1551
DB 301 GCTTCAGTCTTTCAGCAAAATACATGATCCATGAGAGACAGCGGAAAGCCCTGCT 360
QY 1552 CCTAAGATATCCATCTCTCTGAGACACAAATTTCTTCACTTACAGATGACCCCTCA 1611
DB 361 CCTAAGATATCCATCTCTCTGAGACACAAATTTCTTCACTTACAGATGACCCCTCA 420
QY 1612 ATCCCATCATTAATGTTGGTCCAGGAA 1639
DB 421 ATCCCATCATTAATGTTGGTCCAGGAA 448

RESULT 14
CD559384 818 bp mRNA linear EST 11-JUN-2003
LOCUS AGENCOUFT_14401607 NIH_MGC_191 Homo sapiens cDNA clone
DEFINITION IMAGR:30409775 5', mRNA sequence.
ACCESSION CD559384
VERSION CD559384.1 GI:31585452
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 818)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: c9apbs-r@mail.nih.gov
 Tissue Procurement: Narayan Bhat
 cDNA Library Preparation: Clontech Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>
 Plate: NDCM198 row: n column: 24
 High quality sequence stop: 484.

FEATURES

source

1. 818
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 /clone="IMAGE:30409775"
 /tissue_type="Pooled"
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 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggc);
 Site 2: SfiI (ggcgccctggcc); Library is oligo-dT primed
 and directionally cloned. PBMC - Peripheral Blood
 Mononuclear Cells. RNA was pooled from 3/6hour stimulation
 with PMA and ionomycin. 5' and 3' adaptors were used in
 cloning as follows: 5' adaptor sequence:
 5'-CAAGGCGATTAGGCG-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGAGCGCCGACATG-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.69
 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 21.3%; Score 446; DB 6; Length 818;
 Best Local Similarity 99.6%; Pred. No. 6.5e-233;
 Matches 546; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

425 GGATTGCTGAGCTCTGCGCCGAGCCCTTGAAGAAAGATTGTTAGTCAAGACAGACAGAG 484
 3 GGATTGCTGAGCTCTGCGCCGAGCCCTTGAAGAAAGATTGTTAGTCAAGACAGAGAG 62

485 AGATTAGTGGCGACTCCCGGTGGATGACCTGATCTTGAAGACAGACAGCTTGTAGAGT 544
 63 AGATTAGTGGCGACTCCCGGTGGATGACCTGATCTTGAAGACAGACAGCTTGTAGAGT 122

545 CAGAGCTGTACACATGATGATCTCAAGTCAAGTCTTGAAGACAGACAGCTTGTAGAGT 604
 123 CAGAGCTGTACACATGATGATCTCAAGTCAAGTCTTGAAGACAGACAGCTTGTAGAGT 182

605 AGGATTCTGAGGTTTGAAGCAAAATGAGTGAACAGCAACCAATCAATGTTGTAATTG 664
 183 AGGATTCTGAGGTTTGAAGCAAAATGAGTGAACAGCAACCAATCAATGTTGTAATTG 242

665 AAGACTTGAAGTCCATCACTCCGTTGGTACCCCACTTCAAGAGCTCTGGAATA 724
 243 AAGACTTGAAGTCCATCACTCCGTTGGTACCCCACTTCAAGAGCTCTGGAATA 302

725 TTCTGCTTACCCCGAGAAATTTTACAGTACATCTGACAGAGTCTTGGCCAGAGAG 784
 303 TTCTGCTTACCCCGAGAAATTTTACAGTACATCTGACAGAGTCTTGGCCAGAGAG 362

785 AAAGCCAGATCTGTGACTTCAAGATCCAGTTTTCAGAGTCCAAATTTCAAGGCGAG 844
 363 AAAGCCAGATCTGTGACTTCAAGATCCAGTTTTCAGAGTCCAAATTTCAAGGCGAG 422

845 TTCAACTTCTAGAGTATGAGTATGATTAACCACTGCTGAGTGAATGAGCAATTTCAA 904
 423 TTCAACTTCTAGAGTATGAGTATGATTAACCACTGCTGAGTGAATGAGCAATTTCAA 482

905 ATACAGACTTTTCTATCAGCTGAGATGCTTCAAGCTGATCTGCCCTAACAGTGAAT 964
 483 ATACAGACTTTTCTATCAGCTGAGATGCTTCAAGCTGATCTGCCCTAACAGTGAAT 542

QY 965 CTGAGGTA 972
 DB 543 CTGAGGTA 550

RESULT 15

BI025283 591 bp mRNA linear EST 14-JUN-2001
 LOCUS RC5-MT0259-020201-021-G04 MT0259 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BI025283.1 GI:14431913
 VERSION BI025283.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Bukeyeva, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (baes 1 to 591)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
 Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
 Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PABSP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripte/gethtml2.pl?cl=RC5&c2=RC5-MT0259-
 020201-021-G04&t3=2001-02-02&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 78
 High quality sequence stop: 590.

FEATURES

source

1. 591
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 SmaI; A mini-library was made by cloning products derived
 from ORESTER PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN

Query Match 20.7%; Score 434; DB 4; Length 591;
 Best Local Similarity 99.8%; Pred. No. 2.5e-226;
 Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

525 GAGGACAGCTTGTGAAGTCAAGCTGTACACATGATCTCAAGTCAAGCTTGTGAG 584
 102 GAGGACAGCTTGTGAAGTCAAGCTGTACACATGATCTCAAGTCAAGCTTGTGAG 161

585 ATTGCATGATTCAAGAGAAAGAGATTCTGAGGTTTGAAGCAAAATGACGTGAACAGCA 644
 162 ATTGCATGATTCAAGAGAAAGAGATTCTGAGGTTTGAAGCAAAATGACGTGAACAGCA 221

645 CCAATCAATGTTGTAATGAAGACTTGAAGTCTCACTTACCCGTTGGTACCCCACT 704

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Db      222 CCAATCCAAATGTTGTAATTAAGAATTGAGTCTCACTTACCCGTTGGTACCCCACT 281
Qy      705 CTCACAAGCCTCTCTGTAATATTCCTGTTTACCCCGAATATTTACAGGTACATCTGCA 764
Db      282 CTCACAAGCCTCTCTGTAATATTCCTGTTTACCCCGAATATTTACAGGTACATCTGCA 341
Qy      765 GGAGTCTCTTGGCCAGGAGGAAGCCAAAGTATCTGTGACTTCAGCAGATCAAGTTTTC 824
Db      342 GGAGACTCTTGGCCAGGAGGAAGCCAAAGTATCTGTGACTTCAGCAGATCAAGTTTTC 401
Qy      825 AGTGCCAATTTCAAAGCAGTTCACTTACTAGCAATGATGCCATAAAACCACTGCGT 884
Db      402 AGTGCCAATTTCAAAGCAGTTCACTTACTAGCAATGATGCCATAAAACCACTGCGT 461
Qy      885 GGTAGAATTGACATTTCAATAACAGACTTTTCTATCAGCCTGAGATGCCCTTCAGCGT 944
Db      462 GGTAGAATTGACATTTCAATAACAGACTTTTCTATCAGCCTGAGATGCCCTTCAGCGT 521
Qy      945 GATCTGCCCTTAACAGTGAATTTGAGGTACAAAGCCTACTCCAAAGACTGCACTTGAAGA 1004
Db      522 GATCTGCCCTTAACAGTGAATTTGAGGTACAAAGCCTACTCCAAAGACTGCACTTGAAGA 581
Qy      1005 TAAAA 1009
Db      582 TAAAA 586
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GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: August 26, 2005, 19:17:21 ; Search time 5998.62 Seconds
(without alignments)
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Title: US-09-371-347A-45
Perfect score: 2094
Sequence: 1 atgagagaggttcctgcttact.....ttcagatattgtgcataa 2094

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

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1: gb_ba:*
2: gb_hcg:*
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9: gb_pr:*
10: gb_ro:*
11: gb_ses:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1854	88.5	3259	6	AR144976 Sequence
2	1854	88.5	3259	6	AX050463 Sequence
3	1854	88.5	3259	9	AF025794 Homo sapi
4	1854	88.5	3291	9	AF121214 Homo sapi
5	1752	83.7	3241	6	C0726091 Sequence
6	1701	81.2	3310	9	BC054816 Homo sapi
7	1220	58.3	2933	11	BV177620 Bmm95800
8	1220	58.3	2933	11	BV178010 Bmm97986
9	386	18.4	330	6	BD077780 5' EST of
10	381	18.2	1353	9	AF121205 Homo sapi
11	330	15.8	109626	9	AC010346 Homo sapi
12	330	15.8	110756	9	AC025174 Homo sapi
13	279	13.3	158199	2	AC022921 Homo sapi
14	279	13.3	167237	2	AC021609 Homo sapi
15	279	13.3	177596	2	AC091945 Homo sapi
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19	188	9.0	177596	2	AC091945 Homo sapi

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24	158	7.5	2475	6	AX375651	AX375651 Sequence
25	155	7.4	2011	9	FI21202S06	AF121207 Homo sapi
26	146	7.0	2214	9	FI21202S12	AF121213 Homo sapi
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29	121	5.8	1119	9	FI21202S10	AF121211 Homo sapi
30	119	5.7	1200	9	FI21202S03	AF121204 Homo sapi
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32	63	3.0	63	6	AX611833	AX611833 Sequence
33	60	2.9	60	6	CO539377	CO539377 Sequence
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35	54	2.6	54	6	AX611843	AX611843 Sequence
36	51	2.4	51	6	AX162161	AX162161 Sequence
37	48	2.3	48	6	AX611835	AX611835 Sequence
38	48	2.3	48	6	AX611841	AX611841 Sequence
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40	44	2.1	650	9	FI21202S08	AF121209 Homo sapi
41	41	2.0	41	6	AX611845	AX611845 Sequence
42	38	1.8	38	6	AX611837	AX611837 Sequence
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ALIGNMENTS

RESULT 1
LOCUS AR144976 3259 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 23 from patent US 6210950.
ACCESSION AR144976
VERSION AR144976.1 GI:15106843

KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3259)

AUTHORS Johnson, W.G. and Stenroos, R.Scott.
TITLE Methods for diagnosing, preventing, and treating developmental disorders due to a combination of genetic and environmental factors

JOURNAL Patent: US 6210950-A 23 03-APR-2001;
FEATURES Location/Qualifiers

source

ORIGIN
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Query Match	88.5%;	Score 1854;	DB 6;	Length 3259;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 2094;	Conservative	0;	Mismatches 0;	Indels 3; Gaps 1;
QY	1	ATGAGGAGGTTTCTGTACTATATGCTACACGACGAGGCAAGCCATCGAGAA	60	
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DB	140	GAATGTGACAGCTGTGATCATGATTTTGTGAGATCTTCACTGATTAATGA	199	
QY	121	TCGATTAAGTATGACCTTAACAAACGAAACAGCTCTTGTGTGTGTTTACACG	180	
DB	200	TCGATTAAGTATGACCTTAACAAACGAAACAGCTCTTGTGTGTGTTTACACG	259	
QY	181	GGACCGGAGACCCACCCGACAGCCCGCAGTTTGTAAAGAAATACAGAACAA	240	
DB	260	GGACCGGAGACCCACCCGACAGCCCGCAGTTTGTAAAGAAATACAGAACAA	319	
QY	241	CTGCCGTTGATTTCTTCTCACTGCGGTATGGGTACTGGGTCGCGTATTCAGAA	300	

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QY 301 TACACTACTTTTSCAATGGGGGAGATTAATTGATAAGCACTTCAAGAGCTTGAAGCC 360
Db 380 TACACCTACTTTTSCAATGGGGGAGATTAATTGATAAGCACTTCAAGAGCTTGAAGCC 439
QY 361 CGGCAATTTCTATGACACTGACATGACAGATGACTGTGTAGGTTTGAACCTTGTGTGAG 420
Db 440 CGGCAATTTCTATGACACTGACATGACAGATGACTGTGTAGGTTTGAACCTTGTGTGAG 499
QY 421 CCGTGAAATGCTGGAATCTGGCCAGCCCTCAGAAAGCACTTTAGGTCAAGAGAGCA 480
Db 500 CCGTGAAATGCTGGAATCTGGCCAGCCCTCAGAAAGCACTTTAGGTCAAGAGAGCA 559
QY 481 GAGGAGATTAAGTGGCGCACTCCGGTGGACATCACTGCAATCTTGAAGAGACCTTGTG 540
Db 560 GAGGAGATTAAGTGGCGCACTCCGGTGGACATCACTGCAATCTTGAAGAGACCTTGTG 619
QY 541 AAGTCAGAGCTGCTACACATTTGAATCTCAAGTCGAGCTTGAAGATTCAGATTCAGGA 600
Db 620 AAGTCAGAGCTGCTACACATTTGAATCTCAAGTCGAGCTTGAAGATTCAGATTCAGGA 679
QY 601 AGAAGATTTCTGAGTTTGAAGCAAAATGCAATGCAAGCAACCAATCCAATGTTGTA 660
Db 680 AGAAGATTTCTGAGTTTGAAGCAAAATGCAATGCAAGCAACCAATCCAATGTTGTA 739
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Db 740 ATTGAAGACTTGAATCTGCTCACTTACCCGTTCCGTTACCCCACTCTCAAGAGCTCTCTG 799
QY 721 AATATCTGCTGTTTACCCCAAGAAATTTTACAGGTATCATGCAAGAGTCTTGTGGCAG 780
Db 800 AATATCTGCTGTTTACCCCAAGAAATTTTACAGGTATCATGCAAGAGTCTTGTGGCAG 859
QY 781 GAGGAAAGCCAAAGTATCTGGAATCTTCAAGCAATCTCAAGTTTCAAGAGCTTCAAG 840
Db 860 GAGGAAAGCCAAAGTATCTGGAATCTTCAAGCAATCTCAAGTTTCAAGAGCTTCAAG 919
QY 841 GCAATTCACATTTCTCAATGATGATGCAATTAACCACTGCTGTGATGATGATGATGAT 900
Db 920 GCAATTCACATTTCTCAATGATGATGCAATTAACCACTGCTGTGATGATGATGATGAT 979
QY 901 TCAAAATACAGATTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 980 TCAAAATACAGATTTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1039
QY 961 GATTCGAGGTAACAAGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Db 1040 GATTCGAGGTAACAAGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1099
QY 1021 GTCCTTTGAAAATTAAGAGAGACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1100 GTCCTTTGAAAATTAAGAGAGAGACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1159
QY 1081 CCGTGGGAGATGTTCTCTCAAGTCAATTTTAACTGCTGTGTTGAATCCAGCAATTCCT 1140
Db 1160 CCGTGGGAGATGTTCTCTCAAGTCAATTTTAACTGCTGTGTTGAATCCAGCAATTCCT 1219
QY 1141 AAAAAGGCAATTTTGGAGGCGCTTGTGAGATTAATCCAGTGAAGAGAGAGAGAGAGAG 1200
Db 1220 AAAAAGGCAATTTTGGAGGCGCTTGTGAGATTAATCCAGTGAAGAGAGAGAGAGAGAG 1279
QY 1201 CTACAGAGCTGTGCACTAAACAAGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
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LOCUS AX050463
DEFINITION Sequence 23 from Patent WO0071754.

ACCESSION AX050463
VERSION AX050463.1 GI:12226668

KEYWORDS
SOURCE
ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. Johnson, W.G. and Stenroos, E.S.
Methods for diagnosing, preventing, and treating developmental
disorders due to a combination of genetic and environmental factors
Patent: WO 0071754-A 23 NOV-2000;
University of Medicine and Dentistry of New Jersey (US)
Location/Qualifiers
1. 3259
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RESULT 3
AF025794 3259 bp mRNA linear PRI 26-MAR-1998
LOCUS Homo sapiens methionine synthase reductase (MTRR) mRNA, complete
DEFINITION
ACCESSION AF025794
VERSION AF025794.1 GI:2981302
SOURCE Homo sapiens (human)
KEYWORDS Bukavota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3259)
AUTHORS Leclerc, D., Wilson, A., Dumas, R., Gafuick, C., Song, D., Watkins, D., Heng, H.H.Q., Rommens, J.M., Scherer, S.W., Rosenblatt, D.S. and Gravel, R.A.
TITLE Cloning and mapping of a cDNA for methionine synthase reductase, a flavoprotein defective in patients with homocystinuria
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (6), 3059-3064 (1998)
MEDLINE 950169496
PUBMED 9501215
REFERENCE 2 (bases 1 to 3259)
AUTHORS Leclerc, D.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-1997) Human Genetics, McGill University - Montreal Children's Hospital Research Institute, 4060 Ste-Catherine West, Montreal, Que H3Z 2Z3, Canada
3 (bases 1 to 3259)
AUTHORS Leclerc, D.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-1997) Human Genetics, McGill University - Montreal Children's Hospital Research Institute, 4060 Ste-Catherine West, Montreal, Que H3Z 2Z3, Canada
REMARK Sequence update by submitter
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ORIGIN
Query Match 88.5%; Score 1854; DB 9; Length 3259;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2094; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
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LOCUS			
DEFINITION			
Accession			
VERSION			
KEYWORDS			
AF121214.1 GI:6561338			
3291 bp mRNA linear PRI 12-DEC-1999			
Homo sapiens methionine synthase reductase (MTRR) mRNA, complete			

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE AUTHORS	1 (bases 1 to 3291) Leclerc,D., Odievre,M., Wu,Q., Wilson,A., Huitenga,J.J., Rozen,R., Scherer,S.W. and Gravel,R.A. Molecular cloning, expression and physical mapping of the human methionine synthase reductase gene
TITLE	Gene 240 (1), 75-88 (1999)
JOURNAL	10564814
MEDLINE	2 (bases 1 to 3291)
PUBMED	Leclerc,D., Odievre,M.-H., Wu,Q., Wilson,A., Huitenga,J.J., Johns,T., Shoubertidge,E.A., Rosenblatt,D.S., Scherer,S.W., Kozen,R. and Gravel,R.A. Direct Submission
FEATURES	Submitted (18-JUN-1999) Human Genetics, Montreal Children's Hospital, 4060 Ste-Catherine West, Montreal, Quebec H3Z 2Z3, Canada Location/Qualifiers 1..3291 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /chromosome="5" /map="5p15.2-p15.3; between W11755 and D5S1957" 1..3291 /gene="WTRR" 1..30 /gene="WTRR" /evidence=not_experimental 31..2208 /gene="WTRR" /EC_number="2.1.1.135" /function="maintenance of methionine synthase in an active state" /note="alternatively spliced; alternative splicing results in extended 5' sequence compared to Genbank Accession Number AF025794; B12 vitamin; cblB complementation group" /codon_start=1 /product="methionine synthase reductase" /protein_id="AAFI6876.1"
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Query Match 88.5%; Score 1854; DB 9; Length 3291;
Best Local Similarity 99.9%; Pred. No. 0;
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DB 2092 CATGATGCCCTTGTGCAAAATTAATAGCAAAAGAGTTGAGTTGAAAAATCAGAAAGATG 2151
QY 2038 AAAACCTTGCCACTTTAAAGAGAAAAAGCTTACCTTCAAGATATTTTGTCTATA 2094
DB 2152 AAAACCTTGCCACTTTAAAGAGAAAAAGCTTACCTTCAAGATATTTTGTCTATA 2208

RESULT 5

CQ726091 LOCUS CQ726091 3241 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 12025 from Patent WO02068579.
ACCESSION CQ726091
VERSION CQ726091.1 GI:42289134
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1. Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kite, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
hereof
JOURNAL Patent: WO 02068579-A 12025 06-SEP-2002;
PS Corporation (NY) (US)
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Matches 2092; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
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RESULT 6

BC054816

LOCUS

DEFINITION

Homo sapiens 5-methyltetrahydrofolate-homocysteine
methyltransferase reductase, mRNA (CDNA clone IMAGE:5205285),
partial cds.

BC054816

BC054816.1 GI:33392775

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 3310)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Steinman,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buettow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heib,F.,
Diatchenko,L., Matusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Sheezy,T.E., Brownstein,M.U., Uedln,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Locuelli,N.A., Peters,G.J.,
Abramsen,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Hale,S.J., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S.J., Garcia,A.M., Gay,L.J., Hulik,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodighiero,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,S.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalski,U., Smalins,D.E.,
Schnerch,A., Schein,J.B., Jones,S.U. and Marra,M.A.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

2 (bases 1 to 3310)
Strausberg,R.
Direct Submission
Submitted (03-JUL-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

REMARK

COMMENT

DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nigri.nih.gov
Akter,N., Ayala,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Grant,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Lalic,P., Legaspi,R.,
Maduro,Q.L., Masello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantrop,S., Thomas,P.J., Touchman,J.W.,
Tsougen,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LIML at: <http://image.llnl.gov>
Series: IRAX Plate: 115 Row: d Column: 11
This clone was selected for full length sequencing because it
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ORIGIN

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VERSION BVL77620.1 GI:48013757
KEYWORDS STS.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 2933)
AUTHORS Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
Cantor,C.R. and Braun,A.
TITLE Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
JOURNAL Genome Res. (2004) In press
COMMENT Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
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Primer B: No primer sequence submitted
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FEATURES
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QY 1215 CAGTAAACAAGGGGCGAGCCGATTTATAGCCGCTTGTGAGAGATGCTGCTGCTTGT 1274
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RESULT 8
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LOCUS
DEFINITION
Accession
Version
Keywords
Source
Organism
Reference
Authors
Title
Journal
Comment

BV178010 2933 bp DNA linear STS 10-JUN-2004
sqm87986 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
tagged site.
BV178010
BV178010.1 GI:48014252
STS.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 2933)
Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
Cantor,C.R. and Braun,A.
TITLE Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
JOURNAL Genome Res. (2004) In press
COMMENT Contact: Andreas Braun
Pharmaceuticals division
Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted

Primer B: No primer sequence submitted
STS size: 2933.
Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2786 CACTGGACATGACGATGATGCTGTAGATTAGAACTTGTGTAGCCCGTGAATGCTGG 2727
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DB 2006 GCGAGCCCTTGTGACATATACAGTGCAGTGTGAAAAGCGAGCTACAGAGCTGTG 1947
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RESULT 9
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LOCUS BD077780 390 bp DNA linear PAT 27-AUG-2002
DEFINITION 5'EST of secretory protein in brain.
ACCESSION BD077780
VERSION BD077780.1 GI:22623383
KEYWORDS JP 2001512015-A/65.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 390)
AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE 5'EST of secretory protein in brain
JOURNAL Patent: JP 2001512015-A 65 21-AUG-2001;
GENSET

COMMENT OS Homo sapiens (human)
PN JP 2001512015-A/65
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505293
PR 01-AUG-1997 US 08/505223
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO PI
LACROIX
PC C12N15/09,C07K14/47,C12M1/00,C12P21/02,C12Q1/68,C12N15/00 CC
Von Heljne matrix
CC score 6.9
CC seq SLSLSAHSVSC/SN
FH Key Location/Qualifiers
FT sig_peptide 289..357.
Location/Qualifiers
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Query Match 18.4%; Score 386; DB 6; Length 390;
Best Local Similarity 100.0%; Pred. No. 3.7e-199; Indels 0; Gaps 0;
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3 GTACAAAGCTTCTCAAGATGACGCTTGAAGATTAAGAGAGACGCGCTTTTG 62
QY 1030 AAAATTAAGGACAGACAAAGAGAGAGCTTACCTTACCCAGCATATACCTGCGGA 1089
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Db 63 AAAATAAGGACAGACAAAGAAAGAGACTACCTTACCACGATATACCTGGGGA 122
QY 1090 TGTCTCTCCAGTTCAATTTTACTGGTGTCTTGAATTCGAGCAATTCCTAAAAAGCA 1149
Db 123 TGTCTCTCCAGTTCAATTTTACTGGTGTCTTGAATTCGAGCAATTCCTAAAAAGCA 182
QY 1150 TTTTGGAGACCCCTTGGAGCTATACAGTACAGTGTCTGAAAAAGCAGGCTACAGAG 1209
Db 183 TTTTGGAGACCCCTTGGAGCTATACAGTACAGTGTCTGAAAAAGCAGGCTACAGAG 242
QY 1210 CTGTGACGTAAACAGAGGGGAGCGCATATATAGCGCTTTGACAGATGCTGTGCTGC 1269
Db 243 CTGTGACGTAAACAGAGGGGAGCGCATATATAGCGCTTTGACAGATGCTGTGCTGC 302
QY 1270 TTGTGGATCTCTCTCTCGCTTTCCTCTTTCGACGACCACTAGTCTCTGCTGAA 1329
Db 303 TTGTGGATCTCTCTCTCGCTTTCCTCTTTCGACGACCACTAGTCTCTGCTGAA 362
QY 1330 CATCTTCTAACTTCAACCCAGAC 1355
Db 363 CATCTTCTAACTTCAACCCAGAC 388

RESULT 10
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DEFINITION Homo sapiens methionine synthase reductase (MTRR) gene, exon 5.
ACCESSION AF121205 GI:6572530
VERSION AF121205.1 GI:6572530
KEYWORDS 4 of 12
SEGMENT Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1353)
AUTHORS Leclerc,D., Odievre,M., Wu,Q., Wilson,A., Hutzenga,J.J., Rozen,R.,
Scheer,S.W. and Gravel,R.A.
TITLE Molecular cloning, expression and physical mapping of the human
methionine synthase reductase gene
JOURNAL Gene 240 (1), 75-88 (1999)
MEDLINE 20033550
PUBMED 10564814
REFERENCE 2 (bases 1 to 1353)
AUTHORS Leclerc,D.
TITLE Direct Submission
JOURNAL Submitted (20-JAN-1999) Human Genetics, Montreal Children's
Hospital, 4060 Ste-Catherine West, Montreal, Quebec H3Z 2Z3, Canada
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Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 461 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCGGTGGCATCACTGCAT 520
Db 417 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCGGTGGCATCACTGCAT 476
QY 521 CCTTGAGAGACACTTGTGAAGTCAAGCTGCTACACATTGAATCTCAAGTGGAGCTTC 580

Db 477 CTTGAGACAGACCTTGTGAAGTCAGAGCTGTACATTAATCTCAAGTGCAGCTTC 536
QY 581 TGAATTCGATGATTCAGAGAGAAAGATTCTGAGGTTTGAAGCAAAATGCAAGTACA 640
Db 537 TGAATTCGATGATTCAGAGAGAAAGATTCTGAGGTTTGAAGCAAAATGCAAGTACA 596
QY 641 GCAACCAATCCAAATGTTGTAATTGAAGACTTTGAGTCTCACTTACCCTGGTACCCC 700
Db 597 GCAACCAATCCAAATGTTGTAATTGAAGACTTTGAGTCTCACTTACCCTGGTACCCC 656
QY 701 CACTTCACAAGCCTCTGTAATATTCCTGTTTACCCCAAGATATTTACAGGTATC 760
Db 657 CACTTCACAAGCCTCTGTAATATTCCTGTTTACCCCAAGATATTTACAGGTATC 716
QY 761 TGCAGAGTCTCTTGGCCAG 781
Db 717 TGCAGAGTCTCTTGGCCAG 737

RESULT 11
LOCUS AC010346 109626 bp DNA linear PRI 10-NOV-2000
DEFINITION Homo sapiens chromosome 5 clone CITB-H1_201B2, complete sequence.
ACCESSION AC010346
VERSION AC010346.6 GI:11136705
KEYWORDS HTG.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 109626)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
2 (bases 1 to 109626)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 109626)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Nov 10, 2000 this sequence version replaced gi:9256196.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
STS Content:
WI-9255 G05749.

FEATURES

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QY 401 GTTTAGAACTTGTGTGAGCCGTGATGCTGGAATCTGGCCAGCCCTCAGAAACATT 460
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QY 461 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCGGTGGCATCACTGCAT 520
Db 88631 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCGCACTCCGGTGGCATCACTGCAT 88690

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QY 521 CCTTGAGACAGACCTTGTGAAGTCTGAGCTGACATTTGAATCTCAAGTGCAGCTTC 580
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RESULT 12
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LOCUS Homo sapiens chromosome 5 clone CTD-2072124, complete sequence.
DEFINITION AC025174
AC025174.5 GI:19774456
VERSION AC025174.5 GI:19774456
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 110756)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 110756)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 110756)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 4 (bases 1 to 110756)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (28-MAR-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Mar 28, 2002 this sequence version replaced gi:19224767.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
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Best Local Similarity 99.7%; Pred. No. 1,1e-168;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGTTGAGCCGTGATGCTGCTGCACTCTGCGCAGCCCTCAGAAAGCATT 460

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DB 20160 CCTGAGAGACAGACCTTGTGAAGTCTGAGCTGACATTTGAATCTCAAGTGCAGCTTC 20219
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QY 761 TGCAGAGTCTCTTGGCCAGG 781
DB 20400 TGCAGAGTCTCTTGGCCAGG 20420

RESULT 13
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LOCUS Homo sapiens clone RP11-138P20, WORKING DRAFT SEQUENCE, 12
DEFINITION AC022921
AC022921.2 GI:7229868
VERSION AC022921.2 GI:7229868
KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 158199)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 158199)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
Boguslavsky, L., Bouckgalter, B., Brown, A., Burkett, G., Castle, A.,
Choquel, Y., Colangelo, M., Collins, S., Collumore, A., Cooke, P.,
Dearrellano, K., Dewar, K., Domino, M., Doyle, M., Penastor, J.,
Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lehoczeky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Maddison, P., Margulis, N., McEwan, P., McGurk, A., McKernan, K.,
McPheeters, R., Meldrum, J., Menus, L., Morrow, J., Naylor, J.,
Norman, C. H., O'Connor, T., O'Donnell, P., Olivari, T. M., Peterson, K.,
Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Testfaye, S., Theodore, J.,
Tirelli, A., Vassiliou, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Mar 12, 2000 this sequence version replaced gi:6921909.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/XM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu

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Contact:	sequence_submissions@genome.wi.mit.edu
Project Information	
Center project name:	L6314
Center clone name:	138_P_20
Summary Statistics	
Sequencing vector:	M13; M77815; 100% of reads
Chemistry:	Dye-terminator Big Dye; 100% of reads
Assembly program:	Phrap, version 0.960731
Consensus quality:	152636 bases at least Q40
Consensus quality:	155474 bases at least Q30
Consensus quality:	156388 bases at least Q20
Insert size:	178000; agarose-fp
Insert size:	157099; sum-of-contigs
Quality coverage:	4.4 in Q20 bases; agarose-fp
Quality coverage:	5.0 in Q20 bases; sum-of-contigs
NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will still be preserved.	
1	1283: contig of 1283 bp in length
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1384	4203: contig of 2820 bp in length
4204	4303: gap of 100 bp
4304	6786: contig of 2483 bp in length
6787	6886: gap of 100 bp
6887	9683: contig of 2797 bp in length
9684	9783: gap of 100 bp
9784	12902: contig of 3119 bp in length
12903	13002: gap of 100 bp
13003	16429: contig of 3427 bp in length
16430	16529: gap of 100 bp
16530	25201: contig of 6672 bp in length
25202	25301: gap of 100 bp
25302	36759: contig of 11458 bp in length
36760	36925: gap of 100 bp
36926	53921: contig of 17062 bp in length
53922	54021: gap of 100 bp
54022	72054: contig of 18033 bp in length
72055	72154: gap of 100 bp
72155	102527: contig of 30373 bp in length
102528	102628: gap of 100 bp
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Qy	581 TGAAGATTCGATGATTCAGAGAAAGAGATTCGAGGTTTGAAGCAAAATGACATGACAGCA	640
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Qy	761 TGCAGAGATCTCTTGGCCAGG 781	
Db	3806 TGCAGAGATCTCTTGGCCAGG 3826	
RESULT 14		
AC021609	167237 bp	DNA linear HTG 12-MAR-2000
LOCUS		
DEFINITION	Homo sapiens clone RP11-259D10, WORKING DRAFT SEQUENCE, 6 unordered	
ACCESSION	AC021609	
VERSION	AC021609.3	GI:7230210
SOURCE	HTG; HTGS PHASE1; HTGS_DRAFT.	
ORGANISM	Homo sapiens (human)	
REFERENCE	Homo sapiens	
AUTHORS	Mumayyoti; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
TITLE	1 (bases 1 to 167237)	
JOURNAL	Bitren,B., Linton,L., Nuebaum,C. and Lander,E.	
REFERENCE	Unpublished	
AUTHORS	2 (bases 1 to 167237)	
	Bitren,B., Linton,L., Nuebaum,C., Lander,E., Abraham,H., Allen,N.,	
	Anderson,S., Baldwin,J., Barua,N., Beckerly,R., Bede,F.,	
	Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G., Castle,A.,	
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	DeRellano,K., Dewar,K., Domino,M., Doyle,M., Fenebor,J.,	
	Ferreira,S., Flitzhugh,W., Forrest,C., Gage,D., Galagan,J.,	
	Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,	
	Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatae,A., Klein,J.,	
	Landers,T., Lehoczy,J., Levine,R., Liu,C., Liu,G., Locke,K.,	
	Macdonald,P., Margulis,N., McEwan,P., McGurk,A., McKernan,K.,	
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	Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K.,	

Quality coverage: 10.01 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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* 16003 16102: gap of unknown length
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FEATURES

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ORIGIN

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13.3%; Score 279; DB 2; Length 177596;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Gapop 60.0 , Gapext 60.0

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SUMMARIES

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KW	cardiovascular disease; neural tube defect; hyperhomocysteinemia;	
KW	chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.	
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PA	(LECL/) LECLERC D.	

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PA (ROSE/) ROSENBLATT D.
PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX WPI; 2003-576610/54.
XX P-PSDB; ADM43217.
XX
PT New substantially pure nucleic acid encoding a mammalian methionine
PT synthase reductase polypeptide, useful for diagnosing, preventing or
PT treating conditions associated with altered methionine synthase activity,
PT e.g. cancer.
PS Disclosure; SEQ ID NO 45; 26bp; English.
XX
XX The invention relates to a substantially pure nucleic acid that encodes a
CC mammalian methionine synthase reductase polypeptide, HmMTR, or that
CC hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
CC ADM43209. Also included are a non-human animal where one or both genetic
CC alleles encoding the methionine synthase reductase polypeptide are
CC mutated, an antibody that specifically binds the above methionine
CC synthase reductase polypeptide, a method of detecting the presence of the
CC above polypeptide, a method for detecting sequence variants for
CC methionine synthase reductase in a mammal, methods of treating or
CC preventing cancer (or cardiovascular disease or neural tube defects) in a
CC subject, methods of screening for a compound that modulates methionine
CC synthase reductase biological activity and a method for detecting an
CC increased risk of developing a neural tube defect in a mammalian embryo
CC or foetus. The nucleic acid is useful in diagnosing, preventing or
CC treating conditions associated with altered methionine synthase activity,
CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are
CC also associated with hyperhomocysteinaemia. The gene for HmMTR is
CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
CC sequence of a variant human hsmMTR cDNA.
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Matches 2091; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ID AAC91226 standard; DNA; 3259 BP.
 AC
 XX AAC91226;
 AC
 XX 20-MAR-2001 (first entry)
 DT
 XX
 DE Human schizophrenia related gene SEQ ID NO: 23.
 XX
 XX Human; schizophrenia; developmental disorder; spina bifida cystica;
 KM Tourette's syndrome; bipolar illness; autism; conduct disorder;
 KM attention deficit disorder; obsessive compulsive disorder;
 KM chronic multiple tic syndrome; learning disorder; polymorphism; ds.
 XX
 OS Homo sapiens.
 PN
 XX MO200071754-A1.
 PD
 XX 30-NOV-2000.
 PF
 XX 24-MAY-2000; 2000NC-US014354.
 XX
 PR 25-MAY-1999; 99US-00318448.
 PA
 XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
 PI
 XX Johnson WG, Stenroos ES;
 DR WPI; 2001-025174/03.
 XX
 PT Diagnosing a developmental disorder, e.g. schizophrenia, by forming
 PT datasets (DS) of genetic (e.g. genotypes of folate metabolism alleles)
 PT and environmental variables affecting an individual and then comparing
 PT these DS with reference DS.
 XX
 PS Disclosure; Page 142-143, 156pp; English.
 CC
 XX The present invention provides a novel method of estimating the
 CC susceptibility of an individual to a developmental disorder using genetic
 CC and environmental variables. The method can be used in the diagnosis,
 CC prevention and treatment of disorders such as schizophrenia, spina bifida
 CC cystica, Tourette's syndrome, bipolar illness, autism, conduct disorders,
 CC attention deficit disorder, obsessive compulsive disorder, chronic
 CC multiple tic syndrome and learning disorders such as dyslexia
 XX
 SQ Sequence 3259 BP; 944 A; 695 C; 674 G; 946 T; 0 U; 0 Other;

Query Match 88.5%; Score 1854; DB 5; Length 3259;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 204; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

1 ATGAGAGGTTCTGTACTATATGCTACACAGCAGGAGCAGGCAAAAGCCATCGAGAA 60
DB ATGAGAGGTTCTGTACTATATGCTACACAGCAGGAGCAGGCAAAAGCCATCGAGAA 139
QY GAAATGTGACCAAGCTGTGTACATGATTTTCTGAGATCTTCACTGTATATGTA 120
DB GAAATGTGACCAAGCTGTGTACATGATTTTCTGAGATCTTCACTGTATATGTA 199
QY TCCGATTAAGTATGACTTAATAAACCGAAGAGCTCTCTGTGTGTGTGTTCTACAG 180
DB TCCGATTAAGTATGACTTAATAAACCGAAGAGCTCTCTGTGTGTGTGTTCTACAG 259
QY GGCACCGGAGACCCACCGACACAGCCCGCAGTTTGTAAAGAAATACAGAACCAACA 240
DB GGCACCGGAGACCCACCGACACAGCCCGCAGTTTGTAAAGAAATACAGAACCAACA 319
QY CTGCCGGTGAATTTCTTTGCTCACTGCGGTATGGGTACTGGGTCTCGTATTCAGAA 300
DB CTGCCGGTGAATTTCTTTGCTCACTGCGGTATGGGTACTGGGTCTCGTATTCAGAA 379
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DB TACACCTACTTTTGGCAATGGGGGAGATTAATTGATTAACGACTTCAAGAGCTTGAGCC 439
QY CGGCAATTTCTATGACACTGAGACATGACATGATGTATGATTTAGAACCTTGTGTAG 420
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QY CCGTGATTTGCTGGAATCTGCGCCAGCCCTCAGAAACATTTTAAAGTCAAGACAGACA 480
DB CCGTGATTTGCTGGAATCTGCGCCAGCCCTCAGAAACATTTTAAAGTCAAGACAGACA 559
QY GAGAGATTAAGTGGGACATCCCGGAGATCACTCGCATCTTGAGGAGACAGACTTGTG 540
DB GAGAGATTAAGTGGGACATCCCGGAGATCACTCGCATCTTGAGGAGACAGACTTGTG 619
QY AAGTCAGAGCTGTACATGATGATCTCAAGTCGAGCTTCTGAGATTCATGATTCAGGA 600
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DB AATATTCCTGTGTTACCCCAAGATATTTACAGTACATCTGAGAGATCTTGTGACAG 859
QY GAGGAAAGCCAGATCTGTGACTTCAAGCATCAAGTTTCAAGTCCCAATTTCAAG 840
DB GAGGAAAGCCAGATCTGTGACTTCAAGCATCAAGTTTCAAGTCCCAATTTCAAG 919
QY GAGGTTCACTTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB GAGGTTCACTTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 979
QY TCAATATCAGACTTTCTATCAGCTGAGATGCTTCAAGCTGATCTGCTTACAGT 960
DB TCAATATCAGACTTTCTATCAGCTGAGATGCTTCAAGCTGATCTGCTTACAGT 1039
QY GATTTGAGGTACAAAGCTTCTCAAGACATGACAGTGTGAATTAAGAGAGACCTGC 1020
DB GATTTGAGGTACAAAGCTTCTCAAGACATGACAGTGTGAATTAAGAGAGACCTGC 1099

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QY CTTGGGGATGTTCTCTCAGTTCAATTTTACCTGTGTCTTGAATCCGACAAATCTT 1140
DB CTTGGGGATGTTCTCTCAGTTCAATTTTACCTGTGTGTCTTGAATCCGACAAATCTT 1219
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DB CTGCTGAAATCTTCTTAACTTCAACCAAGCATATTCGTGCAAGCTCAAGTTA 1459
QY TTTCAACCCAGAAAGCTCAATTTGTCTTCAATTTGTGAAATTTCTGTACTGACACA 1440
DB TTTCAACCCAGAAAGCTCAATTTGTCTTCAATTTGTGAAATTTCTGTACTGACACA 1519
QY AAGAGTTCTGCGAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
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QY ACAGAGTTCTGCGAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
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DB TCCATCTCTCTGCAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1699
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DB AATATGTTGGTTCAGAAACCGGATAGCCCGTTTATTTGGTCTTACATTAAGAG 1759
QY AATATGTTGGTTCAGAAACCGGATAGCCCGTTTATTTGGTCTTACATTAAGAG 1737
DB AATATGTTGGTTCAGAAACCGGATAGCCCGTTTATTTGGTCTTACATTAAGAG 1819
QY AAGCATTAAGGATTAATCTTATTAAGAAAGAGCTCAGACATTTCTTAAAGATGG 1797
DB AAGCATTAAGGATTAATCTTATTAAGAAAGAGCTCAGACATTTCTTAAAGATGG 1879
QY ATCTTAATCTTAAGGTTTCTTCTCAAGATGCTCTGTGGGAGAGAGAGCC 1857
DB ATCTTAATCTTAAGGTTTCTTCTCAAGATGCTCTGTGGGAGAGAGAGCC 1939
QY AATCTTAATCTTAAGGTTTCTTCTCAAGATGCTCTGTGGGAGAGAGAGCC 1917
DB AATCTTAATCTTAAGGTTTCTTCTCAAGATGCTCTGTGGGAGAGAGAGCC 1999
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DB CAGCAAGATTAATGATCAAGCAATCCAGCTTCAAGTGTGAGAGAGTGTGAGAGTGA 2059
QY CATGATGCTTGTGCAATTAATTAAGCAAGAGTGTGAGAGTGTGAGAGTGA 2037
DB CATGATGCTTGTGCAATTAATTAAGCAAGAGTGTGAGAGTGTGAGAGTGA 2119
QY AAAACCTGCGCACTTTAAAGAAAGAAAGCCTTCAAGATTTTGTGATTA 2094
DB AAAACCTGCGCACTTTAAAGAAAGAAAGCCTTCAAGATTTTGTGATTA 2176

RESULT 4
ADM43206
ID ADM43206 standard; cDNA; 3259 BP.
XX
XX
AC ADM43206;
XX
XX
DT 03-JUN-2004 (first entry)
XX
XX
DE Human full length cDNA encoding methionine synthase reductase.
XX
XX
KW Human; ss; gene; Methionine synthase reductase polypeptide; HemTR; cancer; cardiovascular disease; neural tube defect; hyperhomocysteinemia; chromosome 5p15.2-p15.3; SNP;
KM single nucleotide polymorphism.
XX
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 80..2176
FT /*tag= a
FT /product= "hemTR"
FT /replac= (145, A)
FT variation
FT /*tag= b
FT /strand_name= "Single_nucleotide_polymorphism"
FT /replac= (189, A)
FT /*tag= c
FT /strand_name= "Single_nucleotide_polymorphism"
XX
XX
PN US2003082676-A1.
XX
XX
PD 01-MAY-2003.
XX
XX
PF 10-AUG-1999; 99US-00371347.
XX
XX
PR 16-JAN-1998; 98US-0071622P.
PR 15-JAN-1999; 99US-00232028.
XX
XX
PA (GRAY/) GRAYEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
XX
XX
PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX
XX
DR MPI; 2003-57610/54.
DR P-PSDB; ADM43207.
XX
XX
PT New substantially pure nucleic acid encoding a mammalian methionine
PT synthase reductase polypeptide, useful for diagnosing, preventing or
PT treating conditions associated with altered methionine synthase activity,
PT e.g. cancer.
XX
XX
PS Example 2; SEQ ID NO 24; 26pp; English.
XX
XX
CC The invention relates to a substantially pure nucleic acid that encodes a
CC mammalian methionine synthase reductase polypeptide, HemTR, or that
CC hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
CC ADM43209. Also included are a non-human animal where one or both genetic
CC alleles encoding the methionine synthase reductase polypeptide are
CC mutated, an antibody that specifically binds the above methionine
CC synthase reductase polypeptide, a method of detecting the presence of the
CC above polypeptide, a method for detecting sequence variants for
CC methionine synthase reductase in a mammal, methods of treating or
CC preventing cancer (or cardiovascular disease or neural tube defects) in a
CC subject, methods of screening for a compound that modulates methionine
CC synthase reductase biological activity and a method for detecting an
CC increased risk of developing a neural tube defect in a mammalian embryo
CC or foetus. The nucleic acid is useful in diagnosing, preventing or
CC treating conditions associated with altered methionine synthase activity,
CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are

CC also associated with hyperhomocysteinemia. The gene for HemTR is
CC located on chromosome 5p15.2-p15.3. The present sequence is full length
CC sequence of the wild-type human hemTR cDNA.
XX
XX
SQ Sequence 3259 BP; 944 A; 695 C; 674 G; 946 T; 0 U; 0 Other;
Query Match 88.5%; Score 1854; DB 11; Length 3259;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2094; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 ATGAGAGGTTTCTGTTACTATATGCTACACAGCAGGACGCAAGCCATCGAGAA 60
DB 80 ATGAGAGGTTTCTGTTACTATATGCTACACAGCAGGACGCAAGCCATCGAGAA 139
QY 61 GAAATGTGAGCAAGCTGTGTACATGAGATTTTCTGAGATCTTCACTGATTAAGTAA 120
DB 140 GAAATGTGAGCAAGCTGTGTACATGAGATTTTCTGAGATCTTCACTGATTAAGTAA 199
QY 121 TCCGATTAAGTATGACTTAAACCCGAAACAGCTCTCTGTTGTGTTTCTACACG 180
DB 200 TCCGATTAAGTATGACTTAAACCCGAAACAGCTCTCTGTTGTGTTTCTACACG 259
QY 181 GGCACCGAGACCCACCCGACACAGCCGCAAGTTGTTAAGGAATACAGAACCAACA 240
DB 260 GGCACCGAGACCCACCCGACACAGCCGCAAGTTGTTAAGGAATACAGAACCAACA 319
QY 241 CTGCGGTTGATTTCTTCTCTCACTGCGGTATGAGTTA CTGCGTCTCGGTATTCAGAA 300
DB 320 CTGCGGTTGATTTCTTCTCTCACTGCGGTATGAGTTA CTGCGTCTCGGTATTCAGAA 379
QY 301 TACACCTACTTTTGCAATGGGGGGAATTAATGAATTAACCTTCAAGCTTGGAGCC 360
DB 380 TACACCTACTTTTGCAATGGGGGGAATTAATGAATTAACCTTCAAGCTTGGAGCC 439
QY 361 CCGCATTTCTATGACACTGGAACATGAGATGACTGTGAGTTTGAACCTTGTTGAG 420
DB 440 CCGCATTTCTATGACACTGGAACATGAGATGACTGTGAGTTTGAACCTTGTTGAG 499
QY 421 CCGTGATTTGCTGACTGTGGCCAGCCCTCAGAAACATTTTATGTCAGAGAGACAA 480
DB 500 CCGTGATTTGCTGACTGTGGCCAGCCCTCAGAAACATTTTATGTCAGAGAGACAA 559
QY 481 GAGGATTAATGAGGCGCACTCCCGGTGCACTCCGATCTTGTAGAGACAGACCTTGG 540
DB 560 GAGGATTAATGAGGCGCACTCCCGGTGCACTCCGATCTTGTAGAGACAGACCTTGG 619
QY 541 AAGTCAGAGCTGCTACATGATGATCTCAAGTGAAGCTTCTGAGATTCGATTCAGGA 600
DB 620 AAGTCAGAGCTGCTACATGATGATCTCAAGTGAAGCTTCTGAGATTCGATTCAGGA 679
QY 601 AGAAGGATTTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATTCATGTTGTA 660
DB 680 AGAAGGATTTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATTCATGTTGTA 729
QY 661 ATTGAAGACTTTGAGTCTTCACTTACCCGTTGCTATCCCACTCTCACAAGCTCTTGG 720
DB 740 ATTGAAGACTTTGAGTCTTCACTTACCCGTTGCTATCCCACTCTCACAAGCTCTTGG 799
QY 721 AATATTCCTGTTTACCCCAAGAAATTTTACAGGTACATCTGACAGAGTCTTGGCCAG 780
DB 800 AATATTCCTGTTTACCCCAAGAAATTTTACAGGTACATCTGACAGAGTCTTGGCCAG 859
QY 781 GAGGAAGCCAGATATCTGTGACTTCAGAGATTCAGGTTTTCAGTGCATTTCAAG 840
DB 860 GAGGAAGCCAGATATCTGTGACTTCAGAGATTCAGGTTTTCAGTGCATTTCAAG 919
QY 841 GCGATTCACTTATCTAGATATGATGCTATTAACCACTCTGCTGTATTAATGGACAT 900
DB 920 GCGATTCACTTATCTAGATATGATGCTATTAACCACTCTGCTGTATTAATGGACAT 979
QY 901 TCAATATACAGACTTTTCTATGAGCTTGAAGATGCTTCAAGCTGATTCGCTTAACAGT 960
DB 980 TCAATATACAGACTTTTCTATGAGCTTGAAGATGCTTCAAGCTGATTCGCTTAACAGT 1039

QY 961 GATTCTGAGTACAAAGCCTACTCCAAAGACTGACGCTTGAGATTAAGAGAGACATG 1020
 DB 1040 GATTCTGAGTACAAAGCCTACTCCAAAGACTGACGCTTGAGATTAAGAGAGACATG 1099
 QY 1021 GTCTCTTTGAAAATAAAGGACAGACAAAGAAAGAGAGCTTACCTCCAGCATATA 1080
 DB 1100 GTCTCTTTGAAAATAAAGGACAGACAAAGAAAGAGAGCTTACCTCCAGCATATA 1159
 QY 1081 CTTGCGGGATGTTCTCTCCAGTTCATTTTAACTGCTGCTTGAATTCGAGCAATTCCT 1140
 DB 1160 CTTGCGGGATGTTCTCTCCAGTTCATTTTAACTGCTGCTTGAATTCGAGCAATTCCT 1219
 QY 1141 AAAAAGGCAATTTTGGAGCCCTTGTGACTATACAGTGAACAGCTGTAAGAGCCAGG 1200
 DB 1220 AAAAAGGCAATTTTGGAGCCCTTGTGACTATACAGTGAACAGCTGTAAGAGCCAGG 1279
 QY 1201 CTACAGAGCTGTGACGTAAACAAGGGGACGCCGATTAATAGCCGCTTGTACGAGATGCC 1260
 DB 1280 CTACAGAGCTGTGACGTAAACAAGGGGACGCCGATTAATAGCCGCTTGTACGAGATGCC 1339
 QY 1261 TGTGCTGCTGTTGTTGATCTCTCTGCTTCCCTTCTTGCCAGCCACACTCACTCTC 1320
 DB 1340 TGTGCTGCTGTTGTTGATCTCTCTGCTTCCCTTCTTGCCAGCCACACTCACTCTC 1399
 QY 1321 CTGCTGGAACATCTTCTAACTTCAACCCAGACATATTCGTCAGCAAGCTCAAGTTTA 1380
 DB 1400 CTGCTGGAACATCTTCTAACTTCAACCCAGACATATTCGTCAGCAAGCTCAAGTTTA 1459
 QY 1381 TTTCACCCAGAAAGCTCCATTTTGTCTCAACATTTGTGAAATTTCTGTCTACTGCA 1440
 DB 1460 TTTCACCCAGAAAGCTCCATTTTGTCTCAACATTTGTGAAATTTCTGTCTACTGCA 1519
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 DB 1520 ACAAGAGTTCTGGGAAAGGAGATATGTACAGGCTGGCTGCTTGTGCTTCACTT 1579
 QY 1501 CTTGACCCAAACATATGATGATCCCAATGAAAGACAGGGGAAAGCCCTGCTCTTAAGATA 1560
 DB 1580 CTTGACCCAAACATATGATGATCCCAATGAAAGACAGGGGAAAGCCCTGCTCTTAAGATA 1639
 QY 1561 TCCATCTCTCTGGAACAACAATTCCTTCACTTACAGATGACCCCTCAATCCCATC 1620
 DB 1640 TCCATCTCTCTGGAACAACAATTCCTTCACTTACAGATGACCCCTCAATCCCATC 1699
 QY 1621 ATATAGTGGGTCACAGAACCGGCATAGCCCGTTATTTGAGTTCTTACAACTAGAGAG 1680
 DB 1700 ATATAGTGGGTCACAGAACCGGCATAGCCCGTTATTTGAGTTCTTACAACTAGAGAG 1759
 QY 1681 AAATCTCAAGAAACAACCCAGATGAAATTTTGGAGCAATG--GTTTTTGGCTGC 1737
 DB 1760 AAATCTCAAGAAACAACCCAGATGAAATTTTGGAGCAATG--GTTTTTGGCTGC 1819
 QY 1738 AGGCAATAGGATAGGATTTATCTATTCAAGAAAGCTCAGACATTTCTTAAGATGG 1797
 DB 1820 AGGCAATAGGATAGGATTTATCTATTCAAGAAAGCTCAGACATTTCTTAAGATGG 1879
 QY 1798 ATCTTAATCAATTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1857
 DB 1880 ATCTTAATCAATCTTAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1939
 QY 1858 CCAAGCAAGATATTAACAAGCAATCCAGCTTCAATGCGACAGAGTGGGAGAAATCTTC 1917
 DB 1940 CCAAGCAAGATATTAACAAGCAATCCAGCTTCAATGCGACAGAGTGGGAGAAATCTTC 1999
 QY 1918 CTCACAGAGAACGGCCATATTTATGTTGTGAGATGCAAGAAATATGCAAGATGTA 1977
 DB 2000 CTCACAGAGAACGGCCATATTTATGTTGTGAGATGCAAGAAATATGCAAGATGTA 2059
 QY 1978 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGGTTGAGTTGAAAACTAGAGCAATG 2037
 DB 2060 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGGTTGAGTTGAAAACTAGAGCAATG 2119

QY 2038 AAAACCTGGCCACTTTAAAGAGAGAAAAAGCCTACTTTCAGATATTTGTCATATA 2094
 DB 2120 AAAACCTGGCCACTTTAAAGAGAGAAAAAGCCTACTTTCAGATATTTGTCATATA 2176
 RESULT 5
 ID ADM43208
 ID ADM43208 standard; cDNA; 2094 BP.
 XX
 AC ADM43208;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human wild-type methionine synthase reductase CDS.
 XX
 KW Human; ss; Methionine synthase reductase polypeptide; hsmTRR; cancer;
 KW cardiovascular disease; neural tube defect; hyperhomocysteinemia;
 KW chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2094
 FT /tag= a
 FT /product= "hsmTRR"
 FT /partial
 FT /note= "No stop codon shown"
 FT replace(66, A)
 FT /tag= b
 FT /standard_name= "single_nucleotide_polymorphism"
 FT replace(110, A)
 FT /tag= c
 FT /standard_name= "single_nucleotide_polymorphism"
 PN US2003082676-A1.
 XX
 PD 01-MAY-2003.
 XX
 PP 10-AUG-1999; 99US-00371347.
 XX
 PR 16-JAN-1998; 98US-0071622P.
 PR 15-JAN-1999; 99US-00232028.
 XX
 PA (GRAY/) GRAVEL R. A.
 PA (ROZE/) ROZEN R.
 PA (LECL/) LECLERC D.
 PA (WILS/) WILSON A.
 PA (ROSE/) ROSENBLATT D.
 XX
 PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
 XX
 DR WPI; 2003-576610/54.
 DR P-PSDB; ADM43207.
 XX
 PT New substantially pure nucleic acid encoding a mammalian methionine
 PT synthase reductase polypeptide, useful for diagnosing, preventing or
 PT treating conditions associated with altered methionine synthase activity,
 PT e.g. cancer.
 XX
 PS Claim 3; SEQ ID NO 1; 26pp; English.
 XX
 CC The invention relates to a substantially pure nucleic acid that encodes a
 CC mammalian methionine synthase reductase polypeptide, hsmTRR, or that
 CC hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
 CC ADM43209. Also included are a non-human animal where one or both genetic
 CC alleles encoding the methionine synthase reductase polypeptide are
 CC mutated, an antibody that specifically binds the above methionine
 CC synthase reductase polypeptide, a method of detecting the presence of the
 CC above polypeptide, a method for detecting sequence variants for
 CC methionine synthase reductase in a mammal, methods of treating or
 CC preventing cancer (or cardiovascular disease or neural tube defects) in a
 CC subject, methods of screening for a compound that modulates methionine
 CC synthase reductase biological activity and a method for detecting an

DB 1921 CTCGAGAGAGACGCCATATTTATGTGTGATGCAAGAAATATGCGCAAGATGTA 1980
 QY 1978 CATTGATGCTTGTGCAATTAATTAAGCAAGAGTGTGAGTTGCAAAAACCTAGAGCAATG 2037
 DB 1981 CATTGATGCTTGTGCAATTAATTAAGCAAGAGTGTGAGTTGCAAAAACCTAGAGCAATG 2040
 QY 2038 AAAACCTGCGCCACTTTAAAGAGAGAAAAACCTACTTTCAGAGATTTTGTCTCA 2091
 DB 2041 AAAACCTGCGCCACTTTAAAGAGAGAAAAACCTACTTTCAGAGATTTTGTCTCA 2094
 RESULT 6
 ADM43212
 ID ADM43212 standard; cDNA; 2094 BP.
 XX ADM43212;
 AC
 XX 03-JUN-2004 (first entry)
 DT
 XX Human methionine synthase reductase CDS G110A variant.
 DE
 XX Human; 89; Methionine synthase reductase polypeptide; hsmtrr; cancer;
 KW cardiovascular disease; neural tube defect; hyperhomocysteinemia;
 KW chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2094
 FT /tag= a
 FT /product= "hsmtrr"
 FT /partial
 FT /note= "No stop codon shown"
 FT variation
 FT /tag= b
 FT /standard_name= "Single_nucleotide_polymorphism"
 FT variation
 FT /tag= c
 FT /standard_name= "Single_nucleotide_polymorphism"
 XX
 PN US2003082676-A1.
 XX
 XX 01-MAY-2003.
 XX
 PP 10-AUG-1999; 99US-00371347.
 XX
 PR 16-JAN-1998; 98US-0071622P.
 PR 15-JAN-1999; 99US-00232028.
 XX
 PA (GRAY/) GRAVEL, R. A.
 PA (ROZE/) ROZEN R.
 PA (LECL/) LECLERC D.
 PA (WILS/) WILSON A.
 PA (ROSE/) ROSENBLATT D.
 XX
 PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
 XX
 DR WPI; 2003-576610/54.
 DR P-PSDB; ADM43213.
 XX
 XX
 PT New substantially pure nucleic acid encoding a mammalian methionine
 PT synthase reductase polypeptide, useful for diagnosing, preventing or
 PT treating conditions associated with altered methionine synthase activity,
 PT e.g. cancer.
 PT
 PS Disclosure; SEQ ID NO 43; 26pp; English.
 XX
 XX The invention relates to a substantially pure nucleic acid that encodes a
 CC mammalian methionine synthase reductase polypeptide, hsmtrr, or that
 CC hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
 CC ADM43209. Also included are a non-human animal where one or both genetic
 CC alleles encoding the methionine synthase reductase polypeptide are
 CC mutated, an antibody that specifically binds the above methionine

CC synthase reductase polypeptide, a method of detecting the presence of the
 CC above polypeptide, a method for detecting sequence variants for
 CC methionine synthase reductase in a mammal, methods of treating or
 CC preventing cancer (or cardiovascular disease or neural tube defects) in a
 CC subject, methods of screening for a compound that modulates methionine
 CC synthase reductase biological activity and a method for detecting an
 CC increased risk of developing a neural tube defect in a mammalian embryo
 CC or foetus. The nucleic acid is useful in diagnosing, preventing or
 CC treating conditions associated with altered methionine synthase activity,
 CC such as cancer, cardiovascular disease or neural tube defects, or in
 CC screening for a compound that modulates methionine synthase reductase
 CC biological activity. Naturally occurring variants of the polypeptide are
 CC also associated with hyperhomocysteinemia. The gene for hsmtrr is
 CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
 CC sequence of a variant human hsmtrr cDNA.
 XX
 SQ Sequence 2094 BP; 592 A; 489 C; 480 G; 533 T; 0 U; 0 Other;
 Query Match 86.0%; Score 1800; DB 11; Length 2094;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2090; Conservative 0; Mismatches 1; Indels 3; Gaps 1;
 QY 1 ATGAGAGGTTTCTGTACTATATGCTACAGACGAGGAGCAAGGCAATCGCAGAA 60
 DB 1 ATGAGAGGTTTCTGTACTATATGCTACAGACGAGGAGCAAGGCAATCGCAGAA 60
 QY 61 GAAATGTGACCAAGCTGTGTACATGATTTTCTGCAGATCTTCACTATATGTA 120
 DB 61 GAAATGTGACCAAGCTGTGTACATGATTTTCTGCAGATCTTCACTATATGTA 120
 QY 121 TCGATTAATGATGACCTTAAACCCGAAAGAGCTCTCTGTGTGTGTTTCTACACG 180
 DB 121 TCGATTAATGATGACCTTAAACCCGAAAGAGCTCTCTGTGTGTGTTTCTACACG 180
 QY 181 GGCACCGAGAGACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
 DB 181 GGCACCGAGAGACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
 QY 241 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGAGTTTCTGGTTCGGTATTCAGAA 300
 DB 241 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGAGTTTCTGGTTCGGTATTCAGAA 300
 QY 301 TACACCTACTTTTGCATGAGGAGAAATATGATTAACGACTTCAAGAGCTTGGAGCC 360
 DB 301 TACACCTACTTTTGCATGAGGAGAAATATGATTAACGACTTCAAGAGCTTGGAGCC 360
 QY 361 CGGCAATTTCTATGACACTGACATGACATGACATGACATGACATGACATGACATGAC 420
 DB 361 CGGCAATTTCTATGACACTGACATGACATGACATGACATGACATGACATGACATGAC 420
 QY 421 CCGTGAATGCTGACACTGCGCAGCCCTCAGAAAGCATTTTAAAGTCAAGAGACAA 480
 DB 421 CCGTGAATGCTGACACTGCGCAGCCCTCAGAAAGCATTTTAAAGTCAAGAGACAA 480
 QY 481 GAGAGATTAAGTGGGCACTCCCGGTGACATGACCTGATCTTGAAGACAGACTTGTG 540
 DB 481 GAGAGATTAAGTGGGCACTCCCGGTGACATGACCTGATCTTGAAGACAGACTTGTG 540
 QY 541 AAGTCAGAGCTGACATGACATGACATGACATGACATGACATGACATGACATGACATG 600
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 QY 601 AGAAGAGATTCGAGGTTTGAAGCAAAATGACATGACATGACATGACATGACATGAC 660
 DB 601 AGAAGAGATTCGAGGTTTGAAGCAAAATGACATGACATGACATGACATGACATGAC 660
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 DB 661 ATTTGAAGATTTGAGGCTCCTACCTACCGGTGAGTACCCCACTCAGAGGCTCTG 720
 QY 721 AATATTCCTGTTTACCCCAAGAAATATTTACAGATGATCTGACAGAGTCTTGGCCAG 780
 DB 721 AATATTCCTGTTTACCCCAAGAAATATTTACAGATGATCTGACAGAGTCTTGGCCAG 780

QY 781 GAGGAAAGCCAGATATCTGTGACTTCAGCAGATCCAGTCTTTTCAAGTCCAAATTTCAAG 840
DB 781 GAGGAAAGCCAGATATCTGTGACTTCAGCAGATCCAGTCTTTTCAAGTCCAAATTTCAAG 840
QY 841 GCAGTTCAATTCTCTAGATGATGCAATAAAACCACTGCTGGTAGAATTGGCAATT 900
DB 841 GCAGTTCAATTCTCTAGATGATGCAATAAAACCACTGCTGGTAGAATTGGCAATT 900
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DB 901 TCAATAACAGACTTTTCTATCAGCCCTGAGATGCTTCAAGCTGATCTGCCCTTAACAGT 960
QY 961 GATTCTGAGGTACAAAGCTTACTCCAAAGACTGAGCTTGAAGATAAAAGAGCACTGC 1020
DB 961 GATTCTGAGGTACAAAGCTTACTCCAAAGACTGAGCTTGAAGATAAAAGAGCACTGC 1020
QY 1021 GTGCTTTTGAATAAAGGAGACACAAAGAAAGAGACTTACCTTACCCCAAGCATATA 1080
DB 1021 GTGCTTTTGAATAAAGGAGACACAAAGAAAGAGACTTACCTTACCCCAAGCATATA 1080
QY 1081 CCTGCGGAGATGTTCTCTCAGATTCATTTTACCTGCTGTGTAATCCGAGCAATTCCT 1140
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QY 1141 AAAAAGGCAATTTTGGGAGCCCTTGTGACTATACAGTGAAGTGTGTAATCCGAGCAAG 1200
DB 1141 AAAAAGGCAATTTTGGGAGCCCTTGTGACTATACAGTGAAGTGTGTAATCCGAGCAAG 1200
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DB 1321 CTGCTGGAACATCTTCTTAACTTCAACCAAGACATATTCGTGTGCAAGCTCAAGTTA 1380
QY 1381 TTTTACCCAGAAAGCTCCATTTTGTCTGAACATGTAATTTCTGTCTACGTCACA 1440
DB 1381 TTTTACCCAGAAAGCTCCATTTTGTCTGAACATGTAATTTCTGTCTACGTCACA 1440
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DB 1441 ACAGAGTCTGCGGAGAGATATGTAAGAGCTGCTGCTGTGTGCTTCACTT 1500
QY 1501 CTTGAGCCAAACATACATGATCCCATGAAAGACGCGGAAAGCTGCTCTCTTAAGATA 1560
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DB 1621 ATATATGTTGGTCCAGGAAACCGGATAGCCCGTTTATTTGGGTTCTTACAACATAGAG 1680
QY 1681 AAATCTCAAGAACAAACCCAGATGAAATTTTGGAGCAATGTG--GTTTTTGGCTGC 1737
DB 1681 AAATCTCAAGAACAAACCCAGATGAAATTTTGGAGCAATGTG--GTTTTTGGCTGC 1737
QY 1738 AGGATTAAGATAGGATTAATCTATTCAGAAAGAGCTGACATTTCTTAAAGCAAGG 1797
DB 1741 AGGATTAAGATAGGATTAATCTATTCAGAAAGAGCTGACATTTCTTAAAGCAAGG 1800
QY 1798 ATCTTAATCTCATTAAGGTTCTTCTCAAGAGATCTCTGTGTGGGAGAGAGAGCC 1857
DB 1801 ATCTTAATCTCATTAAGGTTCTTCTCAAGAGATCTCTGTGTGGGAGAGAGAGCC 1860

QY 1858 CCAGCAAGATATGTACAGAACATCCAGCTTCAATGGCAGCAGAGTGGAGAAATCTTC 1917
DB 1861 CCAGCAAGATATGTACAGAACATCCAGCTTCAATGGCAGCAGAGTGGAGAAATCTTC 1920
QY 1918 CTCACAGAGAGCGGCATATTTATGTGTGAGATGCAAGATATATGGCCAAAGATGTA 1977
DB 1921 CTCACAGAGAGCGGCATATTTATGTGTGAGATGCAAGATATATGGCCAAAGATGTA 1980
QY 1978 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGTTGAGTTGAAAACTAGAACATAG 2037
DB 1981 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGTTGAGTTGAAAACTAGAACATAG 2040
QY 2038 AAAACCTTGCCCACTTTAAAGAAAGAAAGCGTACTTCAAGATATTTGTCTA 2091
DB 2041 AAAACCTTGCCCACTTTAAAGAAAGAAAGCGTACTTCAAGATATTTGTCTA 2094

RESULT 7
ADM43209
ID ADM43209 standard; cDNA; 2094 BP.
XX
AC ADM43209;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human methionine synthase reductase CDS G66A variant.
XX
KW Human; ss; Methionine synthase reductase polypeptide; HAMTR; cancer;
KW cardiovascular disease; neural tube defect; hyperhomocysteinemia;
KW chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2094
FT /tag= a
FT /product= "HAMTR"
FT /partial
FT /note= "No stop codon shown"
FT /replace(66,G)
FT /*tag= b
FT /standard_name= "Single_nucleotide_polymorphism"
FT /replace(110,A)
FT /*tag= c
FT /standard_name= "Single_nucleotide_polymorphism"
XX
PN US2003082676-A1.
XX
PD 01-MAY-2003.
XX
XX 10-AUG-1999; 99US-00371347.
XX
PR 16-JAN-1998; 98US-0071622P.
PR 15-JAN-1999; 99US-00232026.
XX
PA (GRAY/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLEIRE D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
XX
ET Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX
XX WPI; 2003-576610/54.
DR P-PSDB; ADM43211.
XX
PT New substantially pure nucleic acid encoding a mammalian methionine
PT synthase reductase polypeptide, useful for diagnosing, preventing or
PT treating conditions associated with altered methionine synthase activity,
PT e.g. cancer.
XX
PS Claim 3; SEQ ID NO 41; 26bp; English.
XX

CC The invention relates to a substantially pure nucleic acid that encodes a
CC mammalian methionine synthase reductase polypeptide, hMTMR, or that
CC hybridizes at high stringency to a nucleic acid appearing as ADM33208 or
CC ADM33209. Also included are a non-human animal where one or both genetic
CC alleles encoding the methionine synthase reductase polypeptide are
CC mutated, an antibody that specifically binds the above methionine
CC synthase reductase polypeptide, a method of detecting the presence of the
CC above polypeptide, a method for detecting sequence variants for
CC methionine synthase in a mammal, methods of treating or
CC preventing cancer (or cardiovascular disease or neural tube defects) in a
CC subject, methods of screening for a compound that modulates methionine
CC synthase reductase biological activity and a method for detecting an
CC increased risk of developing a neural tube defect in a mammalian embryo
CC or foetus. The nucleic acid is useful in diagnosing, preventing or
CC treating conditions associated with altered methionine synthase activity,
CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are
CC also associated with hyperhomocysteinemia. The gene for hMTMR is
CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
CC sequence of a variant human hMTMR cDNA.

XX Sequence 2094 BP; 592 A; 489 C; 480 G; 533 T; 0 U; 0 Other;

Query Match 86.0%; Score 1800; DB 11; Length 2094;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2090; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 ATGAGAGGTTTCTGTTACTATATGCTACACAGAGGAGCAAGGCAAAAGCCATCGAGAA 60
DB 1 ATGAGAGGTTTCTGTTACTATATGCTACACAGAGGAGCAAGGCAAAAGCCATCGAGAA 60
QY 61 GAAATGTGAGAGAACTGTGTGACATGATTTTTCGACAGATCTTCACTGATTAATGAA 120
DB 61 GAAATGTGAGAGAACTGTGTGACATGATTTTTCGACAGATCTTCACTGATTAATGAA 120
QY 121 TCCGATTAATGATGACCTTAATAACCGAAACAGCTCTCTGTGTGTGTGTTTCTACAG 180
DB 121 TCCGATTAATGATGACCTTAATAACCGAAACAGCTCTCTGTGTGTGTGTTTCTACAG 180
QY 121 TCCGATTAATGATGACCTTAATAACCGAAACAGCTCTCTGTGTGTGTGTTTCTACAG 180
DB 121 TCCGATTAATGATGACCTTAATAACCGAAACAGCTCTCTGTGTGTGTGTTTCTACAG 180
QY 181 GGCACCGAGAGACCCAGCCAGACAGCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
DB 181 GGCACCGAGAGACCCAGCCAGACAGCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
QY 241 CTGCGGTGATTTCTTTTGTCTACCTGCGGTATGGTTACTGGTCTCGGTGATTGAA 300
DB 241 CTGCGGTGATTTCTTTTGTCTACCTGCGGTATGGTTACTGGTCTCGGTGATTGAA 300
QY 241 CTGCGGTGATTTCTTTTGTCTACCTGCGGTATGGTTACTGGTCTCGGTGATTGAA 300
DB 241 CTGCGGTGATTTCTTTTGTCTACCTGCGGTATGGTTACTGGTCTCGGTGATTGAA 300
QY 301 TACACCTACTTTTGAATGGGGGAGATTAATTGATTAACGACTTCAAGAGCTTGAAGCC 360
DB 301 TACACCTACTTTTGAATGGGGGAGATTAATTGATTAACGACTTCAAGAGCTTGAAGCC 360
QY 361 CGGCAATTTCTATGACACTGACATGAGATGACTGTGTAGTTTGAACCTTGTGTGAG 420
DB 361 CGGCAATTTCTATGACACTGACATGAGATGACTGTGTAGTTTGAACCTTGTGTGAG 420
QY 421 CCGTGATTTGCTGAGCTCTGGCCAGCCCTCAGAAAGCATTTTATGTCAGAGAGACA 480
DB 421 CCGTGATTTGCTGAGCTCTGGCCAGCCCTCAGAAAGCATTTTATGTCAGAGAGACA 480
QY 481 GAGGAGATTAAGTGGGCACTCCGCGTGGGATCACTGATCTTGAAGAGACAGCTTGG 540
DB 481 GAGGAGATTAAGTGGGCACTCCGCGTGGGATCACTGATCTTGAAGAGACAGCTTGG 540
QY 541 AAGTCAGAGCTGTACATGATGATCTCAAGTCAAGCTTCTGAGATTGATGATGAG 600
DB 541 AAGTCAGAGCTGTACATGATGATCTCAAGTCAAGCTTCTGAGATTGATGATGAG 600
QY 601 AGAAAGATTTGAGGTTTGAAGCAAAATGAGTGAACAGCAACCAATTCATGTTGTA 660
DB 601 AGAAAGATTTGAGGTTTGAAGCAAAATGAGTGAACAGCAACCAATTCATGTTGTA 660
QY 661 ATGAAGACTTTGAGTCTCACTTACCCGTTCCGTAACCCCACTCTCAAGGCTCTG 720

DB 661 ATGAAGACTTTGAGTCTCACTTACCCGTTCCGTAACCCCACTCTCAAGGCTCTG 720
QY 721 AATATTCCTGTTTACCCCGCAAAATTTTACAGTACATCTGACAGAGCTCTGCGCAG 780
DB 721 AATATTCCTGTTTACCCCGCAAAATTTTACAGTACATCTGACAGAGCTCTGCGCAG 780
QY 781 GAGAAAGCAAGTATCTGTGACTTCAGAGATTCAGAGTTTTCAGTGGCAATTTCAAG 840
DB 781 GAGAAAGCAAGTATCTGTGACTTCAGAGATTCAGAGTTTTCAGTGGCAATTTCAAG 840
QY 841 GAGTTCAACTTATCTGTGACTTCAGAGATTCAGAGTTTTCAGTGGCAATTTCAAG 900
DB 841 GAGTTCAACTTATCTGTGACTTCAGAGATTCAGAGTTTTCAGTGGCAATTTCAAG 900
QY 901 TCAATACAGACTTTTCCATATGAGCTGAGATGCTTCAAGGTATCTGCTTAACT 960
DB 901 TCAATACAGACTTTTCCATATGAGCTGAGATGCTTCAAGGTATCTGCTTAACT 960
QY 961 GATTCTGAGGTACAAAGCTTACTCCAAAGACTGACGTTGAAGATTAAGAGAGACTGC 1020
DB 961 GATTCTGAGGTACAAAGCTTACTCCAAAGACTGACGTTGAAGATTAAGAGAGACTGC 1020
QY 1021 GTCTTTTGAATAAAGGAGAGACAAAGAAAGAGGCTTACCTTACCCAGCATATA 1080
DB 1021 GTCTTTTGAATAAAGGAGAGACAAAGAAAGAGGCTTACCTTACCCAGCATATA 1080
QY 1081 CCGCGGAGATGTTCTCTCAAGTTCAATTTTACTGTGCTTGAAGATCCGAGCAATTC 1140
DB 1081 CCGCGGAGATGTTCTCTCAAGTTCAATTTTACTGTGCTTGAAGATCCGAGCAATTC 1140
QY 1141 AAAAAAGCATTTTTCGAGCCCTGTGAGCTATACAGTACAGTGTCTGAAAAGGCGCAG 1200
DB 1141 AAAAAAGCATTTTTCGAGCCCTGTGAGCTATACAGTACAGTGTCTGAAAAGGCGCAG 1200
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DB 1201 CTACAGAGCTGTGAGTAAACAAGGCGCAGATTAATAGCCCTTGTGAGATGAGC 1260
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QY 1381 TTTCAACCGAGAAAGCTCAATTTGTCTTCAATTTGATGATGATGATGATGATGATG 1440
DB 1381 TTTCAACCGAGAAAGCTCAATTTGTCTTCAATTTGATGATGATGATGATGATGATG 1440
QY 1441 ACGAGGTTCTCGGAGGAGATGATGATGATGATGATGATGATGATGATGATGATG 1500
DB 1441 ACGAGGTTCTCGGAGGAGATGATGATGATGATGATGATGATGATGATGATGATG 1500
QY 1501 CTTGAGCCAAATATCATGATGATGATGATGATGATGATGATGATGATGATGATG 1560
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QY 1561 TCCATCTCTCTGAGCAACAATTTCTTCACTTACAGATGATGATGATGATGATGATG 1620
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DB 1621 ATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
QY 1681 AACTCCAAAGCAACACCAAGATGATGATGATGATGATGATGATGATGATGATGATG 1737
DB 1681 AACTCCAAAGCAACACCAAGATGATGATGATGATGATGATGATGATGATGATGATG 1737
QY 1738 AGGCAATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1797
DB 1738 AGGCAATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1797

QY 961 GATTCTGAGGTACAAAGCCTACTCCAAAGCTGACCTGAAAGATTAAGAGAGCACTGC 1020
 DB 1040 GATTCGAGGTCAAAAGCCTACTCCAAAGCTGACCTGAAAGATTAAGAGAGCACTGC 1099
 QY 1021 GTTCCTTTTAAATTAAGGACAGACAAAGAAAGAGCTACTTACCCCGACATATA 1080
 DB 1100 GTTCCTTTTAAATTAAGGACAGACAAAGAAAGAGCTACTTACCCCGACATATA 1159
 QY 1081 CCTGCGGAGATGTTCTCTCAGATTCAATTTTACCTGAGTCTTGAATCCGAGCAATTCCT 1140
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 DB 1460 TTTCAACCGAAGAAAGCTCAATTTTGTCTTCAACATTTGTGGAATTTCTGTCTACTGCAAC 1519
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 DB 1640 TCCATCTCTCTGGAACAACAATTCCTTCCACTTACAGATGACCCCTCAATCCCATC 1699
 QY 1621 ATATAGTGGGTTCAGAAACCGGACATAGCCCGTTTATTTGGGTTCTTACAACTAGAGAG 1680
 DB 1700 ATATAGTGGGTTCAGAAACCGGACATAGCCCGTTTATTTGGGTTCTTACAACTAGAGAG 1759
 QY 1681 AAATCTCAAGAACACACCCAGATGGAATTTTGAAGCAATGTG---GTTTTTGGCTGC 1737
 DB 1760 AAATCTCAAGAACACACCCAGATGGAATTTTGAAGCAATGTG---GTTTTTGGCTGC 1819
 QY 1738 AGGCATTAAGGATGAGGATTAATCTATTCAGAAAGAGCTGACATTTCTTAAGCAATGGG 1797
 DB 1820 AGGCATTAAGGATGAGGATTAATCTATTCAGAAAGAGCTGACATTTCTTAAGCAATGGG 1879
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 DB 1940 CCAGCAAAAGTATTAACAAGACATTCAGCTTCAAGGCAAGAGTGGCGAGAAATCTTC 1999
 QY 1918 CTCACAGAGAACGGCAATTTTATGTTGAGAGATGCAAGAAATATGCGCAAGATGTA 1977
 DB 2000 CTCACAGAGAACGGCAATTTTATGTTGAGAGATGCAAGAAATATGCGCAAGATGTA 2059
 QY 1978 CATGATGCCCTTGTGCAATTAATTAAGCAAAAGAGGTTGAGATTGAAAACTAGAAAGCAATG 2037
 DB 2060 CATGATGCCCTTGTGCAATTAATTAAGCAAAAGAGGTTGAGATTGAAAACTAGAAAGCAATG 2119

QY 2038 AAAACCTGGCCACTTTAAAGAGAAAAACCTACTCTTACAGATATTGTGATATA 2094
 DB 2120 AAAACCTGGCCACTTTAAAGAGAAAAACCTACTCTTACAGATATTGTGATATA 2176
 RESULT 9
 ID ADQ87538
 DB ADQ87538 standard; cDNA; 3270 BP.
 AC ADQ87538;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #4416.
 KW human; tumour-associated antigenic target; TAT; cytosolic; gene therapy;
 KW cancer; cell proliferative disorder; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO2004060270-A2.
 XX
 PD 22-JUL-2004.
 XX
 PF 15-OCT-2003; 2003WO-US029126.
 XX
 PR 18-OCT-2002; 2002US-0418988P.
 XX
 PA (GENT) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 XX
 PI Wu TD, Zhou Y;
 XX
 DR WPI; 2004-534300/51.
 XX
 PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
 PT preventing or treating cell proliferative disorders such as cancer.
 PS
 PS Claim 1; SEQ ID NO 4416; 5504bp; English.
 XX
 CC The present invention describes an isolated tumour-associated antigenic
 CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
 CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
 CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
 CC sequence identity to (a)-(c); or (e) a sequence that hybridizes to (a)-
 CC (c). Also described: (1) an expression vector comprising the above
 CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
 CC a process for producing a polypeptide; (4) an isolated polypeptide
 CC comprising: (a) an amino acid sequence encoded by any of the above
 CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
 CC length coding region of the above nucleotide sequences; or (c) a sequence
 CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
 CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
 CC an isolated antibody that binds to the above polypeptide; (7) a process
 CC for producing the antibody; (8) an isolated oligopeptide that binds to
 CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
 CC binding organic molecule that binds to the above polypeptide; (10) a
 CC composition of matter comprising the above (chimeric) polypeptide;
 CC antibody, oligopeptide or TAT binding organic molecule, in combination
 CC with a carrier; (11) an article of manufacture comprising a container and
 CC the composition of matter contained within the container; (12) methods of
 CC inhibiting the growth of a cell that expresses the above protein, where
 CC the growth of the cell is at least in part dependent upon a growth
 CC potentiating effect of the above protein; (13) a method of
 CC therapeutically treating a mammal having a cancerous tumour comprising
 CC cells that express the above protein; (14) a method of determining the
 CC presence of a protein in a sample suspected of containing the protein
 CC described above; (15) methods of diagnosing the presence of a tumour in a
 CC mammal; (16) a method for treating or preventing a cell proliferative
 CC disorder associated with increased expression or activity of the above
 CC protein; and (17) a method of binding an antibody, oligopeptide or
 CC organic molecule to a cell that expresses the protein described above.


```
DB 2092 CATGAGCCCTTGCAAAATAATACCAAGGTTGAGTTGAAAACTAGAACCAATG 2151
QY 2038 AAAACCCCTGCACTTTAAAGAGAAAAACGTACTCTCAGGATTTTGGTCATTA 2094
DB 2152 AAAACCTGCGCCTTTAAAGAGAAAAACGTACTCTCAGGATTTTGGTCATTA 2208

RESULT 10
ADM43214
ID ADM43214 standard; cDNA; 2091 BP.
XX
AC ADM43214;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human methionine synthase reductase CDS del 1675-1678 variant.
XX
KW Human; ss; Methionine synthase reductase polypeptide; hsmtrr; cancer;
KM cardiovascular disease; neural tube defect; hyperhomocysteinaemia;
XX chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2091
FT /tag= a
FT /product= "hsmtrrdelR559"
FT /partial
FT /note= "No stop codon shown"
FT /replace(66,A)
FT /tag= b
FT /standard name= "single_nucleotide polymorphism"
FT /replace(110,A)
FT /tag= c
FT /standard name= "single_nucleotide polymorphism"
FT /replace(1675,AGAG)
FT /tag= d
FT variation
XX
PN US2003082676-A1.
XX
XX 01-MAY-2003.
XX
PF 10-AUG-1999; 99US-00371347.
XX
PR 16-JAN-1998; 98US-0071622P.
PR 15-JAN-1999; 99US-00232028.
XX
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
XX
PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX
DR WPI; 2003-576610/54.
DR P-PSDB; ADM43215.
XX
PT New substantially pure nucleic acid encoding a mammalian methionine
PT synthase reductase polypeptide, useful for diagnosing, preventing or
PT treating conditions associated with altered methionine synthase activity,
PT e.g. cancer.
XX
PS Disclosure; SEQ ID NO 47; 26pp; English.
XX
XX The invention relates to a substantially pure nucleic acid that encodes a
XX mammalian methionine synthase reductase polypeptide, hsmtrr, or that
XX hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
XX ADM43209. Also included are a non-human animal where one or both genetic
XX alleles encoding the methionine synthase reductase polypeptide are
XX mutated, an antibody that specifically binds the above methionine
XX synthase reductase polypeptide, a method of detecting the presence of the
```

```
CC above polypeptide, a method for detecting sequence variants for
CC methionine synthase reductase in a mammal, methods of treating or
CC preventing cancer (or cardiovascular disease or neural tube defects) in a
CC subject, methods of screening for a compound that modulates methionine
CC synthase reductase biological activity and a method for detecting an
CC increased risk of developing a neural tube defect in a mammalian embryo
CC or foetus. The nucleic acid is useful in diagnosing, preventing or
CC treating conditions associated with altered methionine synthase activity,
CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are
CC also associated with hyperhomocysteinaemia. The gene for hsmtrr is
CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
CC sequence of a variant human hsmtrr cDNA.
XX
SQ Sequence 2091 BP; 589 A; 489 C; 480 G; 533 T; 0 U; 0 Other;
Query Match 79.9%; Score 1674; DB 11; Length 2091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGGAGGTTCTGTACTATATGCTACACAGGAGGACAGGCAAGGCCATCCGAGAA 60
DB 1 ATGAGGAGGTTCTGTACTATATGCTACACAGGAGGACAGGCAAGGCCATCCGAGAA 60
QY 61 GAAATGTGTAGACCAAGCTGTGTACATGATTTTCTGAGATCTTCACTGATTAATGAA 120
DB 61 GAAATGTGTAGACCAAGCTGTGTACATGATTTTCTGAGATCTTCACTGATTAATGAA 120
QY 121 TCCGATTAAGTATGACTTAAACCGAAACAGTCTCTTGTGTGTGTGTCTACACG 180
DB 121 TCCGATTAAGTATGACTTAAACCGAAACAGTCTCTTGTGTGTGTGTCTACACG 180
QY 121 TCCGATTAAGTATGACTTAAACCGAAACAGTCTCTTGTGTGTGTGTCTACACG 180
DB 121 TCCGATTAAGTATGACTTAAACCGAAACAGTCTCTTGTGTGTGTGTCTACACG 180
QY 181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
DB 181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
QY 241 CTGCGGTTGATTTCTTCTGCTACCTGCGGTTATGAGTTCTGAGTTCTGAGTTTCA 300
DB 241 CTGCGGTTGATTTCTTCTGCTACCTGCGGTTATGAGTTCTGAGTTCTGAGTTTCA 300
QY 301 TACACCTACTTTTGCATATGAGGAGGAGAAATATATGATTAACGATTCAGAGCTTGA 360
DB 301 TACACCTACTTTTGCATATGAGGAGGAGAAATATATGATTAACGATTCAGAGCTTGA 360
QY 361 CGGCAATTTTATGACACTGACATGACATGACTGTGTAGTTTAACTTGTGTTGAG 420
DB 361 CGGCAATTTTATGACACTGACATGACATGACTGTGTAGTTTAACTTGTGTTGAG 420
QY 421 CCGTGAATGCTGGAATCTGCGCAGGCGCTCAGAAAGCATTTTAAAGTCAAGAGAGCAA 480
DB 421 CCGTGAATGCTGGAATCTGCGCAGGCGCTCAGAAAGCATTTTAAAGTCAAGAGAGCAA 480
QY 481 GAGAGATTAAGTGGGCACTCCCGGTGAGCATCTGCATCTTGAAGAGACAGACTTGTG 540
DB 481 GAGAGATTAAGTGGGCACTCCCGGTGAGCATCTGCATCTTGAAGAGACAGACTTGTG 540
QY 541 AAGTCAGAGCTGCTACATTTGAATCTCAAGTCAGACTTCTGAATTCATGATTTACAGA 600
DB 541 AAGTCAGAGCTGCTACATTTGAATCTCAAGTCAGACTTCTGAATTCATGATTTACAGA 600
QY 601 AAGAAAGATTCGAGGTTTGAAGCAAAATGAGAGGAAACAGCAACCAATCCAAATGTTGA 660
DB 601 AAGAAAGATTCGAGGTTTGAAGCAAAATGAGAGGAAACAGCAACCAATCCAAATGTTGA 660
QY 661 ATTGAAGACTTGAAGTCTCACTTACCCGTTGAGTACCCCACTCTCACAAGCTCTCTG 720
DB 661 ATTGAAGACTTGAAGTCTCACTTACCCGTTGAGTACCCCACTCTCTCACAAGCTCTCTG 720
QY 721 AATATTCTGTTTACCCCAAGATTTTAAACGATCATCTGCAAGAGTCTTGGCCAG 780
DB 721 AATATTCTGTTTACCCCAAGATTTTAAACGATCATCTGCAAGAGTCTTGGCCAG 780
```


QY	781	GAGAAAGCCAAAGTATCTGTACCTTCACAGATCCAGTTTTCAGTCCCAATTTCAAG	840
Db	781	GAGAAAGCCAAAGTATCTGTACCTTCACAGATCCAGTTTTCAGTCCCAATTTCAAG	840
QY	841	GCAGTTCACCTTACTAGATGATGCCATPAAAACACTCTGTGTGAAATTTGACATT	900
Db	841	GCAGTTCACCTTACTAGATGATGCCATPAAAACACTCTGTGTGAAATTTGACATT	900
QY	901	TCAAAATACAGACTTTTCTATCAGCTGAGATGCTTCAAGGATATCTGCCCTTACAGT	960
Db	901	TCAAAATACAGACTTTTCTATCAGCTGAGATGCTTCAAGGATATCTGCCCTTACAGT	960
QY	961	GATTCTGAGGTACAAAGCCTTACTCCAAAGATCGACGCTTGAAGATPAAAAGAGACATGC	1020
Db	961	GATTCTGAGGTACAAAGCCTTACTCCAAAGATCGACGCTTGAAGATPAAAAGAGACATGC	1020
QY	1021	GTCTCTTTGAAAATPAAAGGACAGACAAAGAAAGAAAGAGCTACTTACCCGATATTA	1080
Db	1021	GTCTCTTTGAAAATPAAAGGACAGACAAAGAAAGAAAGAGCTACTTACCCGATATTA	1080
QY	1081	CCTCGGGGATGTCTCTCAGTTCATTTTACTGTGTCTTGAATCCGAGCAATTCCT	1140
Db	1081	CCTCGGGGATGTCTCTCAGTTCATTTTACTGTGTCTTGAATCCGAGCAATTCCT	1140
QY	1141	AAAAAGCATTTTTCGAGCCCTTGTGACTATACAGTGAACAGTCTGAAAAGCGCAGG	1200
Db	1141	AAAAAGCATTTTTCGAGCCCTTGTGACTATACAGTGAACAGTCTGAAAAGCGCAGG	1200
QY	1201	CTACAGGAGCTGTGAGTAAACAAGGGGACGCCATPAAAGCCGTTTGTGACGATATGC	1260
Db	1201	CTACAGGAGCTGTGAGTAAACAAGGGGACGCCATPAAAGCCGTTTGTGACGATATGC	1260
QY	1261	TGTGCTGTGTTGGATCTCTCTCGCTTTCCTTGTGCAGCCACCACTCAGTCTC	1320
Db	1261	TGTGCTGTGTTGGATCTCTCTCGCTTTCCTTGTGCAGCCACCACTCAGTCTC	1320
QY	1321	CTGTCCGAACATCTTCTTAACTTCAACCCAGACATATTTGTGTGCAAGCTCAAGTTTA	1380
Db	1321	CTGTCCGAACATCTTCTTAACTTCAACCCAGACATATTTGTGTGCAAGCTCAAGTTTA	1380
QY	1381	TTTCAACCAGAAAAGCTCATTTTGTCTTCAACATTTGGAAATTTCTGTACTGSCACA	1440
Db	1381	TTTCAACCAGAAAAGCTCATTTTGTCTTCAACATTTGGAAATTTCTGTACTGSCACA	1440
QY	1441	ACAGAGGTTCTGCGAAGGAGATATGACAGGCTGCTGCGCTTGTGTGTTCACTTCACTT	1500
Db	1441	ACAGAGGTTCTGCGAAGGAGATATGACAGGCTGCTGCGCTTGTGTGTTCACTTCACTT	1500
QY	1501	CTTACAGCCAAACATACATGATGCCATGAAAGACGGGAAAAGCCCTGCTCTTAAAGTAA	1560
Db	1501	CTTACAGCCAAACATACATGATGCCATGAAAGACGGGAAAAGCCCTGCTCTTAAAGTAA	1560
QY	1561	TCCATCTCTCTCGAACAAATTCCTTCCACTTACAGATGACCCCTCATCCCCATC	1620
Db	1561	TCCATCTCTCTCGAACAAATTCCTTCCACTTACAGATGACCCCTCATCCCCATC	1620
QY	1621	ATATATGTGGGTCCAGAAACCGGCATAGCCCCGTTTATTTGGTTCCTTCAACAT	1674
Db	1621	ATATATGTGGGTCCAGAAACCGGCATAGCCCCGTTTATTTGGTTCCTTCAACAT	1674

Accession	Gene	Protein	Enzyme	EC	Ref
AA058977	RESULT 11				
AAA58977	ID	AAA58977	standard; DNA, 3256 BP.		
XX	AC	AAA58977;			
XX	DT	07-NOV-2000	(first entry)		
XX	DE	A human methionine synthase reductase DNA sequence with polymorphism			
XX	XX	Human; methionine synthase reductase; MTRR; cancer; cardiovascular disease; Down's Syndrome; neural tube defect;			
KW	XX				

XX premature coronary artery disease; ss.
OS Homo sapiens.
PN W0200042196-A2.
PP 20-JUL-2000.
XP 14-JAN-2000; 2000MOC-IH000209.
XX 15-JAN-1999; 99US-00232028.
PR 10-AUG-1999; 99US-00371347.
XX (UTMC-) UNIV MCGILL.
PA
XX
XX Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
PI WPJ; 2000-466131/40.
DR
XX
XX Mammalian methionine synthase reductase nucleic acid used for detecting
PT an increased risk of developing a neural tube defect, Down's Syndrome or
PT cardiovascular disease in a mammalian embryo or fetus.
XX
XX
XX Claim 8; Page; 85pp; English.

The present sequence represents a human methionine synthase reductase (MTRR) DNA sequence, with a polymorphism comprising of a deletion of nucleotides 1726-1728. Inhibitors of MTRR polypeptide and polynucleotide are used for treating or preventing cancer, cardiovascular disease, Down's Syndrome or neural tube defects in a subject. The cardiovascular disease is premature coronary artery disease. The compounds are detected by methods which screen for modulators of MTRR biological activity. MTRR polypeptide or nucleic acid is examined for the presence of a polymorphism in the parents or the embryo or foetus, and the information used for detecting an increased risk of an embryo or foetus developing cancer, cardiovascular disease, Down's Syndrome or neural tube defects. CC note: the present sequence does not appear in the specification; it was created using information provided

Sequence 3256 BP; 943 A; 705 C; 662 G; 946 T; 0 U; 0 Other;

Query Match	76.2% ; Score 1595 ; DB 3 ; Length 3256 ;
Best Local Similarity	99.9% ; Pred. No. 0 ;
Matches 1645 ; Conservative	0 ; Mismatches 1 ; Indels 0 ; Gaps 0
QY 1 ATGAGGAGGTTCTGTTACTATATATGCTACACAGAGGACAGGACAAAGCCATGCGAGAA	60
Db 80 ATGAGGAGGTTCTGTTACTATATATGCTACACAGAGGACAGGACAAAGCCATGCGAGAA	139
QY 61 GAAATGTGTGAGCAAGCTGTGTGTACATGGAATTTTCTGCAGATCTTCACTGTATTAGTGA	120
Db 140 GAAATGTGTGAGCAAGCTGTGTGTACATGGAATTTTCTGCAGATCTTCACTGTATTAGTGA	199
QY 121 TCCGATATAGTATGACCTTAAAAACGAAACAGCTCCTCTGTGTGTGTGTTCTTACACAG	180
Db 200 TCCGATATAGTATGACCTTAAAAACGAAACAGCTCCTCTGTGTGTGTGTTCTTACACAG	259
QY 181 GGCACCCGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA	240
Db 260 GGCACCCGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA	319
QY 241 CTGCGCGGTGATTTCTTTGTGCACCTGCGGTATGCGGTATCTGCGGTCTCGGTATTCAAGA	300
Db 320 CTGCGCGGTGATTTCTTTGTGCACCTGCGGTATGCGGTATCTGCGGTATTCAAGA	379
QY 301 TACACTACTTCTTGGCAATGGGGGGAGATATTGATAAACGACTTCAAGACTTGGAGCC	360
Db 380 TACACTACTTCTTGGCAATGGGGGGAGATATTGATAAACGACTTCAAGACTTGGAGCC	439
QY 361 CGGCAATTTCTATGACACTGGAACATGACAGATGACTGTGATGTTTAAAGACTTGTGTGAG	420
Db 440 CGGCAATTTCTATGACACTGGAACATGACAGATGACTGTGATGTTTAAAGACTTGTGTGAG	499


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QY 421 CCGTGGATTTGCTGACTCTGGCCAGCCCTCAGAAAGCATTTTATAGTCAAGAGAGACAA 480
DB 500 CCGTGGATTTGCTGACTCTGGCCAGCCCTCAGAAAGCATTTTATAGTCAAGAGAGACAA 559
QY 481 GAGGAGATTAAGTGGGCACTCCCGGTGGGATCACTGATCTTTGAGGACAGACCTTGG 540
DB 560 GAGGAGATTAAGTGGGCACTCCCGGTGGGATCACTGATCTTTGAGGACAGACCTTGG 619
QY 541 AAGTCAGAGCTGCTACACATTTGAATCTCAAGTCAGAGCTTCTGAGATTCGATGATTCAGGA 600
DB 620 AAGTCAGAGCTGCTACACATTTGAATCTCAAGTCAGAGCTTCTGAGATTCGATGATTCAGGA 679
QY 601 AGAAAGATTTCTAGGTTTGAAGCAAAATGCAAGTGAACAGAACCAATCCATGTTTGA 660
DB 680 AGAAAGATTTCTAGGTTTGAAGCAAAATGCAAGTGAACAGAACCAATCCATGTTTGA 739
QY 661 ATTGAAGACTTGAAGTCTGACTTACCTCGGTGGGATCCCGCACTCTCAGAGCTCTCTG 720
DB 740 ATTGAAGACTTGAAGTCTGACTTACCTCGGTGGGATCCCGCACTCTCAGAGCTCTCTG 799
QY 721 AATATTTCTGCTGTTTACCCCGAATTTTACAGGTATCTGCAAGAGTCTCTGGCCAG 780
DB 800 AATATTTCTGCTGTTTACCCCGAATTTTACAGGTATCTGCAAGAGTCTCTGGCCAG 859
QY 781 GAGGAAAGCCAGATCTGCTGACTTCAAGAGATCCAGTTTTCAGTGGCAATTTCAAG 840
DB 860 GAGGAAAGCCAGATCTGCTGACTTCAAGAGATCCAGTTTTCAGTGGCAATTTCAAG 919
QY 841 GCAATTCAACTTATCTAGATGATGCAATTAACCACTCTGCTGATGATTTGACAT 900
DB 920 GCAATTCAACTTATCTAGATGATGCAATTAACCACTCTGCTGATGATTTGACAT 979
QY 901 TGAATATACAGACTTTTCTATCAGGCTGAGATGCTTCAAGGTGATCTGCTTACAGT 960
DB 980 TGAATATACAGACTTTTCTATCAGGCTGAGATGCTTCAAGGTGATCTGCTTACAGT 1039
QY 961 GATTCGAGGTACAAAGCTTACTCAAAAGCTGCACTTGAAGATTAAGAGAGACACTGC 1020
DB 1040 GATTCGAGGTACAAAGCTTACTCAAAAGCTGCACTTGAAGATTAAGAGAGACACTGC 1099
QY 1021 GTCTTTTGAATAAAGGAGACACAAAGAAAGAGCTACCTTACCCGACATATA 1080
DB 1100 GTCTTTTGAATAAAGGAGACACAAAGAAAGAGCTACCTTACCCGACATATA 1159
QY 1081 CCGTGGGAGATTTCTCTCAGATTCATTTTCTGCTGCTTGAATCCGAGCAATTCCT 1140
DB 1160 CCGTGGGAGATTTCTCTCAGATTCATTTTCTGCTGCTTGAATCCGAGCAATTCCT 1219
QY 1141 AAAAAGGCAATTTTGGGAGCCCTTGTGACTATACAGTGAAGTGTGAAAAAGGCGAG 1200
DB 1220 AAAAAGGCAATTTTGGGAGCCCTTGTGACTATACAGTGAAGTGTGAAAAAGGCGAG 1279
QY 1201 CTACAGAGCTGTGCAATTAACAGAGGGGAGCGATTAATAGCCGCTTGTGACAGATGCC 1260
DB 1280 CTACAGAGCTGTGCAATTAACAGAGGGGAGCGATTAATAGCCGCTTGTGACAGATGCC 1339
QY 1261 TGTGCTGCTTGTGATCTCTCTGCTTTCCTTCTTGGCAGGACCACTCACTCTC 1320
DB 1340 TGTGCTGCTTGTGATCTCTCTGCTTTCCTTCTTGGCAGGACCACTCACTCTC 1399
QY 1321 CTGCTGGAACATTTCTTAACCTTCAACCCAGACATATTCGTGTGACAGCTCAAGTTTA 1380
DB 1400 CTGCTGGAACATTTCTTAACCTTCAACCCAGACATATTCGTGTGACAGCTCAAGTTTA 1459
QY 1381 TTTACCCAGAAAGTCCATTTTGTCTTCAACATTTGTGAATTTGTCTACCTGACACA 1440
DB 1460 TTTACCCAGAAAGTCCATTTTGTCTTCAACATTTGTGAATTTGTCTACCTGACACA 1519
QY 1441 ACAGAGATTTGCGGAAAGGAGATGATACAGGCTGCTGCTTGTGCTTGTGCTTCAAGTT 1500
DB 1520 ACAGAGATTTGCGGAAAGGAGATGATGATGAGGCTGCTGCTTGTGCTTGTGCTTCAAGTT 1579
QY 1501 CTTCAGCCAAACATACATGATCCCATGGAAGACGCGGAGAAAGCCTGCTCTTAAGATA 1560

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DB 1580 CTTACGCCAAACATACATGATCCCATGAAAGCACGCGGAAAGCCCTGCTCTTAAGATA 1639
QY 1561 TCCATCTCTCCCGGAAACAAATCTTTCACCTTACAGATGATGCCCTCAATCCCATC 1620
DB 1640 TCCATCTCTCCCGGAAACAAATCTTTCACCTTACAGATGATGCCCTCAATCCCATC 1699
QY 1621 ATATATGTTGGTCCAGAAACCGGCAT 1646
DB 1700 ATATATGTTGGTCCAGAAACCGGCAT 1725

RESULT 12
ID AA58976
ID AA58976 standard; DNA; 3255 BP.
XX
AC AA58976;
XX
DT 07-NOV-2000 (first entry)
XX
DE A human methionine synthase reductase DNA sequence with polymorphism.
XX
KW Human; methionine synthase reductase; MTRR; cancer;
KW cardiovascular disease; Down's Syndrome; neural tube defect;
KW premature coronary artery disease; ss.
XX
OS Homo sapiens.
XX
PN WO200042196-A2.
XX
PD 20-JUL-2000.
XX
PF 14-JAN-2000; 2000MO-1B000209.
XX
PR 15-JAN-1999; 99US-00232028.
XX
PR 10-AUG-1999; 99US-00371347.
XX
PA (UWMC-) UNIV MCGILL.
XX
PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX
DR WPI; 2000-466131/40.
XX
PT Mammalian methionine synthase reductase nucleic acid used for detecting
PT an increased risk of developing a neural tube defect, Down's Syndrome or
PT cardiovascular disease in a mammalian embryo or fetus.
XX
PS Claim 7; Page; 85pp; English.
XX
CC The present sequence represents a human methionine synthase reductase
CC (MTRR) DNA sequence, with a polymorphism comprising of a deletion of
CC nucleotides 1675-1678. Inhibitors of MTRR polypeptide and polynucleotide
CC are used for treating or preventing cancer, cardiovascular disease,
CC Down's Syndrome or neural tube defects in a subject. The cardiovascular
CC disease is premature coronary artery disease. The compounds are detected
CC by methods which screen for modulators of MTRR biological activity. MTRR
CC polypeptide or nucleic acid is examined for the presence of a
CC polymorphism in the parents or the embryo or foetus and the information
CC used for detecting an increased risk of an embryo or foetus developing
CC cancer, cardiovascular disease, Down's Syndrome or neural tube defects.
CC note: the present sequence does not appear in the specification; it was
CC created using information provided.
XX
SQ Sequence 3255 BP; 942 A; 704 C; 663 G; 946 T; 0 U; 0 Other;

Query Match 73.7%; Score 1544; DB 3; Length 3255;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1594; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAGAGAGTTTCTGTTACTATATGCTACACAGGAGGACAGGCAAGGCCATTCGAGAA 60
DB 80 ATGAGAGAGTTTCTGTTACTATATGCTACACAGGAGGAGGCAAGGCCATTCGAGAA 139

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QY	61	GAATGTGTGAGCAGCTGTGTGTAATGATATTTCTGCAGATCTTCACTGTATTAAGAA	120
Db	140	GAATGTGTGAGCAGCTGTGTGTAATGATATTTCTGCAGATCTTCACTGTATTAAGAA	199
QY	121	TCCGATAGTATGACCTTAAACCGAAACAGCTCCTCTGTGTGTGTGGTTTCTAACAGC	180
Db	200	TCCGATAGTATGACCTTAAACCGAAACAGCTCCTCTGTGTGTGTGGTTTCTAACAGC	259
QY	181	GGCACCCGAGACCCACCCGACACAGCCCGCAAGTTTGTTAAGAAATACAGAACCAACA	240
Db	260	GGCACCCGAGACCCACCCGACACAGCCCGCAAGTTTGTTAAGAAATACAGAACCAACA	319
QY	241	CTGCCGGTGAATTTCTTTTGTCTACCTGGGGTAATGGGTTACTGGGTCTCGGATTTCAAA	300
Db	320	CTGCCGGTGAATTTCTTTTGTCTACCTGGGGTAATGGGTTACTGGGTCTCGGATTTCAAA	379
QY	301	TACACCTTACTTTTGCAATGGGGGGGAAGTAATTAATTAACGACTTCAAGAGCTTGAGCC	360
Db	380	TACACCTTACTTTTGCAATGGGGGGGAAGTAATTAATTAACGACTTCAAGAGCTTGAGCC	439
QY	361	CGGCAATTTCTATGACATGACATGACAGATGACTGTGAGTTTGAACCTTGTGGTTAG	420
Db	440	CGGCAATTTCTATGACATGACATGACAGATGACTGTGAGTTTGAACCTTGTGGTTAG	499
QY	421	CCGTGAGATGCTGGACTCTGTGGCCAGCCTTCAGAAAGCAATTTAGTCAAGCAGACAA	480
Db	500	CCGTGAGATGCTGGACTCTGTGGCCAGCCTTCAGAAAGCAATTTAGTCAAGCAGACAA	559
QY	481	GAGGAGATTAATGGCGGCACTCCGGTGGCACTGTCGATCCTTGAGAGCAGACCTTGTG	540
Db	560	GAGGAGATTAATGGCGGCACTCCGGTGGCACTGTCGATCCTTGAGAGCAGACCTTGTG	619
QY	541	AAGTCAGAGCTGTACACATTTGAATCTTCATGTCAGACTTCTGAGATTCGATTCAGAA	600
Db	620	AAGTCAGAGCTGTACACATTTGAATCTTCATGTCAGACTTCTGAGATTCGATTCAGAA	679
QY	601	AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAACAGAACCAATCCATGTTGTA	660
Db	680	AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAACAGAACCAATCCATGTTGTA	739
QY	661	ATTGAAGCTTGAAGTCTCTCACTTAACCGGTGGTAACCCCACTCAACAGCCTCTCTG	720
Db	740	ATTGAAGCTTGAAGTCTCTCACTTAACCGGTGGTAACCCCACTCAACAGCCTCTCTG	799
QY	721	AATATTCCTGGTTTACCCCGAGAATATTTACAGGTACATCTGCAGAGTCTCTTGGCCAG	780
Db	800	AATATTCCTGGTTTACCCCGAGAATATTTACAGGTACATCTGCAGAGTCTCTTGGCCAG	859
QY	781	GAGAAAGCCAGATCTGTGACTTCAGCAGATCCAGTTTTCAGATGTCACAAATTCAAAG	840
Db	860	GAGAAAGCCAGATCTGTGACTTCAGCAGATCCAGTTTTCAGATGTCACAAATTCAAAG	919
QY	841	GCAGTTTCACTTACAGAAATGATGCCATAAACCACTCTGCTGTGTAAGAAATTTGACATT	900
Db	920	GCAGTTTCACTTACAGAAATGATGCCATAAACCACTCTGCTGTGTAAGAAATTTGACATT	979
QY	901	TCAAAATACAGACTTTTCTATCAGGCTGGAATGCTTCAGCGTATCTGCGCTTAACGT	960
Db	980	TCAAAATACAGACTTTTCTATCAGGCTGGAATGCTTCAGCGTATCTGCGCTTAACGT	1039
QY	961	GATTCGTAGGTACAAAGCCTTCTCAAGAGCTGCAGCTTGAAGTAATAAGAGCACTGC	1020
Db	1040	GATTCGTAGGTACAAAGCCTTCTCAAGAGCTGCAGCTTGAAGTAATAAGAGCACTGC	1099
QY	1021	GTCCTTTGAAAATTAAGGCAACACAAAGAAAGAGGCTTACCTTACCCAGCATATA	1080
Db	1100	GTCCTTTGAAAATTAAGGCAACACAAAGAAAGAGGCTTACCTTACCCAGCATATA	1159
QY	1081	CCTGGGGAGTGTCTCTCAGTTCAATTTTACCTGGGTCTTGAATCCAGAGCAATTCCT	1140
Db	1160	CCTGGGGAGTGTCTCTCAGTTCAATTTTACCTGGGTCTTGAATCCAGAGCAATTCCT	1219
QY	1141	AAAAAGGCAATTTTTCGAGCCCTTGTGACTATACAGTGAACAGTGTGAAAAGCGCAGG	1200

Db	1220	AAAAAGGCAATTTTGGCAGAGCCCTTGTTGSACTATACAGTACAGTGTCTGAAGAGCCAGG	1279
Qy	1201	CTACAGAGAGCTGTGACGTAAACAGAGGGCAGCCGATTTATAGCCGCTTTGTACAGATGCC	1260
Db	1280	CTACAGGAGGCTGTGACGTAAACAGAGGGCAGCCGATTTATAGCCGCTTTGTACAGATGCC	1339
Qy	1261	TGTGCTGCTGTTGTTGGATCTCTCTCTGCTTTTCCCTTCTTGCCAGCCACCACTCAGCTC	1320
Db	1340	TGTGCTGCTGTTGTTGGATCTCTCTCTGCTTTTCCCTTCTTGCCAGCCACCACTCAGCTC	1399
Qy	1321	CTGCTCGAACACTTCTCTTAACCTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTA	1380
Db	1400	CTGCTCGAACACTTCTCTTAACCTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTA	1459
Qy	1381	TTTTCACCCAGGAAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTCTGTACTGCCACA	1440
Db	1460	TTTTCACCCAGGAAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTCTGTACTGCCACA	1519
Qy	1441	ACAGAGGTTCTGCGGAAAGGAGATGTATACAGAGCTGCGCTGCTGTTGTTGCTTCAGTT	1500
Db	1520	ACAGAGGTTCTGCGGAAAGGAGATGTATACAGAGCTGCGCTGCTGTTGTTGCTTCAGTT	1579
Qy	1501	CTTGAGGCCAAACATATCATGTGATCCCATGAAGACAGCGGGAAAGCCCTGCTCTAAGATA	1560
Db	1580	CTTGAGGCCAAACATATCATGTGATCCCATGAAGACAGCGGGAAAGCCCTGCTCTAAGATA	1639
Qy	1561	TTCCATCTCTCTCGAACACAAATTTCTTCCACTT	1595
Db	1640	TTCCATCTCTCTCGAACACAAATTTCTTCCACTT	1674
RESULT 13			
ACN42470			
ID	ACN42470	standard; cDNA; 3189 BP.	
AC	ACN42470;		
XX			
XX			
DT	18-NOV-2004	(first entry)	
XX			
DE		Human diagnostic and therapeutic polynucleotide SEQ ID NO:1345.	
XX			
KM		ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;	
XX		dihnp.	
OS		Homo sapiens.	
XX			
XX	WO2004023973-A2.		
PN			
XX			
PD	25-MAR-2004.		
XX			
PF	12-SEP-2003; 2003WO-US028227.		
XX			
PR	12-SEP-2002; 2002US-0410259P.		
XX	12-SEP-2002; 2002US-0410260P.		
PA	(INCY-) INCYTE CORP.		
XX			
PI	Schmidt JP, Wright RJ, Bruns CM, Marjanovic NM, Shen F;		
PI	Harthorne TA, Suchorolski MT, Altus CM, Fites SU, Elder LV;		
PI	Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;		
PI	Steven KM, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;		
PI	Perilla CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LB;		
PI	Laegre RE, Spito PH, Stewart EA, Wingrove J, Vilt UB, Kiron ES;		
PI	Ku Y, Kwong H, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;		
PI	Patury S, Shi X, Suarez CJ;		
XX			
XX			
DR	WPI; 2004-329368/30.		
XX	P-PsDB; ABM83818.		
PT		New diagnostic and therapeutic polynucleotides and polypeptides, useful	
PT		in diagnosing a condition, disease or disorder associated with human	
PT		molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or	

PT in gene mapping.

PS Claim 1; Page; 190pp; English.

The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dthp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dthp polynucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from www.wipo.int/pct/en/sequences/listing.htm

SQ Sequence 3189 BP; 916 A; 679 C; 665 G; 929 T; 0 U; 0 Other;

Query Match	Score	DB	Length
45.7%	956	13	3189

Best Local Similarity 99.8%; pred. No. 0;
Matches 1056; Conservative 0; Mismatches

Matches 1056; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	ATAGAGAGGTTCTGTATCACTAATATGTCACAGACAGGGACAGGCAAAAGCCATGCGAGAA	60
Db	ATAGAGAGGTTCTGTATCACTAATATGTCACAGACAGGGACAGGCAAAAGCCATGCGAGAA	1712
QY	GAATGTGTAGCAGACGTGTGTACATGTGATTTTCTGCAGATCTTCACTGTATTAGTAA	120
Db	GAATATGTAGCAGACGTGTGTACATGTGATTTTCTGCAGATCTTCACTGTATTAGTAA	231
QY	TCCGATTAAGTATGACTTAAACCCGAAACAGCTCCTCTTGTGTGTGTCTTACACACG	180
Db	TCCGATTAAGTATGACTTAAACCCGAAACAGCTCCTCTTGTGTGTGTCTTACACACG	291
QY	GGACACGGAGACCCACCCGACACAGCCGCGCAAGTTGTTAAGGAAATACAGAACCAAC	240
Db	GGACACGGAGACCCACCCGACACAGCCGCGCAAGTTGTTAAGGAAATACAGAACCAAC	351
QY	CTGCGGGTGAATTTCTTGTCTCACTCGCGGTATGGGTTACTGGGCTCGGTGATTCAGAA	300
Db	CTGCGGGTGAATTTCTTGTCTCACTCGCGGTATGGGTTACTGGGCTCGGTGATTCAGAA	411
QY	TACACCTACTTTTGCATATGAGGAGAAAGATTAATTTGATTAACGATTCGAAGCTTGGAGCC	360
Db	TACACCTACTTTTGCATATGAGGAGAGAAATTAATTTGATTAACGATTCGAAGCTTGGAGCC	471
QY	CGGATTTCTATATGACATGAGATGTGACTGTATGAGTTTGAACCTTGCGTGTAG	420
Db	CGGATTTCTATATGACATGAGATGTGACTGTATGAGTTTGAACCTTGCGTGTAG	531
QY	CCGTGATTTCTGAACTGTGCGCAGCCCTCAAAAAGCAATTTAGGTCAAGCAGAGACAA	480
Db	CCGTGATTTCTGAACTGTGCGCAGCCCTCAAAAAGCAATTTAGGTCAAGCAGAGACAA	591
QY	GAGAGATTAAGTGGCCACATCCCGGTGGCATCACTGCATCTTCAAGCAGACACTTGTG	651
Db	GAGAGATTAAGTGGCCACATCCCGGTGGCATCACTGCATCTTCAAGCAGACACTTGTG	761
QY	AAAGTCAGAGCTGTACACATGTGAATCTCAAGGTGAGGCTTCTGAGTTGAGATTCAGGA	600
Db	AAAGTCAGAGCTGTACACATGTGAATCTCAAGGTGAGGCTTCTGAGTTGAGATTCAGGA	711
QY	AGAAAGATTCGAGGTTTGAAGCAAAATGACGTGACAGCAACAAATCCATGTTGTA	660
Db	AGAAAGATTCGAGGTTTGAAGCAAAATGACGTGACAGCAACAAATCCATGTTGTA	771
QY	ATTGAGACTTTGATCTCACTTACCCGTTGGGTACCCCACTTCAACAGCTCTGTG	720

Db	772	ATTGAAGACTTGTAGTCTCACTTACCCGGTGGTACCCCCCACTCTCAAGACCTCTCTG	831
Qy	721	AATTTCTCTGTTTACCCCCAGAAATATTTACAGGTACATCTGCAGAGATCTCTTGGCAG	780
Db	832	AATTTCTCTGTTTACCCCAAGATATTTACAGGTACATCTGCAGAGATCTCTTGGCCAG	891
Qy	781	GAGGAAGCCAGATCTGTGACTTTCAGAGATCAGTTTTCAGAGCCAAATTTCAGAG	840
Db	892	GAGGAAGCCAGATCTGTGACTTTCAGAGATCAGTTTTCAGAGCCAAATTTCAGAG	951
Qy	841	GCAGTTCAACTTACTACGATGATGACATTAACCACTCTGCTGTGATTTGACATTT	900
Db	952	GCAGTTCAACTTACTACGATGATGACATTAACCACTCTGCTGTGATTTGACATTT	1011
Qy	901	TCAAAATACAGCTTTTCTATACGCTCGAGATGCTTACGCGTATCTGCTTAAACGT	960
Db	1012	TCAAAATACAGCTTTTCTATACGCTCGAGATGCTTACGCGTATCTGCTTAAACGT	1071
Qy	961	GATTCTGAGGTACAAAGCTTACTCCAAAGACTGACGCTTGAAGTAAAGAGACACTGC	1020
Db	1072	GATTCTGAGGTACAAAGCTTACTCCAAAGACTGACGCTTGAAGTAAAGAGACACTGC	1131
Qy	1021	GTCTCTTTGAAAATTAAGGACGACACAAAGAGAAGG	1058
Db	1132	GTCTCTTTGAAAATTAAGGACGACACAAAGAGAAGG	1169

RESULT 14

ID ADQ39029 standard; DNA; 3256 BP

AC ADQ39029

DT 18-NOV-2004 (first entry)

DE Human SNP containing myocardial infarction-associated gene, SEQ ID 692.

KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;

XX

XX 5

XX

XX

XX

PR 10-MAR-2003; 2003US-0453135P

PR 23-SEP-2003; 2003US-0504955P

PA (APPL-) APPLERA CORP.

PI Cargill M, Devlin JJ, Iakubova O;

DR WPI; 2004-533949/51.

XX

PT myocardial infarct

XX

XX

CC has an altered risk for developing myo-

CC the nucleotide sequences given in the

CC further comprises: an isolated nucleic acid molecule comprising at least

CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardant activity.
CC The nucleic acids in the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 3256 BP; 927 A; 691 C; 669 G; 940 T; 0 U; 29 Other;

Query Match 42.8%; Score 896; DB 13; Length 3256;

Best Local Similarity 99.1%; Pred. No. 0;

Matches 1646; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 67 TGTGAGCAAGCTGTGATCATGATTTTCTGACAGATCTTCACTGATATGATCCGAT 126
DB 160 TGTGAGCAAGCTGTGATCATGATTTTCTGACAGATCTTCACTGATATGATCCGAT 219
QY 127 AAGTATGACCTAAACACCGAAACAGCTCTCTTGTGTGTGTTTTCACAGGCGAC 186
DB 220 AAGTATGACCTAAACACCGAAACAGCTCTCTTGTGTGTGTTTTCACAGGCGAC 279
QY 187 GAGAGCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACATCCG 246
DB 280 GAGAGCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACATCCG 339
QY 247 GTTGATTTCTTGTCTCACTGCGGTATGGTTACTGCGTCTCGGTATTCAGATACCC 306
DB 340 GTTGATTTCTTGTCTCACTGCGGTATGGTTACTGCGTCTCGGTATTCAGATACCC 399
QY 307 TACTTTTGCATGGGGGGAAGATATGATTAACGACTTCAAGAGCTTGAAGCCCGCAT 366
DB 400 TACTTTTGCATGGGGGGAAGATATGATTAACGACTTCAAGAGCTTGAAGCCCGCAT 459
QY 367 TTCTATGACCTGACATGACATGATGATGATGATTTAGAACTTGTGTGAGCCGTG 426
DB 460 TTCTATGACCTGACATGACATGATGATGATGATTTAGAACTTGTGTGAGCCGTG 519
QY 427 ATTGCTGAGCTGTGCGCAGCCCTCAGAAAGCATTTTGTAGCAAGCAGAGCAAGAG 486
DB 520 ATTGCTGAGCTGTGCGCAGCCCTCAGAAAGCATTTTGTAGCAAGCAGAGCAAGAG 579
QY 487 ATAAGTGGCGCATCTCCGGTGGCATCACTGCACTCTTGAAGAGACCTTGTGAAGTCA 546
DB 580 ATAAGTGGCGCATCTCCGGTGGCATCACTGCACTCTTGAAGAGACCTTGTGAAGTCA 639
QY 547 GAGCTGTACACATGATGATCAAGTGGAGCTTGTGATTCATGATTCAGGAAGAAG 606
DB 640 GAGCTGTACACATGATGATCAAGTGGAGCTTGTGATTCATGATTCAGGAAGAAG 699
QY 607 GATTTGAGGTTTGAAGCAAAATGACGTAAACAGCAACCAATCCAATGTTGTAATGAA 666
DB 700 GATTTGAGGTTTGAAGCAAAATGACGTAAACAGCAACCAATCCAATGTTGTAATGAA 759
QY 667 GACTTTGAGTCTCATCTTACCGTTGGATACCCCACTCTCAAGCCTCTGTAATATT 726
DB 760 GACTTTGAGTCTCATCTTACCGTTGGATACCCCACTCTCAAGCCTCTGTAATATT 819
QY 727 CTTGTTTACCCCGAATATTTTACAGTACATTCGAGAGAGTCTCTTGGCCAGAGAGAA 786

DB 820 CTTGTTTACCCCGAATATTTTACAGTACATTCGAGAGAGTCTCTTGGCCAGAGAGAA 879
QY 787 AGCCAAATATCTGTGACTTCAAGCATTCAGATTTTCAAGTGGCAATTTCAAGAGCAT 846
DB 880 AGCCAAATATCTGTGACTTCAAGCATTCAGATTTTCAAGTGGCAATTTCAAGAGCAT 939
QY 847 CAATTTACTACGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 906
DB 940 CAATTTACTACGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 999
QY 907 ACAGATTTTCTATGAGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 966
DB 1000 ACAGATTTTCTATGAGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 1059
QY 967 GAGTTCACAAAGCTTCTCAAGATGATGATGATGATGATGATGATGATGATGATGAT 1026
DB 1060 GAGTTCACAAAGCTTCTCAAGATGATGATGATGATGATGATGATGATGATGATGAT 1119
QY 1027 TTGAAATATTAAGGACACCAAGAAAGAGGATGATGATGATGATGATGATGATGAT 1086
DB 1120 TTGAAATATTAAGGACACCAAGAAAGAGGATGATGATGATGATGATGATGATGAT 1179
QY 1087 GATGTTTCTCTCAAGTTCATTTTACCTGATGATGATGATGATGATGATGATGATGAT 1146
DB 1180 GATGTTTCTCTCAAGTTCATTTTACCTGATGATGATGATGATGATGATGATGATGAT 1239
QY 1147 GATTTTTCAGAGCCCTTGTGACATTAACAGTACAGTGTGAAAGGCGAGGCTACAG 1206
DB 1240 GATTTTTCAGAGCCCTTGTGACATTAACAGTACAGTGTGAAAGGCGAGGCTACAG 1299
QY 1207 GAGCTGTGACATTAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1266
DB 1300 GAGCTGTGACATTAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1359
QY 1267 TGTGTTGATGATCTCTCTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1326
DB 1360 TGTGTTGATGATCTCTCTCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1419
QY 1327 GAAATCTTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1386
DB 1420 GAAATCTTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1479
QY 1387 CAGGAAAGCTCATTTTGTCTTCAATTTGAGATTTTGTCTTCACTGACCAACAGAG 1446
DB 1480 CAGGAAAGCTCATTTTGTCTTCAATTTGAGATTTTGTCTTCACTGACCAACAGAG 1539
QY 1447 GTTCTGCGAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1506
DB 1540 GTTCTGCGAAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1599
QY 1507 CCAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1566
DB 1600 CCAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1659
QY 1567 TCTCTCTGAAACCAATTTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1626
DB 1660 TCTCTCTGAAACCAATTTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 1719
QY 1627 GTGAGTTCAGAAACCGGATAGCCGTTTATTTGAGTTCATCAATAGAGAAATTC 1686
DB 1720 GTGAGTTCAGAAACCGGATAGCCGTTTATTTGAGTTCATCAATAGAGAAATTC 1779
QY 1687 CAAGAACCAACCCAGATGAAATTTTGAAGCAATGTGTT 1727
DB 1780 CAAGAACCAACCCAGATGAAATTTTGAAGCAATGTGTT 1820

RESULT 15
ADQ39030
ID ADQ39030 standard; DNA; 3274 BP.
XX
XX ADQ39030;
XX

DT 18-NOV-2004 (first entry)
XX Human SNP containing myocardial infarction-associated gene, SEQ ID 693.
DE Myocardial infarction; detection; single nucleotide polymorphism; SNP;
XX cardiant; gene therapy; human; gene; ds.
KW
XX Homo sapiens.
OS
XX MO2004058052-A2.
FN
XX 15-JUL-2004.
XX
XX 22-DEC-2003; 2003WO-US040978.
XX
XX 20-DEC-2002; 2002US-0434778P.
XX 10-MAR-2003; 2003US-0453135P.
XX 30-APR-2003; 2003US-0466412P.
XX 23-SEP-2003; 2003US-0504955P.
XX
XX (APPL-) APPLERA CORP.
PI Cargill M, Devlin JJ, Iakubova O;
XX
XX WPI; 2004-533949/51.
DR P-PSDB; ADQ39858.
XX
XX Identifying an individual who has an altered risk for developing
PT myocardial infarction by detecting a single nucleotide polymorphism in
PT the individual's nucleic acids.
XX
XX Claim 7; SEQ ID NO 693; 145pp; English.
XX
XX The invention relates to a novel method for identifying an individual who
CC has an altered risk for developing myocardial infarction. The method
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
CC the nucleotide sequences given in the specification in the individual's
CC nucleic acids, where the presence of the SNP is correlated with an
CC altered risk for myocardial infarction in the individual. The invention
CC further comprises: an isolated nucleic acid molecule comprising at least
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.
XX
SO Sequence 3274 BP; 932 A; 694 C; 672 G; 946 T; 0 U; 30 Other;

Query Match 42.8%; Score 896; DB 13; Length 3274;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1646; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 67 TGTGACCAAGCTGTGTGACATGATTTTGTGACAGATCTTACATGTAATGTAATCCGAT 126
DB 178 TGTGACCAAGCTGTGTGACATGATTTTGTGACAGATCTTACATGTAATGTAATCCGAT 237
QY 127 AAGTATGACCTTAATAAACCGAAGCAGCTCTCTGTGTGTGTGTGTCTACACGGGACCC 186
|||||

DB 238 AAGTATGACCTTAATAAACCGAAGCAGCTCTCTGTGTGTGTGTGTCTACACGGGACCC 297
QY 187 GGAAGACCCACCCGACACAGCCCGCAGTTTGTAAAGAAATACAGAACCAACACTGCGG 246
DB 298 GGAAGACCCACCCGACACAGCCCGCAGTTTGTAAAGAAATACAGAACCAACACTGCGG 357
QY 247 GTTGAATTTCTTTGTCTACCTGCGGTATGGGTACTGCGGTCTGCGTATTCAGAAATACAC 306
DB 358 GTTGAATTTCTTTGTCTACCTGCGGTATGGGTACTGCGGTCTGCGTATTCAGAAATACAC 417
QY 307 TACTTTTGCAATGAGGGGGAGAAATATGATTAACAACATTCAAGAGCTTGAAGCCGCAAT 366
DB 418 TACTTTTGCAATGAGGGGGAGAAATATGATTAACAACATTCAAGAGCTTGAAGCCGCAAT 477
QY 367 TTCTATGACATGACATGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426
DB 478 TTCTATGACATGACATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 537
QY 427 ATTGCTGACCTGTGCGCAGCCCTCAGAAAGCATTTTATGATCAAGACAGAGAGAGAG 486
DB 538 ATTGCTGACCTGTGCGCAGCCCTCAGAAAGCATTTTATGATCAAGACAGAGAGAGAGAG 597
QY 487 ATTAAGTGGCGACCTCCGCTGATCATCTGATCTTGAAGACAGACATCTTGAAGTCA 546
DB 598 ATTAAGTGGCGACCTCCGCTGATCATCTGATCTTGAAGACAGACATCTTGAAGTCA 657
QY 547 GAGCTGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 606
DB 658 GAGCTGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 717
QY 607 GATTCGAGTTTGTGAAGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
DB 718 GATTCGAGTTTGTGAAGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 777
QY 667 GACTTGAAGTCTCACTTACCCGCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 726
DB 778 GACTTGAAGTCTCACTTACCCGCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 837
QY 727 CCTGTTTACCCCGCAAAATTTTACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 786
DB 838 CCTGTTTACCCCGCAAAATTTTACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 897
QY 787 AGCAAGTATCTGTGATCTCAGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 846
DB 898 AGCAAGTATCTGTGATCTCAGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 957
QY 847 CAATCTACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 906
DB 958 CAATCTACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1017
QY 907 ACAAGCTTTTCTATCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 966
DB 1018 ACAAGCTTTTCTATCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1077
QY 967 GAGGTACAAAGCTCTCAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1026
DB 1078 GAGGTACAAAGCTCTCAAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1137
QY 1027 TTGAAATATTAAGGACAGACAAAGAAAGAGTACTTACCCAGATATATCTGCGG 1086
DB 1138 TTGAAATATTAAGGACAGACAAAGAAAGAGTACTTACCCAGATATATCTGCGG 1197
QY 1087 GGAATGTTCTCTCAGTTCATTTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1146
DB 1198 GGAATGTTCTCTCAGTTCATTTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1257
QY 1147 GCAATTTTTCGAGCCCTTGTGACATATACAGTACAGTGTGATGATGATGATGATGATGATGATGAT 1206
DB 1258 GCAATTTTTCGAGCCCTTGTGACATATACAGTACAGTGTGATGATGATGATGATGATGATGATGAT 1317
QY 1207 GAGCTGTGACATTAACAAAGGAGGACCGGATTAAGCCGCTTTGTATGAGATGCTGTGCTC 1266
DB 1318 GAGCTGTGACATTAACAAAGGAGGACCGGATTAAGCCGCTTTGTATGAGATGCTGTGCTC 1377
|||||

QY	1267	TGCTGTGGATCTCCCTCGGCTTCCCTCTTGCCAGGCAACAATCAGCTCTGCTC	1326
Db	1378	TGCTGTGGATCTCCCTCGGCTTCCCTCTTGCCAGGCAACAATCAGCTCTGCTC	1437
QY	1327	GAACATCTTCTTAAACTTCAACCCAGACCATATTCGTGTGAAGCTCAAGTTATTTTAC	1386
Db	1438	GAACATCTTCTTAAACTTCAACCCAGACCATATTCGTGTGAAGCTCAAGTTATTTTAC	1497
QY	1387	CCAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACTGTGCACAACAGAG	1446
Db	1498	CCAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACTGTGCACAACAGAG	1557
QY	1447	GTTCTGCGGAAGGAGATGTATACAGGGCTGGGCTTGTGGTGGCTTCAGTCTTCAG	1506
Db	1558	GTTCTGCGGAAGGAGATGTATACAGGGCTGGGCTTGTGGTGGCTTCAGTCTTCAG	1617
QY	1507	CCAAACATATCATGCAATGCCATGAAAGACGCGGAAAGCCCTGGCTCCTAAGATATTCATC	1566
Db	1618	CCAAACATATCATGCAATGCCATGAAAGACGCGGAAAGCCCTGGCTCCTAAGATATTCATC	1677
QY	1567	TCTCTCGAACAACAAATTTCTTTCACATTCACATGACGCCCTCAATCCCATATATG	1626
Db	1678	TCTCTCGAACAACAAATTTCTTTCACATTCACATGACGCCCTCAATCCCATATATG	1737
QY	1627	GTGGGTCAGGAACCGGCGATAGCCCCGTTTATTTGGTTCCTAACAATAGAGAACTC	1686
Db	1738	GTGGGTCAGGAACCGGCGATAGCCCCGTTTATTTGGTTCCTAACAATAGAGAACTC	1797
QY	1687	CAAGAACAAACCCAGATGAAATTTTGGACCAATATGCTT	1727
Db	1798	CAAGAACAAACCCAGATGAAATTTTGGACCAATATGCTT	1838

Search completed: August 27, 2005, 01:18:41
Job time : 737.44 secs

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OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 23:30:25 ; Search time 235.42 Seconds
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14554.251 Million cell updates/sec

Title: US-09-371-347a-45

Perfect score: 2094

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Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*

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- 6: /cgn2_6/prodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1854	88.5	3259	3 US-09-318-448-23	Sequence 23, Appl
2	1701	81.2	3242	4 US-09-949-016-4215	Sequence 4215, Ap
3	386	18.4	390	3 US-08-905-223-71	Sequence 71, Appl
4	330	15.8	601	4 US-09-949-016-150019	Sequence 150019, A
5	330	15.8	35916	4 US-09-949-016-15957	Sequence 15957, A
6	279	13.3	601	4 US-09-949-016-150020	Sequence 150020, A
7	189	9.0	601	4 US-09-949-016-150037	Sequence 150037, A
8	158	7.5	2475	4 US-09-566-921-88	Sequence 88, Appl
9	155	7.4	601	4 US-09-949-016-150030	Sequence 150030, A
10	145	6.9	601	4 US-09-949-016-150031	Sequence 150031, A
11	137	6.5	601	4 US-09-949-016-150046	Sequence 150046, A
12	137	6.5	601	4 US-09-949-016-150047	Sequence 150047, A
13	125	6.0	601	4 US-09-949-016-150029	Sequence 150029, A
14	121	5.8	601	4 US-09-949-016-150041	Sequence 150041, A
15	121	5.8	601	4 US-09-949-016-150042	Sequence 150042, A
16	119	5.7	601	4 US-09-949-016-150008	Sequence 150008, A
17	119	5.7	601	4 US-09-949-016-150055	Sequence 150055, A
18	110	5.3	601	4 US-09-949-016-150048	Sequence 150048, A
19	94	4.5	601	4 US-09-949-016-150032	Sequence 150032, A
20	78	3.7	244	4 US-09-471-276-495	Sequence 495, Appl
21	78	3.7	601	4 US-09-949-016-150007	Sequence 150007, A
22	76	3.6	601	4 US-09-949-016-150018	Sequence 150018, A
23	30	1.4	1681	4 US-09-023-655-453	Sequence 453, Appl
24	20	1.0	273	4 US-09-513-999C-14761	Sequence 14761, A
25	20	1.0	440	3 US-09-397-787-305	Sequence 305, Appl
26	20	1.0	444	4 US-09-621-976-14139	Sequence 14139, A
27	20	1.0	445	3 US-09-397-787-274	Sequence 274, Appl

c 28	20	1.0	174259	4 US-09-949-016-11968	Sequence 11968, A
c 29	20	1.0	174262	4 US-09-949-016-14259	Sequence 14259, A
c 30	19	0.9	169	1 US-08-166-346A-8	Sequence 8, Appl
c 31	19	0.9	459	4 US-09-621-976-8324	Sequence 8324, Ap
c 32	19	0.9	3969	3 US-09-518-386B-4	Sequence 4, Appl
c 33	19	0.9	4396	3 US-09-821-736-1	Sequence 1, Appl
c 34	19	0.9	14721	4 US-09-949-016-13507	Sequence 13507, A
c 35	19	0.9	25199	4 US-09-949-016-13361	Sequence 13361, A
c 36	19	0.9	129658	4 US-09-949-016-17195	Sequence 17195, A
c 37	19	0.9	186734	4 US-09-949-016-14870	Sequence 14870, A
c 38	19	0.9	193689	4 US-09-949-016-12350	Sequence 12350, A
c 39	19	0.9	193689	4 US-09-949-016-13088	Sequence 13088, A
c 40	19	0.9	200663	4 US-09-949-016-12569	Sequence 12569, A
c 41	19	0.9	203093	4 US-09-949-016-14445	Sequence 14445, A
c 42	18	0.9	78	2 US-08-749-852-56	Sequence 56, Appl
c 43	18	0.9	78	2 US-08-749-852-58	Sequence 58, Appl
c 44	18	0.9	511	4 US-09-902-540-1374	Sequence 1374, Ap
c 45	18	0.9	531	4 US-09-252-991A-2223	Sequence 2223, Ap

ALIGNMENTS

RESULT 1					
US-09-318-448-23					
Sequence 23, Application US/09318448					
Patent No. 6210950					
GENERAL INFORMATION:					
APPLICANT: Johnson, William G.					
APPLICANT: Steenroos, Edward S.					
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING					
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS					
FILE REFERENCE: 601-1-057					
CURRENT APPLICATION NUMBER: US/09/318,448					
CURRENT FILING DATE: 1999-05-25					
NUMBER OF SEQ ID NOS: 46					
SOFTWARE: PatentIn Ver. 2.0					
SEQ ID NO 23					
LENGTH: 3259					
TYPE: DNA					
ORGANISM: Homo sapiens					
US-09-318-448-23					
Query Match					
Best Local Similarity 99.9%; Pred. No. 0;					
Matches 2094; Conservative 0; Mismatches 0; Indels 3; Gaps 1;					
QY	1	ATGAGGAGGTTCTGTACTATATGCTACACAGGAGGAGCAAGGCCATCGCAGAA	60		
DB	80	ATGAGGAGGTTCTGTACTATATGCTACACAGGAGGAGCAAGGCCATCGCAGAA	139		
QY	61	GAATGTGTGACCAAGCTGTGTACATGATTTTCTGCAGATCTTCACTGTATTAGTAA	120		
DB	140	GAATGTGTGACCAAGCTGTGTACATGATTTTCTGCAGATCTTCACTGTATTAGTAA	199		
QY	121	TCCGATAGTATGACTTAAACCGAAACAGCTCTTGTGTGTGTCTTCTCCAG	180		
DB	200	TCCGATAGTATGACTTAAACCGAAACAGCTCTTGTGTGTGTCTTCTCCAG	259		
QY	181	GGCAGCGAGACCCACCGACAGCCCGCAGTTGTTAAGAAATACAGAACCAACA	240		
DB	260	GGCAGCGAGACCCACCGACAGCCCGCAGTTGTTAAGAAATACAGAACCAACA	319		
QY	241	CTGCGGTGATTTCTTCTCACTGCGGTATGGTTACTGCGTCTCGGTATTCAGAA	300		
DB	320	CTGCGGTGATTTCTTCTCACTGCGGTATGGTTACTGCGTCTCGGTATTCAGAA	379		
QY	301	TACACTACTTTTGAATGGGGGAATTAATGATTAACGACTTCAAGAGCTGGAGCC	360		
DB	380	TACACTACTTTTGAATGGGGGAATTAATGATTAACGACTTCAAGAGCTGGAGCC	439		
QY	361	CGGCAATTTCTATGACACTGACATGACATGATGATGATTTAGAACTTGTGTAG	420		

Db	440	CGCGATTTCTATGACACTGCGACATGCGAGANTGACTGTGAGGTTTAAACAATTGTGTTGAG	499
Qy	421	CCGTGGAATGTGGAGCTCTGTGGCCGAGCCCTCAGAAAGCATTTTAAAGTCAAGCAGAGCA	480
Db	500	CCGTGGAATGTGGAGCTCTGTGGCCGAGCCCTCAGAAAGCATTTTAAAGTCAAGCAGAGCA	559
Qy	481	GAGGAGATTAAGTGGCGGACTCCGGGTGGCACTGATGATCTCTTGAAGACAGACCTTGTG	540
Db	560	GAGGAGATTAAGTGGCGGACTCCGGGTGGCACTGATGATCTCTTGAAGACAGACCTTGTG	619
Qy	541	AAGTCAGAGCTGTCAACATTTGAATCTCAAGTCAGCTTCTGAGATTCGATGATTCAGGA	600
Db	620	AAGTCAGAGCTGTCAACATTTGAATCTCAAGTCAGCTTCTGAGATTCGATGATTCAGGA	679
Qy	601	AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCATGTTGTGA	660
Db	680	AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCATGTTGTGA	739
Qy	661	ATTGAAGCTTTGAGTCCCTCACTTACCCGTTGGGATCCCGCACTCAAGACCTCTCTG	720
Db	740	ATTGAAGCTTTGAGTCCCTCACTTACCCGTTGGGATCCCGCACTCAAGACCTCTCTG	799
Qy	721	AATATTCCTGGTTTACCCCGAGAAATATTGAAGGTACATCTGCAAGAGTCTTGTGGCAG	780
Db	800	AATATTCCTGGTTTACCCCGAGAAATATTGAAGGTACATCTGCAAGAGTCTTGTGGCAG	859
Qy	781	GAGAAAGCCAAAGTACTGTGACTTCAGCAGATCCAGTTTTCAGATGCCAATTTCAAAG	840
Db	860	GAGAAAGCCAAAGTACTGTGACTTCAGCAGATCCAGTTTTCAGATGCCAATTTCAAAG	919
Qy	841	GCAGTTCAACTTACAGAAATGATGCCATATAAACCACTCTGCTGTGTGAATTTGGAATT	900
Db	920	GCAGTTCAACTTACAGAAATGATGCCATATAAACCACTCTGCTGTGTGAATTTGGAATT	979
Qy	901	TCAATAACAGACTTTTCCCTATCAGGCTGAGATGCTTCAGGCGATCTGCTCAACAGT	960
Db	980	TCAATAACAGACTTTTCCCTATCAGGCTGAGATGCTTCAGGCGATCTGCTCAACAGT	1039
Qy	961	GATTCTGAGTACAAAGCTTACTCCAAAGACTGACGACTTGAAGATTAAGAGAGCACTGC	1020
Db	1040	GATTCTGAGTACAAAGCTTACTCCAAAGACTGACGACTTGAAGATTAAGAGAGCACTGC	1099
Qy	1021	GTCCTTTTGAATAATTAAGGAGACACAAAGAAAGAGAGCTACTTATCCCGACATATA	1080
Db	1100	GTCCTTTTGAATAATTAAGGAGACACAAAGAAAGAGAGCTACTTATCCCGACATATA	1159
Qy	1081	CCTGGGGAGATGTTCTCTCAGTTCATTTTACCTGTGTCTTGAATCCGAGCAATTCCT	1140
Db	1160	CCTGGGGAGATGTTCTCTCAGTTCATTTTACCTGTGTGTCTTGAATCCGAGCAATTCCT	1219
Qy	1141	AAAAAGGCAATTTTGTGCGAGCCCTGTGTGACTATACAGTGAACAGTGTGAAGACGACG	1200
Db	1220	AAAAAGGCAATTTTGTGCGAGCCCTGTGTGACTATACAGTGAACAGTGTGAAGACGACG	1279
Qy	1201	CTACAGAGCTGTGCAATTAACAAAGGGGCAAGCCATTATAGCCGTTTGTACAGAGTCC	1260
Db	1280	CTACAGAGCTGTGCAATTAACAAAGGGGCAAGCCATTATAGCCGTTTGTACAGAGTCC	1339
Qy	1261	TGTGCTGTCTGTTGGATCTCTGCTGTGCTTCCCTTGTGCGAGCCACACTAGTCTC	1320
Db	1340	TGTGCTGTCTGTTGGATCTCTGCTGTGCTTCCCTTGTGCGAGCCACACTAGTCTC	1399
Qy	1321	CTGCTCGAATCTTCTCTTAACTTTCACCCAGACCATATTCGTGTGCAAGTCAAGTTTA	1380
Db	1400	CTGCTCGAATCTTCTCTTAACTTTCACCCAGACCATATTCGTGTGCAAGTCAAGTTTA	1459
Qy	1381	TTTCACCCAAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACTGCCACA	1440
Db	1460	TTTCACCCAAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACTGCCACA	1519
Qy	1441	ACAGAGGTTTCCCGAAGAGGAGTATGTACAGGCTGGCGGCTTGTGTTGTTCTCACTT	1500
Db	1520	ACAGAGGTTTCCCGAAGAGGAGTATGTACAGGCTGGCGGCTTGTGTTGTTCTCACTT	1579

[illegible]

Db 80 ATGAGAGGTTTCTGTATATATATGCTACACAGAGGACAGGCAAGGCCATCCGACAA 139
Qy 61 GAAATGTGACCAAGCTGTGTATCAATGATTTTCTGAGATCTTCACTGTATTAATGTA 120
Db 140 GAAATATGTGACCAAGCTGTGTATCAATGATTTTCTGAGATCTTCACTGTATTAATGTA 199
Qy 121 TCCGATTAAGTATGACCTTAATAAACCCGAAACAGCTCTCTGTGTGTGTGTCTACACAG 180
Db 200 TCCGATTAAGTATGACCTTAATAAACCCGAAACAGCTCTCTGTGTGTGTGTCTACACAG 259
Qy 181 GGCACCGAGAGCCCAACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
Db 260 GGCACCGAGAGCCCAACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACA 319
Qy 241 CTGCGCGGTGATTTCTTTTGTCTCACTGCGGTATAGGTTTCTGGGTCTCGGTATTCAGAA 300
Db 320 CTGCGCGGTGATTTCTTTTGTCTCACTGCGGTATAGGTTTCTGGGTCTCGGTATTCAGAA 379
Qy 301 TACACTACTTTTGCATGGGGGGAAGATTAATGATTAACGACTTCAAGAGCTTGAGCC 360
Db 380 TACACTACTTTTGCATGGGGGGAAGATTAATGATTAACGACTTCAAGAGCTTGAGCC 439
Qy 361 CGGCAATTTCTATGACATGAGACATGAGATGACTGTAGGTTTGAACCTTGTGTAG 420
Db 440 CGGCAATTTCTATGACATGAGACATGAGATGACTGTAGGTTTGAACCTTGTGTAG 499
Qy 421 CCGTGATTTGCTGAGATCTGCGGCAAGCCCTCAGAAAGATTTTATGCTCAGAGAGACAA 480
Db 500 CCGTGATTTGCTGAGATCTGCGGCAAGCCCTCAGAAAGATTTTATGCTCAGAGAGACAA 559
Qy 481 GAGAGATTAAGTGTGAGCACTCCCGGTGAGATCACTGCAATCTTGAGAGACAGCTTGTG 540
Db 560 GAGAGATTAAGTGTGAGCACTCCCGGTGAGATCACTGCAATCTTGAGAGAGACAGCTTGTG 619
Qy 541 AAGTCAGAGCTGCTACATGATTAATCTCAAGTCGACCTTCTGAGATTCAGATTCAGGA 600
Db 620 AAGTCAGAGCTGCTACATGATTAATCTCAAGTCGACCTTCTGAGATTCAGATTCAGGA 679
Qy 601 AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCAAATGTTGA 660
Db 680 AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCAAATGTTGA 739
Qy 661 ATTGAAGCTTTGAGGCTCACTTACCCGTTGGGTACCCCACTCTCAGAAAGCTCTCTG 720
Db 740 ATTGAAGCTTTGAGGCTCACTTACCCGTTGGGTACCCCACTCTCAGAAAGCTCTCTG 799
Qy 721 AATATTTCTGTGTTTACCCCAAGATATTTTACAGGTATCATCTGAGAGATCTTGTGCGCAG 780
Db 800 AATATTTCTGTGTTTACCCCAAGATATTTTACAGGTATCATCTGAGAGATCTTGTGCGCAG 859
Qy 781 GAGGAAAGCCAGATATCTGTGATCTCAGAGATCCAGTTTTCAGTCCCAATTTCAAG 840
Db 860 GAGGAAAGCCAGATATCTGTGATCTCAGAGATCCAGTTTTCAGTCCCAATTTCAAG 919
Qy 841 GAGGTTCAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 920 GAGGTTCAACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 979
Qy 901 TCAATATCAGACTTTTCTATCAGCTTGAGATGCTTCAAGCTGTCTGCTTCAAGAT 960
Db 980 TCAATATCAGACTTTTCTATCAGCTTGAGATGCTTCAAGCTGTCTGCTTCAAGAT 1039
Qy 961 GATTCTGAGTACAAAGCTTATCTCAAAAGCTGAGTGTGAAGTAAAGAGAGAGCTGC 1020
Db 1040 GATTCTGAGTACAAAGCTTATCTCAAAAGCTGAGTGTGAAGTAAAGAGAGAGAGCTGC 1099
Qy 1021 GTCTTTTGAATTAAGGACACAAAGAAAGAAAGAGCTTACCCCGACATAT 1080
Db 1100 GTCTTTTGAATTAAGGACACAAAGAAAGAAAGAGCTTACCCCGACATAT 1159
Qy 1081 CCGTGGGAGATGTTCTCTCCAGTTCAATTTTACCTGTGTCTTGAATTCGAGCAATTCCT 1140
Db 1160 CCGTGGGAGATGTTCTCTCCAGTTCAATTTTACCTGTGTCTTGAATTCGAGCAATTCCT 1219

Qy 1141 AAAAGCATTTTTCGAGCCCTTGTGACTATACAGTGAACAGTGTGAAGGCGAG 1200
Db 1220 AAAAGCATTTTTCGAGCCCTTGTGACTATACAGTGAACAGTGTGAAGGCGAG 1279
Qy 1201 CTACAGAGCTGTGAGTAAACAGAGGCGAGCGATTAATAGCCGTTTGTACAGATGCC 1260
Db 1280 CTACAGAGCTGTGAGTAAACAGAGGCGAGCGATTAATAGCCGTTTGTACAGATGCC 1339
Qy 1261 TGTGCTGTGTGTGATCTCTCTGCTTTCCTTCTGAGAGCCAGCTCAGTCTC 1320
Db 1340 TGTGCTGTGTGTGATCTCTCTGCTTTCCTTCTGAGAGCCAGCTCAGTCTC 1399
Qy 1321 CTGCTGAAACCTTCTTAACTTCAACCCAGACCAATTAATGCTGTGACAGCTCAAGTTTA 1380
Db 1400 CTGCTGAAACCTTCTTAACTTCAACCCAGACCAATTAATGCTGTGACAGCTCAAGTTTA 1459
Qy 1381 TTTCAACCCAGAAAGCTCAATTTTGTCTTCAATTTGTGAAATTTCTGTACTGACCA 1440
Db 1460 TTTCAACCCAGAAAGCTCAATTTTGTCTTCAATTTGTGAAATTTCTGTACTGACCA 1519
Qy 1441 ACAGAGTTCTGCGGAGAGGATATGTAAGGCTGTGCTGTGTGTGTGTGTGTGTGTGT 1500
Db 1520 ACAGAGTTCTGCGGAGAGGATATGTAAGGCTGTGCTGTGTGTGTGTGTGTGTGTGT 1579
Qy 1501 CTTGAGCCAAACATCATGATCCCATGAAAGACAGCGGAAAGCCCTGCTCTTAAGATA 1560
Db 1580 CTTGAGCCAAACATCATGATCCCATGAAAGACAGCGGAAAGCCCTGCTCTTAAGATA 1639
Qy 1561 TCCATCTCTCTGAAACCAAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
Db 1640 TCCATCTCTCTGAAACCAAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1699
Qy 1621 ATATATGTGTGTGTGAGAACCGGCAATGCGGTTTATGTGTGTGTGTGTGTGTGTGT 1680
Db 1700 ATATATGTGTGTGTGAGAACCGGCAATGCGGTTTATGTGTGTGTGTGTGTGTGTGT 1759
Qy 1681 AAATCCCAAGAACCAACCCAGATGAAATTTTGTGAGCAATGTG--GTTTTTGGCTGC 1737
Db 1760 AAATCCCAAGAACCAACCCAGATGAAATTTTGTGAGCAATGTG--GTTTTTGGCTGC 1819
Qy 1738 AGCATTAAGATAGGATTAATCTATTCAGAAAGAGCTCAGACATTTCTTAAAGATGG 1797
Db 1820 AGCATTAAGATAGGATTAATCTATTCAGAAAGAGCTCAGACATTTCTTAAAGATGG 1879
Qy 1798 ATCTTAATCTATTAAGGTTTCTTCTGAGAGATGCTCTGTTGGGAGAGAGAGCC 1857
Db 1880 ATCTTAATCTATTAAGGTTTCTTCTGAGAGATGCTCTGTTGGGAGAGAGAGCC 1939
Qy 1858 CCAGCAAGATATGTAAGAGAACCATCCAGCTTCAATGCGCAGAGGTGCGAGATCTCTC 1917
Db 1940 CCAGCAAGATATGTAAGAGAACCATCCAGCTTCAATGCGCAGAGGTGCGAGATCTCTC 1999
Qy 1918 CTCAGAGAGAACGGCATATTAATGATGTGTGTGAGATGCAAGAAATATGCGCAAGATGTA 1977
Db 2000 CTCAGAGAGAACGGCATATTAATGATGTGTGTGAGATGCAAGAAATATGCGCAAGATGTA 2059
Qy 1978 CATGATGCCCTTGTGCAATTAATAGCAAAAGGTTGAGATTGAAAATCTAAGCAATG 2037
Db 2060 CATGATGCCCTTGTGCAATTAATAGCAAAAGGTTGAGATTGAAAATCTAAGCAATG 2119
Qy 2038 AAAACCTGCGCACTTTTAAAGAAAGAAAGGCTACCTTCAAGATTTTGTGATTA 2094
Db 2120 AAAACCTGCGCACTTTTAAAGAAAGAAAGGCTACCTTCAAGATTTTGTGATTA 2176

RESULT 3
US-08-905-223-71
; Sequence 71, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclercq, Aymeric

```

1  APPLICANT: Lacroix, Bruno
2  NUMBER OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
3  NUMBER OF SEQUENCES: 503
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Knobbe, Martens, Olson & Bear
6  STREET: 501 West Broadway
7  CITY: San Diego
8  STATE: California
9  COUNTRY: USA
10 ZIP: 92101-3505
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Floppy disk
13 COMPUTER: IBM PC compatible
14 OPERATING SYSTEM: Win95
15 SOFTWARE: Word
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/08/905,223
18 FILING DATE:
19 CLASSIFICATION: 536
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Israelsen, Ned A.
22 REGISTRATION NUMBER: 29,655
23 REFERENCE/DOCKET NUMBER:
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (619) 235-8550
26 TELEFAX: (619) 235-0176
27 INFORMATION FOR SEQ ID NO: 71:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 390 base pairs
30 TYPE: NUCLEIC ACID
31 STRANDEDNESS: DOUBLE
32 TOPOLOGY: LINEAR
33 MOLECULE TYPE: CDNA
34 ORIGINAL SOURCE:
35 ORGANISM: Homo Sapiens
36 TISSUE TYPE: Brain
37 FEATURE:
38 NAME/KEY: sig_peptide
39 LOCATION: 289-357
40 IDENTIFICATION METHOD: Von Heijne matrix
41 OTHER INFORMATION: score 6.9
42 OTHER INFORMATION: seq SLSLASHSVSC/SN
43 JS-08-905-223-71

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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 15957
LENGTH: 35916
TYPE: DNA
ORGANISM: Human
US-09-949-016-15957

Query Match 15.8%; Score 330; DB 4; Length 35916;
Best Local Similarity 99.7%; Pred. No. 2.4e-159;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 GTTTGAACCTTGCTGTTGAGCCGTGATGCTGGAAGCTGCGCCAGCCCTCAGAAAGCATT 460
DB 10781 GTTTGAACCTTGCTGTTGAGCCGTGATGCTGGAAGCTGCGCCAGCCCTCAGAAAGCATT 10840
QY 461 TTAGGTCAAGCAGAGCAGAGCAGAGATTAAGTGGCCACTCCCGGTGGATCAGCTGCAT 520
DB 10841 TTAGGTCAAGCAGAGCAGAGCAGAGATTAAGTGGCCACTCCCGGTGGATCAGCTGCAT 10900
QY 521 CCTTGAAGCAGACCTTGTGAAGTCAAGCTGCTCAACATGTAATCTCAAGTCAGCTTC 580
DB 10901 CCTTGAAGCAGACCTTGTGAAGTCAAGCTGCTCAACATGTAATCTCAAGTCAGCTTC 10960
QY 581 TGAGATTCATGATTTGAGAAAGAAAGATTTGAGATTTTGAAGAAATGCAAGTAACA 640
DB 10961 TGAGATTCATGATTTGAGAAAGAAAGATTTGAGATTTTGAAGAAATGCAAGTAACA 11020
QY 641 GCAACCAATCCAAATGTTGATTAAGAGCTTGAAGCTTCACTTACCCGTCGGTACCC 700
DB 11021 GCAACCAATCCAAATGTTGATTAAGAGCTTGAAGCTTCACTTACCCGTCGGTACCC 11080
QY 701 CACTCTCAAGCCTCTCTGATATATTCCTGTTTACCCCGCAATATTTACAGATACATC 760
DB 11081 CACTCTCAAGCCTCTCTGATATATTCCTGTTTACCCCGCAATATTTACAGATACATC 11140
QY 761 TGCAGAGTCTCTTGGCCAGG 781
DB 11141 TGCAGAGTCTCTTGGCCAGG 11161

RESULT 6

US-09-949-016-150020
Sequence 150020, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 150020
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-150020

Query Match 13.3%; Score 279; DB 4; Length 601;

Best Local Similarity 99.5%; Pred. No. 3.7e-133;
Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTTGAACCTTGCTGTTGAGCCGTGATGCTGGAAGCTGCGCCAGCCCTCAGAAAGCATT 460
DB 165 GTTTGAACCTTGCTGTTGAGCCGTGATGCTGGAAGCTGCGCCAGCCCTCAGAAAGCATT 224
QY 461 TTAGGTCAAGCAGAGCAGAGCAGAGATTAAGTGGCCACTCCCGGTGGATCAGCTGCAT 520
DB 225 TTAGGTCAAGCAGAGCAGAGCAGAGATTAAGTGGCCACTCCCGGTGGATCAGCTGCAT 284
QY 521 CCTTGAAGCAGACCTTGTGAAGTCAAGCTGCTCAACATGTAATCTCAAGTCAGCTTC 580
DB 285 CCTTGAAGCAGACCTTGTGAAGTCAAGCTGCTCAACATGTAATCTCAAGTCAGCTTC 344
QY 581 TGAGATTCATGATTTGAGAAAGAAAGATTTGAGATTTTGAAGAAATGCAAGTAACA 640
DB 345 TGAGATTCATGATTTGAGAAAGAAAGATTTGAGATTTTGAAGAAATGCAAGTAACA 404
QY 641 GCAACCAATCCAAATGTTGATTAAGAGCTTGAAGCTTCACTTACCCGTCGGTACCC 700
DB 405 GCAACCAATCCAAATGTTGATTAAGAGCTTGAAGCTTCACTTACCCGTCGGTACCC 464
QY 701 CACTCTCAAGCCTCTCTGATATATTCCTGTTTACCCCGCAATATTTACAGATACATC 760
DB 465 CACTCTCAAGCCTCTCTGATATATTCCTGTTTACCCCGCAATATTTACAGATACATC 524
QY 761 TGCAGAGTCTCTTGGCCAGG 781
DB 525 TGCAGAGTCTCTTGGCCAGG 545

RESULT 7

US-09-949-016-150037
Sequence 150037, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 150037
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-150037

Query Match 9.0%; Score 189; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 8.9e-87;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1369 AGCTCAAGTTTATTTTACCCAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTCTG 1428
DB 18 AGCTCAAGTTTATTTTACCCAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTCTG 77
QY 1429 TCTACTGCCAACAAGAGTTCTGCGAAGGAGTATGTAACAGGCTGCGCTGTGTG 1488
DB 78 TCTACTGCCAACAAGAGTTCTGCGAAGGAGTATGTAACAGGCTGCGCTGTGTG 137
QY 1489 GTTGCTTCAAGTTCTTCAAGCAATATATTCATGATCCATGAAAGACGCGGAAAGCCCTG 1548
DB 138 GTTGCTTCAAGTTCTTCAAGCAATATATTCATGATCCATGAAAGACGCGGAAAGCCCTG 197

Qy	1549	GCTCCTAAG	1557
Db	198	GCTCCTAAG	206

RESULT 8
US-09-566-921-88
; Sequence 88, Application US/09566921

Query Match 7.5%; Score 158; DB 4; Length 2475;
Best Local Similarity 100.0%; Pred. No. 9.2e-71;
Matches 158; Conservative 0; Indels 0; Gaps 0

DY 585 ATTGCATGATT CAGGAAGAAGCATTC TAGGCTTTTGAACAAATGCAGTGAA CAGCA 644
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 76 ATTCGATGATT CAGGAAGAAGCATTC TAGGCTTTTGAACAAATGCAGTGAA CAGCA 139

Oy	645	CCAATCCATGTTGTAAATTGAAGACTTGAAGTCCTCAC	682
Db	136	CCAATCCATGTTGTAAATTGAAGACTTGAAGTCCTCAC	173

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RESULT 9
US-09-949-016-150030
: Sequence 150030, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 150030
:
: LENGTH: 601
: TYPE: DNA
: ORGANISM: Human
: US-09-949-016-150030

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Query Match	7.4%	Score 155;	DB 4;	Length 601;
Best Local Similarity	100.0%	Pred. No. 3e-69;		
Matches 155;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 964 TCTAGGTACAAAGCCATCTACCTCAAAGCTGAGCTTAAAGTAAAGAGACACCTGCCTC 1022

Db 380 TCTAGGTACAAAGCCATCTACCTCAAAGCTGAGCTTAAAGTAAAGAGACACCTGCCTC 439

QY 1024 CTTTGGAAATTAAGGCGACACAAAGAAGAAAAG 1058

Db 440 CTTTGGAAATTAAGGCGACACAAAGAAGAAAAG 474

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OY      1024 CTTTGAATAAAGCACAACAAAGAAGAAAG 1055  
        |||||  
DB      440 CTTTGAATAAAGCACAACAAAGAAGAAAG 474
```

RESULT 10
 US-09-949-016-150031
 : Sequence 150031, Application US/09949016
 : Patent No. 6812339
 : GENERAL INFORMATION:
 : APPLICANT: VENTER, J. Craig et al.
 : TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 : TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 : FILE REFERENCE: C1001307
 : CURRENT APPLICATION NUMBER: US/09/949,016
 : CURRENT FILING DATE: 2000-04-14
 : PRIOR APPLICATION NUMBER: 60/241,755
 : PRIOR FILING DATE: 2000-10-20
 : PRIOR APPLICATION NUMBER: 60/237,768
 : PRIOR FILING DATE: 2000-10-03
 : PRIOR APPLICATION NUMBER: 60/231,498
 : PRIOR FILING DATE: 2000-09-08
 : NUMBER OF SEQ ID NOS: 207012
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 150031
 : LENGTH: 601
 : TYPE: DNA
 : ORGANISM: Human
 : US-09-949-016-150031

Query Match	6.9%	Score 145	DB 4	Length 601
Best Local Similarity	100.0%	Pred. No. 4	2e-64	
Matches 145	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	964	TCTGAGGATCAAAAGCTCTCCAAAGATCGACGTTGAAGATAAAGAGAGCATCGCGTC	1022
Db	216	TCTGAGGATCAAAAGCTCTCCAAAGATCGACGTTGAAGATAAAGAGAGCATCGCGTC	275

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QY      1024 CTTTGGAAATTAAGGCAGACACAAA 1048  
        |||||  
Db      276 CTTTGGAAATTAAGGCAGACACAAA 300
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RESULT 11
US-09-949-016-150046
; Sequence 150046, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

```

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? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/231,498
? PRIOR FILING DATE: 2000-09-08
? NUMBER OF SEQ ID NOS: 207012
? SOFTWARE: FASTSEQ For Windows Version 4.0.0
? SEQ ID NO: 150046
? LENGTH: 601
? TYPE: DNA
? ORGANISM: Human
US-09-949-016-150046
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Query Match	6.5%	Score 137;	DB 4;	Length 601;
Best Local Similarity	99.5%;	Pred. No. 5.6e-60;		
Matches 187;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

QY	1762	TTGAGAAAGAGCTCAGACATTTCTCTTAAGATGGATCTTAACTCACTAAAGTTTCC	1821
Db	413	TTGAGAAAGAGCTCAGACATTTCTCTTAAGATGGATCTTAACTCACTAAAGTTTCC	472
QY	1822	TTCTCAAGAGATGCTCTCTGTTGGGAGAGAGAGCCACAGAAAGTATGTATCAAGACAAC	1881
Db	473	TTCTCAAGAGATGCTCTCTGTTGGGAGAGAGAGCCACAGAAAGTATGTATCAAGACAAC	532
QY	1882	ATCCAGCTTCAATGCGCCAGACAGGTGGCCAGAAATCTCTCTCCAGAGAAAGGCGCATTTAT	1941
Db	533	ATCCAGCTTCAATGCGCCAGACAGGTGGCCAGAAATCTCTCTCCAGAGAAAGGCGCATTTAT	592
QY	1942	GTGTGTGG	1949
Db	593	GTGTGTGG 600	

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RESULT 12
US-09-949-016-150047
; Sequence 150047, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001037
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150047
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-150047

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	Query Match	Similarity	6.5%	Score 137;	DB 4;	Length 601;	
	Best Local	Similarity	99.5%;	Pred. No.	5.6e-60;		
	Matches	187;	Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;
Oy	1762	TTCAGAAAAGAGCTCAGACATTTCCTTTAGCATGTGGATCTTAACAATCTAAAGGTTTTCC					1821
Db	191	TTCAAAAAAGAGCTCAGACATTTCCTTTAGCATGTGGATCTTAACAATCTAAAGGTTTTCC					250
Oy	1822	TTCTCAAGAGATGCTCTCTGTTTGGGGAAGAAGGCCCCAGCAAAGTAGTACTAAGCAAC					1881
Db	251	TTCTCAAGAGATGCTCTCTGTTGSGGAGAGGAAGCCCAAGCAAATAGTGTACAAAGCAAC					310
Oy	1882	ATTCAGCTTCATGCGGCAGAGGTGGCGAAGATCTCTTCACAGAGAAAGGCAATTTAT					1941
Db	311	ATTCAGCTTCATGCGGCAGAGGTGGCGAAGATCTCTCTTCAGAGAAAGGCAATTTAT					370

QY	1942	GTGTGTGG	1943
Db	371	GTGTGTGG	378

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RESULT 13
US-09-949-016-150029
: Sequence 150029, Application US/09949016
: Patent No. 681239
:
GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C0001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: PRIOR FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 150029
:
LENGTH: 601
:
TYPE: DNA
:
ORGANISM: Human
:
US-09-949-016-150029

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	Query Match	Best Local Similarity	6.0% Score 125; DB 4; Length 601;	100.0% Pred. No. 8.6e-54;	Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	779	AGGAGGAAGCCAGAGTCTGTGACCTTCACGACATCCAGTTTTCAGAGTCCCAATTTCAA	838		
Db	379	AGGAGGAAGCCAGAGTCTGTGACCTTCACGACATCCAGTTTTCAGTGCCTCAATTTCAA	438		
Qy	839	AGGCAAGTTCAACTTACTACGAGATGATGCCATTAATAACACTCTGCTGTGATCAATTGACA	898		
Db	439	AGGCAAGTTCAACTTACTACGAGATGATGCCATTAATAACAACACTCTGCTGTGATCAATTGACA	498		
Qy	899	TTTCA 903			
Db	499	TTTCA 503			

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RESULT 14
US-09-949-016-150041
; Sequence 150041: Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OR INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150041
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150041

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Query Match 5.8%; Score 121; DB 4; Length 601;

Best Local Similarity 100.0%; Pred. No. 9.9e-52;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1556 AGATATCCATCTCTCTCGAACAACAATTTCTTCCATTACAGATGACCCCTCAATCC 1615
DB 124 AGATATCCATCTCTCTCGAACAACAATTTCTTCCATTACAGATGACCCCTCAATCC 183

QY 1616 CCATCATTAATGGTGGGTCCAGGAACCGGCATAGCCCGTTATTGGGTTCTTCAACATA 1675
DB 184 CCATCATTAATGGTGGGTCCAGGAACCGGCATAGCCCGTTATTGGGTTCTTCAACATA 243

QY 1676 G 1676
DB 244 G 244

RESULT 15

US-09-949-016-150042
Sequence 150042, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CU001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 150042
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-150042

Query Match 5.8%; Score 121; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 9.9e-52;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1556 AGATATCCATCTCTCTCGAACAACAATTTCTTCCATTACAGATGACCCCTCAATCC 1615
DB 95 AGATATCCATCTCTCTCGAACAACAATTTCTTCCATTACAGATGACCCCTCAATCC 154

QY 1616 CCATCATTAATGGTGGGTCCAGGAACCGGCATAGCCCGTTATTGGGTTCTTCAACATA 1675
DB 155 CCATCATTAATGGTGGGTCCAGGAACCGGCATAGCCCGTTATTGGGTTCTTCAACATA 214

QY 1676 G 1676
DB 215 G 215

Search completed: August 27, 2005, 16:18:20
Job time : 237.42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 00:17:56 ; Search time 899.113 Seconds
(without alignments)
15238.608 Million cell updates/sec

Title: US-09-371-347a-45

Perfect score: 2094

Sequence: 1 atgaggaggttctgtact.....ttcaggatcttgcataca 2094

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 7331713 seqs, 3271544945 residues

Word size : 0

Total number of hits satisfying chosen parameters: 14663426

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA.*

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2094	100.0	2094	10	US-09-371-347-45
2	1854	88.5	2097	10	US-09-371-347-1
3	1854	88.5	3259	10	US-09-371-347-24
4	1803	86.1	2097	10	US-09-371-347-41
5	1803	86.1	2097	10	US-09-371-347-43
6	1677	80.1	2093	10	US-09-371-347-47
7	896	42.8	3256	21	US-10-741-600-692

8	896	42.8	3274	21	US-10-741-600-693	Sequence 693, App
9	330	15.8	591	16	US-10-029-386-6369	Sequence 6369, App
10	328	15.7	379	16	US-10-029-386-20100	Sequence 20100, A
11	279	13.3	591	16	US-10-029-386-1735	Sequence 1735, App
12	277	12.7	379	16	US-10-029-386-15435	Sequence 15435, A
13	266	12.7	43985	21	US-10-741-600-17757	Sequence 17757, A
14	188	9.0	525	16	US-10-029-386-653	Sequence 653, App
15	175	8.4	175	16	US-10-029-386-14338	Sequence 14338, A
16	158	7.5	2475	22	US-09-909-5578-38	Sequence 38, App1
17	158	7.5	2475	22	US-10-741-600-88	Sequence 88, App1
18	158	7.5	21852	21	US-10-741-600-17986	Sequence 17986, A
19	150	7.2	201	21	US-10-741-600-15583	Sequence 15583, A
20	150	7.2	201	21	US-10-741-600-15584	Sequence 15584, A
21	150	7.2	201	21	US-10-741-600-15589	Sequence 15589, A
22	150	7.2	201	21	US-10-741-600-15590	Sequence 15590, A
23	150	7.2	201	21	US-10-741-600-15592	Sequence 15592, A
24	150	7.2	201	21	US-10-741-600-15594	Sequence 15594, A
25	150	7.2	201	21	US-10-741-600-15598	Sequence 15598, A
26	150	7.2	201	21	US-10-741-600-15599	Sequence 15599, A
27	150	7.2	201	21	US-10-741-600-15600	Sequence 15600, A
28	150	7.2	201	21	US-10-741-600-15605	Sequence 15605, A
29	150	7.2	201	21	US-10-741-600-15609	Sequence 15609, A
30	150	7.2	201	21	US-10-741-600-15610	Sequence 15610, A
31	150	7.2	201	21	US-10-741-600-15612	Sequence 15612, A
32	150	7.2	201	21	US-10-741-600-15613	Sequence 15613, A
33	150	7.2	201	21	US-10-741-600-15614	Sequence 15614, A
34	150	7.2	201	21	US-10-741-600-15620	Sequence 15620, A
35	150	7.2	201	21	US-10-741-600-15621	Sequence 15621, A
36	150	7.2	201	21	US-10-741-600-15623	Sequence 15623, A
37	150	7.2	201	21	US-10-741-600-15625	Sequence 15625, A
38	150	7.2	201	21	US-10-741-600-15629	Sequence 15629, A
39	150	7.2	201	21	US-10-741-600-15630	Sequence 15630, A
40	150	7.2	201	21	US-10-741-600-15631	Sequence 15631, A
41	150	7.2	201	21	US-10-741-600-15637	Sequence 15637, A
42	150	7.2	201	21	US-10-741-600-15640	Sequence 15640, A
43	150	7.2	201	21	US-10-741-600-15641	Sequence 15641, A
44	150	7.2	201	21	US-10-741-600-15643	Sequence 15643, A
45	150	7.2	201	21	US-10-741-600-53894	Sequence 53894, A

ALIGNMENTS

RESULT 1
US-09-371-347-45
; Publication 45, Application US/09371347
; General Information:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE;
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; FILE REFERENCE: 50004/003003
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-45

Query Match 100.0%; Score 2094; DB 10; Length 2094;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2094; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGAGGAGTTCTGTACTATATGCTACAGCAGGAGCAGGCAAGGCATCGCAGAA 60
|||||

TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
 TITLE OF INVENTION: DEFECTS CARDIOVASCULAR DISEASE, AND CANCER
 FILE REFERENCE: 50004/003003
 CURRENT APPLICATION NUMBER: US/09/371,347
 PRIOR FILING DATE: 1999-08-10
 PRIOR APPLICATION NUMBER: 60/071,622
 PRIOR FILING DATE: 1998-01-16
 PRIOR APPLICATION NUMBER: 09/232,028
 PRIOR FILING DATE: 1999-01-15
 NUMBER OF SEQ ID NOS: 51
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 2097
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-371-347-1

Query Match 88.5%; Score 1854; DB 10; Length 2097;
 Best Local Similarity 99.9%; Pred. No. 0;

Matches 2094; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 ATGAGAGGTTCTGTTACTATATGCTACACAGGAGGAGCAAGGCAAGCCATGCGAGA 60
 DB 1 ATGAGAGGTTCTGTTACTATATGCTACACAGGAGGAGCAAGGCAAGCCATGCGAGA 60
 QY 61 GAAATGCTGACCAAGCTGTGTACATGATTTCTGAGATCTTCACTGTATTAGTGA 120
 DB 61 GAAATGCTGACCAAGCTGTGTACATGATTTCTGAGATCTTCACTGTATTAGTGA 120
 QY 121 TCCGATTAAGTATGACCTTAATAACCGAAGAGCTCTCTGTTGTTGTTGTTCTACAG 180
 DB 121 TCCGATTAAGTATGACCTTAATAACCGAAGAGCTCTCTGTTGTTGTTGTTCTACAG 180
 QY 181 GGCACCGAGAGCCACCGACACAGCCGCGAAGTTGTTAAGAAATACAGAACCAACA 240
 DB 181 GGCACCGAGAGCCACCGACACAGCCGCGAAGTTGTTAAGAAATACAGAACCAACA 240
 QY 241 CCGCCGTTGATTTCTTCTGCTACCTGCGGTAGGTTTCTGCTGCTGCTGCTGCTGCT 300
 DB 241 CCGCCGTTGATTTCTTCTGCTACCTGCGGTAGGTTTCTGCTGCTGCTGCTGCTGCT 300
 QY 301 TACACCTACTTTTGGCAATGGGGGAGATTAATTGATTAACGACTTCAAGAGCTTGGAGCC 360
 DB 301 TACACCTACTTTTGGCAATGGGGGAGATTAATTGATTAACGACTTCAAGAGCTTGGAGCC 360
 QY 361 CGGCAATTTCTATGACACTGACATGCAATGACTGTGAGTTTGAACCTTGTGTTGAG 420
 DB 361 CGGCAATTTCTATGACACTGACATGCAATGACTGTGAGTTTGAACCTTGTGTTGAG 420
 QY 421 CCGTGAATGCTGAGATCTGCGGCGACCTTCAAGAAAGATTTTAAAGCAAGAGAGCA 480
 DB 421 CCGTGAATGCTGAGATCTGCGGCGACCTTCAAGAAAGATTTTAAAGCAAGAGAGCA 480
 QY 481 GAGGAGATTAAGTGGCCACTCCCGGTGGCATCTGCACTCTTGAAGGAGAGCTTGTG 540
 DB 481 GAGGAGATTAAGTGGCCACTCCCGGTGGCATCTGCACTCTTGAAGGAGAGCTTGTG 540
 QY 541 AAGTCAGAGCTGCTACATGATGATCTCAAGTGAAGCTTCTGAGATTCGATTCAGGA 600
 DB 541 AAGTCAGAGCTGCTACATGATGATCTCAAGTGAAGCTTCTGAGATTCGATTCAGGA 600
 QY 601 AGAAAGAGATTTGAGGTTTGAAGCAAAATGCAAGTGAAGCAAGCAACCAATTCGAAT 660
 DB 601 AGAAAGAGATTTGAGGTTTGAAGCAAAATGCAAGTGAAGCAAGCAACCAATTCGAAT 660
 QY 661 ATTGAAGATTTGAGGTTTGAAGCAAAATGCAAGTGAAGCAAGCAACCAATTCGAAT 720
 DB 661 ATTGAAGATTTGAGGTTTGAAGCAAAATGCAAGTGAAGCAAGCAACCAATTCGAAT 720
 QY 721 AATATTCCTGTTTACCCCAAGATATTTAAGATATCTGAGAGAGTCTTGGCCAG 780
 DB 721 AATATTCCTGTTTACCCCAAGATATTTAAGATATCTGAGAGAGTCTTGGCCAG 780

QY 781 GAGAAAGCAGATATCTGATCTTCAAGATCCAGTTTCAAGTGCATTTCAAG 840
 DB 781 GAGAAAGCAGATATCTGATCTTCAAGATCCAGTTTCAAGTGCATTTCAAG 840
 QY 841 GAGTTCAATCTTACAGATATGATCCATAAACAACCTCTGCTGTAGATTTGACATT 900
 DB 841 GAGTTCAATCTTACAGATATGATCCATAAACAACCTCTGCTGTAGATTTGACATT 900
 QY 901 TCAATACAGATTTTCTATCAGCTGAGATGCTTCAAGGATATCTGCTTACAGT 960
 DB 901 TCAATACAGATTTTCTATCAGCTGAGATGCTTCAAGGATATCTGCTTACAGT 960
 QY 961 GATTCGAGTACCAAGCTTCAAGAGCTGACCTTGAAGATTAAGAGAGAGAGAGAG 1020
 DB 961 GATTCGAGTACCAAGCTTCAAGAGCTGACCTTGAAGATTAAGAGAGAGAGAGAG 1020
 QY 1021 GTCTTTTGAATAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 DB 1021 GTCTTTTGAATAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
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 DB 1081 CCGGCGGAGATGTTCTCTCAGTTCAATTTTACCTGCTGCTGAAATCCAGAGATTCT 1140
 QY 1141 AAAAAGCATTTTTCGAGCCCTTGTGACATATACAGTACAGTGTGAGAGAGAGAG 1200
 DB 1141 AAAAAGCATTTTTCGAGCCCTTGTGACATATACAGTACAGTGTGAGAGAGAGAG 1200
 QY 1201 CTACAGAGCTGTGACATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 DB 1201 CTACAGAGCTGTGACATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 QY 1261 TGTGCTGCTGTTGATGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 DB 1261 TGTGCTGCTGTTGATGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 QY 1321 CTTGCTGAAATCTTCTTAACTTCAACCCAGACATATCTGCTGCTGCTGCTGCTGCT 1380
 DB 1321 CTTGCTGAAATCTTCTTAACTTCAACCCAGACATATCTGCTGCTGCTGCTGCTGCT 1380
 QY 1381 TTTCAACCAAG 1440
 DB 1381 TTTCAACCAAG 1440
 QY 1441 ACAAGGTTCTGCGAG 1500
 DB 1441 ACAAGGTTCTGCGAG 1500
 QY 1501 CTTGAGCCAAATACATGATCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
 DB 1501 CTTGAGCCAAATACATGATCCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
 QY 1561 TCCATCTCTCTGAG 1620
 DB 1561 TCCATCTCTCTGAG 1620
 QY 1621 ATTAATGTTGTTGAG 1680
 DB 1621 ATTAATGTTGTTGAG 1680
 QY 1681 AAATCTCAAG 1740
 DB 1681 AAATCTCAAG 1740
 QY 1741 AGGCAATTAAG 1800
 DB 1741 AGGCAATTAAG 1800
 QY 1801 ATCTTAATCTTAAG 1860
 DB 1801 ATCTTAATCTTAAG 1860
 QY 1858 CAGCAAGATATGATCAAG 1917

Accession	Sequence	Length
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D8	1861	
D8	1918	
D8	1921	
D8	1978	
D8	1981	
D8	2038	
D8	2041	

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? RESULT 3
? US-09-371-347-24
? Sequence 24, Application US/09371347
? Publication No. US20030082676A1
? GENERAL INFORMATION:
? APPLICANT: Roy A. Gravel et al.
? TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
? TITLE OF INVENTION: CLOTHING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
? TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
? FILE REFERENCE: 50004/003003
? CURRENT APPLICATION NUMBER: US/09/371,347
? CURRENT FILING DATE: 1999-08-10
? PRIOR APPLICATION NUMBER: 60/071,622
? PRIOR FILING DATE: 1998-01-16
? PRIOR APPLICATION NUMBER: 09/232,028
? PRIOR FILING DATE: 1999-01-15
? NUMBER OF SEQ ID NOS: 51
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 24
? LENGTH: 3259
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-371-347-24

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Query Match	88.5%	Score 1854	DB 10	Length 3259
Best Local Similarity	99.9%	Pred. No. 0		
Matches 2094	Conservative 0	Mismatches 0	Indels 3	Gaps 1

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Db	80	ATGAGGAGGTTTCTGTTACTATATAGCTACACAGCAGGAGCAGGCGAAGGCCATGCGCAGAA	139
Qy	61	GAATATGATGAGCAAGCTGTGCTACATAGGATTTTCTGCAGATCTTCACTGTATTAAGGAA	120
Db	140	GAATATGATGAGCAAGCTGTGCTACATAGGATTTTCTGCAGATCTTCACTGTATTAAGGAA	199
Qy	121	TCCGATTAAGTATGACCTTAAAAACGAAACAGCTCCTGTGTGTGTGTGTGTGTGTAAACAG	180
Db	200	TCCGATTAAGTATGACCTTAAAAACGAAACAGCTCCTGTGTGTGTGTGTGTGTGTAAACAG	259
Qy	181	GGCACCCGAGACCCACCCGACACAGCCCGCAGTTTGTATAGAAATACAGAACCAACA	240
Db	260	GGCACCCGAGACCCACCCGACACAGCCCGCAGTTTGTATAGAAATACAGAACCAACA	319
Qy	241	CTGCCGGTTGATTTCTTTTGCTCACTCGCGGTATGGGTTACTGGGCTCGGATTCAGAA	300
Db	320	CTGCCGGTTGATTTCTTTTGCTCACTCGCGGTATGGGTTACTGGGCTCGGATTCAGAA	379
Qy	301	TACACCTACTTTTGCATATGGGGGAGATTAATTGATTAACGACTTCAAGACTTGGAGCC	360
Db	380	TACACCTACTTTTGCATATGGGGGAGATTAATTGATTAACGACTTCAAGACTTGGAGCC	439
Qy	361	CGGCATTTCTATGACACTGGAACATGCAGATGACTGTGAGTTTGAACCTTGTGTTGAG	420
Db	440	CGGCATTTCTATGACACTGGAACATGCAGATGACTGTGAGTTTGAACCTTGTGTTGAG	499
Qy	421	CCGTGATTTGCTGGACTCTGCGCAGCCCTCAGAAAGCAATTTTAGCTCAGCAGAGCAAA	480

Db	500	CCGCGAATCTGACACTCTGACCAGCCCTGAGAAAGCATTTTAAAGTCAACGAGGACAA	559
Qy	481	GAGAGATTAATGAGCGCACTCCGCGTGGCATCACTTGACATCTTGAAGACAGACCTTGTG	540
Db	560	GAGAGAGTTAATGGCCGACCTCCGCGTGGCATCACTTGACATCTTGAAGACAGACCTTGTG	619
Qy	541	AAGTCAGAGCTGCTACACATGTAATCTCAAGTCGAGCTTGTAGATTCGATGATTCAGGA	600
Db	620	AAGTCAGAGCTGCTACACATGTAATCTCAAGTCGAGCTTGTAGATTCGATGATTCAGGA	679
Qy	601	AGAAAGATCTGAGGTTTTGAAAGCAAAAGCAGTGAACGACAAACCAATCCATGTTGTA	660
Db	680	AGAAAGATCTGAGGTTTTGAAAGCAAAAGCAGTGAACGACAAACCAATCCATGTTGTA	739
Qy	661	ATTGAAAGACTTGGAGTCTCTACATTAACCGTTCGGTACCCCACTCTCAAGAGCTCTGTG	720
Db	740	ATTGAAAGACTTGGAGTCTCTACATTAACCGTTCGGTACCCCACTCTCAAGAGCTCTGTG	799
Qy	721	AATATTCCTGAGTTTACCCCGAATAATTTACAGTACATCTGACGAGAGTCTCTTGGCCAG	780
Db	800	AATATTCCTGAGTTTACCCCGAATAATTTACAGTACATCTGACGAGAGTCTCTTGGCCAG	859
Qy	781	GAGAAAGCCAAAGTATCTGTGACTTTCAGCAGATCCAGTTTTCAGAGGCCAATTTCAAG	840
Db	860	GAGAAAGCCAAAGTATCTGTGACTTTCAGCAGATCCAGTTTTCAGAGGCCAATTTCAAG	919
Qy	841	GCAAGTTCAACTTACAGATGATGCGCATTAATAACCACTCTGCTGTGTAAGATTGACATT	900
Db	920	GCAAGTTCAACTTACAGATGATGCGCATTAATAACCACTCTGCTGTGTAAGATTGACATT	979
Qy	901	TCAAAATACAGACTTTTCTATCAAGCTGAGATGCTTTCAGCGTATCTGCTCCCTAACAGT	960
Db	980	TCAAAATACAGACTTTTCTATCAAGCTGAGATGCTTTCAGCGTATCTGCTCCCTAACAGT	1039
Qy	961	GATTCGAGGTACAAAGCCTTATCTCCAAAGACTGAGCTTGAAGATTAAGAAGCACTGC	1020
Db	1040	GATTCGAGGTACAAAGCCTTATCTCCAAAGACTGAGCTTGAAGATTAAGAAGCACTGC	1099
Qy	1021	GTCTCTTTGAAAATTAAGGACAGACAAATAAGAAAGAGACTACCTTACCCCGACATATA	1080
Db	1100	GTCTCTTTGAAAATTAAGGACAGACAAATAAGAAAGAGACTACCTTACCCCGACATATA	1159
Qy	1081	CCTGCGGAGATGTTCTCTCCAGTTCAATTTTACCTGATGTGTGAATCCGAGCAATTTCT	1140
Db	1160	CCTGCGGAGATGTTCTCTCCAGTTCAATTTTACCTGATGTGTGAATCCGAGCAATTTCT	1219
Qy	1141	AAAAAGCATTTTTCGACGCCCTTGTGTGACTTATACAGTGAACAGTGTGAAAAAGCGAGG	1200
Db	1220	AAAAAGCATTTTTCGACGCCCTTGTGTGACTTATACAGTGAACAGTGTGAAAAAGCGAGG	1279
Qy	1201	CTACAGAGAGCTGTGACATTAACAAAGGGGACGCAATTAATGCGGCTTTGTACGAGATGCC	1260
Db	1280	CTACAGAGAGCTGTGACATTAACAAAGGGGACGCAATTAATGCGGCTTTGTACGAGATGCC	1339
Qy	1261	TGTGCTGTGTTGTGATCTCTCTCTCGCTTTCCTTCTTTCGACGCCACCTCAAGTCTC	1320
Db	1340	TGTGCTGTGTTGTGATCTCTCTCTCGCTTTCCTTCTTTCGACGCCACCTCAAGTCTC	1399
Qy	1321	CTGTGCGAATCTTCTCTAACTTTCACCCAGACATATTGCGTGTGCAACACTCAAGTTTA	1380
Db	1400	CTGTGCGAATCTTCTCTAACTTTCACCCAGACATATTGCGTGTGCAACACTCAAGTTTA	1459
Qy	1381	TTTTCACCCAGAAAGCTCCATTTTGTCTTCACACATGTGTGAATTTCTGTCTACGCGACA	1440
Db	1460	TTTTCACCCAGAAAGCTCCATTTTGTCTTCACACATGTGTGAATTTCTGTCTACGCGACA	1519
Qy	1441	ACAGAGGTTCTGCGGAAGGAGTATGTACAGGCTGAGCTGTGTGTGTTCACTTCAGTT	1500
Db	1520	ACAGAGGTTCTGCGGAAGGAGTATGTACAGGCTGAGCTGTGTGTGTTCACTTCAGTT	1579
Qy	1501	CTTCAGCCAAACATACATGATCCCATGAAGACAGCGGAAAGCCTTGCTCCTTAAGATA	1560

1580 CTTGAGCCAAACATACATGATCCCATGAGAGAGCGGGAAGCCCTGCTCTTAAGATA 1639
1561 TCCATCTCTCTGGAACAATCTTCACTTAACGATGACCCCTCAATGCCCATC 1620
1640 TCCATCTCTCTGGAACAATCTTCACTTAACGATGACCCCTCAATGCCCATC 1699
1621 ATATGCTGCTGCAAGAACCGGATAGCCCGTTTATTTGGTTCTCAACATAGAGAG 1680
1700 ATATGCTGCTGCAAGAACCGGATAGCCCGTTTATTTGGTTCTCAACATAGAGAG 1759
1681 AAATCTCAAGAACCAACCCAGATGGAATTTTGAAGCATGTG--GTTTTTGGCTGC 1737
1760 AAATCTCAAGAACCAACCCAGATGGAATTTTGAAGCATGTG--GTTTTTGGCTGC 1819
1728 AGGCAATAGAGATGAGATTAATCTATTCAGAAAAGCTCAGACATTTCTTAAGATGAG 1797
1820 AGGCAATAGAGATGAGATTAATCTATTCAGAAAAGCTCAGACATTTCTTAAGATGAG 1879
1798 ATCTTAATCTATTAAGATTTCTCTGCAAGATGCTCTGTTGGAGAGAGAGAGCC 1857
1880 ATCTTAATCTATTAAGATTTCTCTGCAAGATGCTCTGTTGGAGAGAGAGAGCC 1939
1858 CCAGCAAGATATGACAGAACATCCAGCTTCATGCGCAGAGAGTGGCAGATCTTC 1917
1940 CCAGCAAGATATGACAGAACATCCAGCTTCATGCGCAGAGAGTGGCAGATCTTC 1999
1918 CTCGAGAGAAAGGCTATTTATGCTGATGAGATGCAAAATATGCGCAAGATGTA 1977
2000 CTCGAGAGAAAGGCTATTTATGCTGATGAGATGCAAAATATGCGCAAGATGTA 2059
1978 CATGATGCTGCTGCAATTAATTAAGCAAGAGTGGAGTTGAAAACTAGAGCATG 2037
2060 CATGATGCTGCTGCAATTAATTAAGCAAGAGTGGAGTTGAAAACTAGAGCATG 2119
2038 AAAACCTGCGCACTTTAAAGAGAAAAAGCTTACAGATTTTGTCTATA 2094
2120 AAAACCTGCGCACTTTAAAGAGAAAAAGCTTACAGATTTTGTCTATA 2176

RESULT 4
US-09-371-347-41
; Sequence 41, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE.
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-41

Query Match 86.1%; Score 1803; DB 10; Length 2097;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

1 ATGAGAGAGTTCTGTTACTATATGCTACAGCAGAGAGCAGGCAAGGCATCGAGAA 60
1 ATGAGAGAGTTCTGTTACTATATGCTACAGCAGAGAGCAGGCAAGGCATCGAGAA 60
61 GAAATGTGAGCAAGCTGTGATACATGATTTTCTGAGATCTTCACTGATTAAGAA 120

61 GAAATGTGAGCAAGCTGTGATACATGATTTTCTGAGATCTTCACTGATTAAGAA 120
121 TCCGATTAAGTATGACCTTAACCAAGCAAGCTCTCTGTTGTTGTTCTACACAG 180
121 TCCGATTAAGTATGACCTTAACCAAGCAAGCTCTCTGTTGTTGTTCTACACAG 180
181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCA 240
181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCA 240
241 CTGCGGTGATTTCTTTGCTCACTGCGGTATGAGTTATCTGGGTCTCGGTATTCAGA 300
241 CTGCGGTGATTTCTTTGCTCACTGCGGTATGAGTTATCTGGGTCTCGGTATTCAGA 300
301 TACACCTACTTTTGGCAATGCGGAGAAAGATTAATGATTAACGACTTCAAGAGCTTGA 360
301 TACACCTACTTTTGGCAATGCGGAGAAAGATTAATGATTAACGACTTCAAGAGCTTGA 360
361 CGGCAATTTCTATGACACTGACATGACATGAGATGATGATGATTTGAACTTGTGAG 420
361 CGGCAATTTCTATGACACTGACATGACATGAGATGATGATGATTTGAACTTGTGAG 420
421 CCGTGATGCTGACCTGCGCAGAGCTTCAAGAACATTTTAAGTCAAGAGAGACA 480
421 CCGTGATGCTGACCTGCGCAGAGCTTCAAGAACATTTTAAGTCAAGAGAGACA 480
481 GAGGAGATTAAGTGGGCACTCCCGGTGATACCTGATGAGAGAGAGAGAGAGAGAG 540
481 GAGGAGATTAAGTGGGCACTCCCGGTGATACCTGATGAGAGAGAGAGAGAGAGAG 540
541 AAGTCAAGCTCTACACATTAATCTCAAGTGAAGCTTCAAGATTCAGATTCAGAG 600
541 AAGTCAAGCTCTACACATTAATCTCAAGTGAAGCTTCAAGATTCAGATTCAGAG 600
601 AAAAAAGATTCGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCAATGTTGA 660
601 AAAAAAGATTCGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCAATGTTGA 660
661 ATTGAAGATTTGAGTCCCTCACTTACCGGTGATACCCCACTCTCAAGAGCTCTG 720
661 ATTGAAGATTTGAGTCCCTCACTTACCGGTGATACCCCACTCTCAAGAGCTCTG 720
721 AATATTCCTGTTTACCCCAAGATTAATTAAGATTCAGATTCAGAGAGCTCTGCGCAG 780
721 AATATTCCTGTTTACCCCAAGATTAATTAAGATTCAGATTCAGAGAGCTCTGCGCAG 780
781 GAGGAAAGCAAGTATCTGTGACTTCAGAGATTCAGATTCAGATTCAGATTCAGAG 840
781 GAGGAAAGCAAGTATCTGTGACTTCAGAGATTCAGATTCAGATTCAGATTCAGAG 840
841 GCAATTCATTAATCAAGATGATGCAATTAACCACTCTGCTGTGATTAATTCAGATT 900
841 GCAATTCATTAATCAAGATGATGCAATTAACCACTCTGCTGTGATTAATTCAGATT 900
901 TCAAAATACAGACTTTTCTATCAGAGCTGAGAGTCTTCAAGAGTATCTGCTTACAG 960
901 TCAAAATACAGACTTTTCTATCAGAGCTGAGAGTCTTCAAGAGTATCTGCTTACAG 960
961 GATTCGAGTACCAAGCTCTTCAAGAGCTGAGAGTCTTCAAGAGTATCTGCTTACAG 1020
961 GATTCGAGTACCAAGCTCTTCAAGAGCTGAGAGTCTTCAAGAGTATCTGCTTACAG 1020
1021 GTTCCTTTGAAAATTAAGGACACACAAAGAAAGAGAGCTTACCTTACCCGAGATTA 1080
1021 GTTCCTTTGAAAATTAAGGACACACAAAGAAAGAGAGCTTACCTTACCCGAGATTA 1080
1081 CCGCGGAGATTTCTCTCAGTTCAATTTTACCTGCTGCTTGAATCCGAGCAATTCCT 1140
1081 CCGCGGAGATTTCTCTCAGTTCAATTTTACCTGCTGCTTGAATCCGAGCAATTCCT 1140
1141 AAAAAGCAATTTTGGAGCCCTTGTGAGCTATACAGTGAAGAGTGTGAAAAGCGCAG 1200
1141 AAAAAGCAATTTTGGAGCCCTTGTGAGCTATACAGTGAAGAGTGTGAAAAGCGCAG 1200

QY 1201 CTACAGAGCTGTGCACTAATAACAAGGGGACGGGATTATAGCCGTTTGTACAGATGCC 1260
DB 1201 CTACAGAGCTGTGCACTAATAACAAGGGGACGGGATTATAGCCGTTTGTACAGATGCC 1260
QY 1261 TGTGCGCTGTGTTGATGATCTCCCTCTCGCTTTCCCTTTCCGACGACCACTCACTTC 1320
DB 1261 TGTGCGCTGTGTTGATGATCTCCCTCTCGCTTTCCCTTTCCGACGACCACTCACTTC 1320
QY 1321 CTGCTGGAACATCTTCTTAACCTTCAACCCAGACCATATTCGTGTGAAGCTCAAGTTTA 1380
DB 1321 CTGCTGGAACATCTTCTTAACCTTCAACCCAGACCATATTCGTGTGAAGCTCAAGTTTA 1380
QY 1381 TTTACCCAGGAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTGTCTACTGCCACA 1440
DB 1381 TTTACCCAGGAAGCTCCATTTTGTCTTCAACATTTGTGAAATTTGTCTACTGCCACA 1440
QY 1441 ACAGAGTTTCTGGGGAAGGAGATATGACAGGCTGGCTGTGTTGTGTTCTTCAATT 1500
DB 1441 ACAGAGTTTCTGGGGAAGGAGATATGACAGGCTGGCTGTGTTGTGTTCTTCAATT 1500
QY 1501 CTTCAGCCAAACATACATGATCCCATGAAGACAGCGGAAAGCCCTGCTCCTAAGATA 1560
DB 1501 CTTCAGCCAAACATACATGATCCCATGAAGACAGCGGAAAGCCCTGCTCCTAAGATA 1560
QY 1561 TCCATCTCTCTGGAACAACAATTTCTTTCACCTTACAGATGACCCCTCAATCCCCTATC 1620
DB 1561 TCCATCTCTCTGGAACAACAATTTCTTTCACCTTACAGATGACCCCTCAATCCCCTATC 1620
QY 1621 ATTAATGTGGGTCCAGGAACCGGCAATGCCCCGTTTATTTGGGTTCTTCAACAATAAGAG 1680
DB 1621 ATTAATGTGGGTCCAGGAACCGGCAATGCCCCGTTTATTTGGGTTCTTCAACAATAAGAG 1680
QY 1681 AAATCCAAAGAACACACCCAGATGGAATTTTGGAGCAATGTG---GTTTTTGGCTGC 1737
DB 1681 AAATCCAAAGAACACACCCAGATGGAATTTTGGAGCAATGTG---GTTTTTGGCTGC 1737
QY 1738 AGGCATTAAGATAGGATTAATCTATTCAGAAAAGAGCTCAGACATTTCTTTAAGCATGG 1797
DB 1741 AGGCATTAAGATAGGATTAATCTATTCAGAAAAGAGCTCAGACATTTCTTTAAGCATGG 1800
QY 1798 ATCTTAATCTATTAAGATTTCTTCTCAAGAGATGCTCTGTGGGGAGAGAGAGCC 1857
DB 1801 ATCTTAATCTATTAAGATTTCTTCTCAAGAGATGCTCTGTGGGGAGAGAGAGCC 1860
QY 1858 CCAGCAAGATATACAGACAAATCATCATGAGCCAGAGAGGTGGAGAAATCTCTC 1917
DB 1861 CCAGCAAGATATATGACAAACATCATGAGCCAGAGAGGTGGAGAAATCTCTC 1920
QY 1918 CTCAGAGAGAGCGCATATTTATGTGTGTGAGATCAAAAGATATGCGCAAGATGTA 1977
DB 1921 CTCAGAGAGAGCGCATATTTATGTGTGTGAGATCAAAAGATATGCGCAAGATGTA 1980
QY 1978 CAGATAGCTCTTGTGCAAAATTAATGAGAGAGTTGAGTAAAAAATGAAAGCATG 2037
DB 1981 CAGATAGCTCTTGTGCAAAATTAATGAGAGAGTTGAGTAAAAAATGAAAGCATG 2040
QY 2038 AAAAACCCTGGCACTTTAAAGAAAGAAAGCTACCTTCAGAGATTTTGTGATTA 2094
DB 2041 AAAAACCCTGGCACTTTAAAGAAAGAAAGCTACCTTCAGAGATTTTGTGATTA 2097

RESULT 5
US-09-371-347-43
; Sequence 43, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347

; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FASTSEQ For Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-43

Query Match 86.1%; Score 1803; DB 10; Length 2097;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 ATGAGAGAGTTTCTGTACTATATATGTTACACAGAGGACAGGCAAGGCCATCCGAGAA 60
DB 1 ATGAGAGAGTTTCTGTACTATATATGTTACACAGAGGACAGGCAAGGCCATCCGAGAA 60
QY 61 GAAATGTGAGCAAGCTGTGTAACATGATTTTCTGAGATCTTCACTGATTAATGAA 120
DB 61 GAAATGTGAGCAAGCTGTGTAACATGATTTTCTGAGATCTTCACTGATTAATGAA 120
QY 121 TCCGATTAAGTATGACCTTAAACCGAAGACGCTCTTGTGTGTGTTGTTCTACACG 180
DB 121 TCCGATTAAGTATGACCTTAAACCGAAGACGCTCTTGTGTGTGTTGTTCTACACG 180
QY 181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
DB 181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
QY 241 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGAGTTACTGGGTCTCGGTATTCAGAA 300
DB 241 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGAGTTACTGGGTCTCGGTATTCAGAA 300
QY 301 TACACCTACTTTTGCAATGAGGGGGAATATATGATTAACGACTTCAAGACTTGAAGCC 360
DB 301 TACACCTACTTTTGCAATGAGGGGGAATATATGATTAACGACTTCAAGACTTGAAGCC 360
QY 361 CGGCAATTTCTATGACATGAGCAATGAGATGATGATGATGATTAACCTGTGGTTGAG 420
DB 361 CGGCAATTTCTATGACATGAGCAATGAGATGATGATGATGATTAACCTGTGGTTGAG 420
QY 421 CGGTGATGCTGGAATCTGCGCAGCCCTCAGAAACATTTTATGATCAAGAGACAA 480
DB 421 CGGTGATGCTGGAATCTGCGCAGCCCTCAGAAACATTTTATGATCAAGAGACAA 480
QY 481 GAGAGATTAAGTGGGCACTCCCGGTGGATCACTGCACTCTTGAAGACAGACTTTGTG 540
DB 481 GAGAGATTAAGTGGGCACTCCCGGTGGATCACTGCACTCTTGAAGACAGACTTTGTG 540
QY 541 AAGTCAGAGCTGTACACATTAATCTCAAGTGAAGCTTGAAGATTTCAATGATTAAGGA 600
DB 541 AAGTCAGAGCTGTACACATTAATCTCAAGTGAAGCTTGAAGATTTCAATGATTAAGGA 600
QY 601 AGAAGAGTTCTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATGATTTGTA 660
DB 601 AGAAGAGTTCTGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATGATTTGTA 660
QY 661 ATTGAAGACTTGAAGTCTCACTTACCCGTTGGGATACCCCACTCTCAAGCCTCTCTG 720
DB 661 ATTGAAGACTTGAAGTCTCACTTACCCGTTGGGATACCCCACTCTCAAGCCTCTCTG 720
QY 721 AATATTCCTGTTTACCCCAAGAAATTTTAACAGATCACTGAGAGAGTCTTTGGCCAG 780
DB 721 AATATTCCTGTTTACCCCAAGAAATTTTAACAGATCACTGAGAGAGTCTTTGGCCAG 780
QY 781 GAGGAAGCAAGATATCTGATCTTCAAGAGATCCAGATTTTCAAGTGCATTTCAAG 840
DB 781 GAGGAAGCAAGATATCTGATCTTCAAGAGATCCAGATTTTCAAGTGCATTTCAAG 840

Qy	841	GCAGTCAACTTACTAGAAAGAGCCATAAACCACTCGCTGAGTAATGGACATT	900
Db	841	GCAGTCAACTTACTAGAAAGAGCCATAAACCACTCGCTGAGTAATGGACATT	900
Qy	901	TCAATAACAGACTTTTCCCTATCAGCCCTGAGATGCTTACAGCTGATCTGACCTTAACGT	960
Db	901	TCAATAACAGACTTTTCCCTATCAGCCCTGAGATGCTTACAGCTGATCTGACCTTAACGT	960
Qy	961	GATTCTGAGGTACAAAGCTTATCTCCAAAGACTGAGCTTGAAGATAAAGAGCACTGC	1020
Db	961	GATTCTGAGGTACAAAGCTTATCTCCAAAGACTGAGCTTGAAGATAAAGAGCACTGC	1020
Qy	1021	GTCTCTTTGAAATAATTAAGGCGACACAAAGAAAGAAAGAGCTACTTATCCCCACATATA	1080
Db	1021	GTCTCTTTGAAATAATTAAGGCGACACAAAGAAAGAAAGAGCTACTTATCCCCACATATA	1080
Qy	1081	CCTCGGGGATGTTCCTCTCAGTTCATTTTATCTGAGTCTTTGAATCCGAGCAATTCCT	1140
Db	1081	CCTCGGGGATGTTCCTCTCAGTTCATTTTATCTGAGTCTTTGAATCCGAGCAATTCCT	1140
Qy	1141	AAAAAGGCAATTTTTCGAGCCCTTGTGAGCTATACCAATGACAGTGTGAAGAACGACAG	1200
Db	1141	AAAAAGGCAATTTTTCGAGCCCTTGTGAGCTATACCAATGACAGTGTGAAGAACGACAG	1200
Qy	1201	CTACAGAGCTGTGCTAGTAAACAAAGGGGACGCCGATTATAGCCGCTTTGTATCGAGATGCC	1260
Db	1201	CTACAGAGCTGTGCTAGTAAACAAAGGGGACGCCGATTATAGCCGCTTTGTATCGAGATGCC	1260
Qy	1261	TGTGCTGTCTGTTGGATCTCTCTCGCTTCCCTCTTGCACAGCCACACTAGTCTC	1320
Db	1261	TGTGCTGTCTGTTGGATCTCTCTCGCTTCCCTCTTGCACAGCCACACTAGTCTC	1320
Qy	1321	CTGCTCGAACAATCTTCTTAACTTCAACCAGACCATATTCGTGTGCAAGCTCAAGTTTA	1380
Db	1321	CTGCTCGAACAATCTTCTTAACTTCAACCAGACCATATTCGTGTGCAAGCTCAAGTTTA	1380
Qy	1381	TTTCAACCCAGAAAGCTCATTTTGTCTTCAACATTTGTGAATTTCTGTCTATCTGCCACA	1440
Db	1381	TTTCAACCCAGAAAGCTCATTTTGTCTTCAACATTTGTGAATTTCTGTCTATCTGCCACA	1440
Qy	1441	ACAGAGGTTGCGGGAAGGGAGTATGTACAGGCTGCGCTGCTTGTGTGCTTCAAGTT	1500
Db	1441	ACAGAGGTTGCGGGAAGGGAGTATGTACAGGCTGCGCTGCTTGTGTGCTTCAAGTT	1500
Qy	1501	CTTGAGCCAAACATATCATGTATCCCATGTAAAGACAGCGGAAAGCCCTGCTCTTAAGTA	1560
Db	1501	CTTGAGCCAAACATATCATGTATCCCATGTAAAGACAGCGGAAAGCCCTGCTCTTAAGTA	1560
Qy	1561	TCCATCTCTCTGTAACAACAATTTCTTTCACATTACAGATGACCCCTCAATCCCATC	1620
Db	1561	TCCATCTCTCTGTAACAACAATTTCTTTCACATTACAGATGACCCCTCAATCCCATC	1620
Qy	1621	ATATATGTGGGTCCAGGAACCGGCATAGCCCCGTTATATGGGTTCTTACATATAGAGAG	1680
Db	1621	ATATATGTGGGTCCAGGAACCGGCATAGCCCCGTTATATGGGTTCTTACATATAGAGAG	1680
Qy	1681	AAACTCCAAAGAACCAACCCAGATGGAATTTTGGAGCAATGTG---GTTTTTTGGCTGC	1737
Db	1681	AAACTCCAAAGAACCAACCCAGATGGAATTTTGGAGCAATGTG---GTTTTTTGGCTGC	1740
Qy	1738	AGGCATTAAGATAGGATTAATCTAATTCGAAAAGAGCTCAGACATTTCTTAAAGCATGGG	1797
Db	1741	AGGCATTAAGATAGGATTAATCTAATTCGAAAAGAGCTCAGACATTTCTTAAAGCATGGG	1800
Qy	1798	ATCTTAATCTCATTAAGGTTTCTTCTCAAGAGATGCTCTGTGTGGGAGAGGAAGCC	1857
Db	1801	ATCTTAATCTCATTAAGGTTTCTTCTCAAGAGATGCTCTGTGTGGGAGAGGAAGCC	1860
Qy	1858	CCAGCAAGTATGTATCAGACAAACATCCAGCTTCATGSCACAGAGTGGCGAGAACTCTC	1917
Db	1861	CCAGCAAGTATGTATCAGACAAACATCCAGCTTCATGSCACAGAGTGGCGAGAACTCTC	1920
Qy	1918	CTCCAGAGAAACGGCATATTTATGTGTGTGAGATGCAAGAAATATGSCCAAGATGTA	1977

Accession	Sequence	Year
Dd	1221 CTCGAGGAAAGCGCCATATTTATGTGTGTGAGATCCAAAGATATGCGCAAGAGTGA	1980
Oy	1978 CATGATGCGCTTGTGCAATATATAGCAAAAGGTTGAGTTGAAAACTTGAAGCAATG	2037
Dd	1981 CATATGCGCCCTTGTGCAATATATAGCAAAAGGTTGAGTTGAAAACTTGAAGCAATG	2040
Oy	2038 AAAACCGTGGCACTTTAAAGAAGAAAAAGCTACCTTCAAGATATTTGGTCATTA	2094
Dd	2041 AAAACCGTGGCACTTTAAAGAAGAAAAAGCTACCTTCAAGATATTTGGTCATTA	2097

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RESULT 6
US-09-371-347-47
Sequence 47, Application US/09371347
Publication No. US20030082676A1
GENERAL INFORMATION:
APPLICANT: Roy A. Gravel et al.
TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
FILE REFERENCE: 50004/003003
CURRENT APPLICATION NUMBER: US/09/371,347
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/071,622
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 09/232,028
PRIOR FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47
LENGTH: 2093
TYPE: DNA
ORGANISM: Homo sapiens
US-09-371-347-47

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Query Match	80.1%;	Score 1677;	DB 10;	Length 2093;
Beet Local Similarity	100.0%;	Pred. No. 0;		
Matches 1677;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGAGAGAGGTTCTGTACTTATGTCACACAGAGGACAGGCAAAAGCCATCGCAGAA	60	
Db	1	ATGAGAGAGGTTCTGTACTTATGTCACACAGAGGACAGGCAAAAGCCATCGCAGAA	60	
Qy	61	GAAATGTGTGAGCAAGCTGTGTACATGAAATTTCTGCAGATCTTCACTGATTTAGTGA	120	
Db	61	GAAATGTGTGAGCAAGCTGTGTACATGAAATTTCTGCAGATCTTCACTGATTTAGTGA	120	
Qy	121	TCCGATTAAGTATGACCTTAAAAACCGAAACAGCTCTCTTGTGTGTGTGTTTCTACACG	180	
Db	121	TCCGATTAAGTATGACCTTAAAAACCGAAACAGCTCTCTTGTGTGTGTGTTTCTACACG	180	
Qy	181	GGCACCCGAGACCCACCCGACACAGCCCGCAAGTTTGTATTAAGAAATACAGAACCAACA	240	
Db	181	GGCACCCGAGACCCACCCGACACAGCCCGCAAGTTTGTATTAAGAAATACAGAACCAACA	240	
Qy	241	CTGC CGGTGATTTCTTTTGCTCACTCGCGGTATGGGTTACTGGGCTTCGATTCAGAA	300	
Db	241	CTGC CGGTGATTTCTTTTGCTCACTCGCGGTATGGGTTACTGGGCTTCGATTCAGAA	300	
Qy	301	TACACCTTACTTTTGCAATGGGGGGAAGTAAATTGATTAACGACTTCAAGAGCTTGAAGCC	360	
Db	301	TACACCTTACTTTTGCAATGGGGGGAAGTAAATTGATTAACGACTTCAAGAGCTTGAAGCC	360	
Qy	361	CGGATTTCTATGACACTGACATGACAGATGACCTGTGAGGTTTAAAGACTTGTGGTTGAG	420	
Db	361	CGGATTTCTATGACACTGACATGACAGATGACCTGTGAGGTTTAAAGACTTGTGGTTGAG	420	
Qy	421	CCGTGATTTGTGAGACTCTGGCCAGAGCCCTCAGAAAGACTTTTAGTCAAGCAGAGACAA	480	
Db	421	CCGTGATTTGTGAGACTCTGGCCAGAGCCCTCAGAAAGACTTTTAGTCAAGCAGAGACAA	480	
Qy	481	GAGAGATTAAGTCGCGCATCCCGGTGGCATCACTTGATCTTTGAGACAGACCTTGTG	540	

481 GAGAGGTAAGTGGCGATCCCGGTGGCATCACCTGATCTTGGAGACAGACCTTGTG 540
541 AAGTCAGAGCTGTACATCATTTGAATCTCAAGTCGAGCTTCTGAGATTGATTCAGGA 600
541 AAGTCAGAGCTGTACATCATTTGAATCTCAAGTCGAGCTTCTGAGATTGATTCAGGA 600
601 AGAAGGATTTCTGAGCTTTTGAAGCAAAATGCACTGAACAGCAACCAATCCAAATGTTGA 660
601 AGAAGGATTTCTGAGCTTTTGAAGCAAAATGCACTGAACAGCAACCAATCCAAATGTTGA 660
661 ATTGAAGACTTTGAGCTCTGATACCTTACCGGTGATCCCACTCTGACAAAGCTCTGTG 720
661 ATTGAAGACTTTGAGCTCTGATACCTTACCGGTGATCCCACTCTGACAAAGCTCTGTG 720
721 AATATTCCTGTTTACCCCGAATATTTAAGGTATCATCTGACAGAGTCTCTTGGCCAG 780
721 AATATTCCTGTTTACCCCGAATATTTAAGGTATCATCTGACAGAGTCTCTTGGCCAG 780
781 GAGGAAAGCCCAAGTATCTGTGATCTTCAAGCATTCAGATCTTCAAGTCCAAATTTCAAAG 840
781 GAGGAAAGCCCAAGTATCTGTGATCTTCAAGCATTCAGATCTTCAAGTCCAAATTTCAAAG 840
841 GCAGTTCAACTTCTACGAATGATGCGATATAAACACTGCGGTGAGAAATTTGACATT 900
841 GCAGTTCAACTTCTACGAATGATGCGATATAAACACTGCGGTGAGAAATTTGACATT 900
901 TCAATATCAGACTTTTCTATCAGCCCTGAGATGCTTCAAGCTGATCTGCTTAAACAT 960
901 TCAATATCAGACTTTTCTATCAGCCCTGAGATGCTTCAAGCTGATCTGCTTAAACAT 960
961 GATTCTGAGGTACAAAGCTTACTCTCAAAAGCTGACCTTGAAGATTAAGAGAGCACTGC 1020
961 GATTCTGAGGTACAAAGCTTACTCTCAAAAGCTGACCTTGAAGATTAAGAGAGCACTGC 1020
1021 GTCCTTTTGAATTAAGAGCAACAAGAAAGAGAGCTACCTTACCCGACATATA 1080
1021 GTCCTTTTGAATTAAGAGCAACAAGAAAGAGAGCTACCTTACCCGACATATA 1080
1081 CCGTGGGATGTTCTCTCAGATTCATTTTAACTGTGTCTTGAATCCGAGCAATTCCT 1140
1081 CCGTGGGATGTTCTCTCAGATTCATTTTAACTGTGTCTTGAATCCGAGCAATTCCT 1140
1141 AAAAAGGCAATTTTGGCAAGCCCTTGTGACTATACAGTGAAGTGTGAAAAGCCGAG 1200
1141 AAAAAGGCAATTTTGGCAAGCCCTTGTGACTATACAGTGAAGTGTGAAAAGCCGAG 1200
1201 CTACAGAGAGCTGTGCACTTAACAAAGGGGAGCCGATTAATAGCCGCTTGTGACGAGATGCC 1260
1201 CTACAGAGAGCTGTGCACTTAACAAAGGGGAGCCGATTAATAGCCGCTTGTGACGAGATGCC 1260
1261 TGTGCTGCTGTGTGATCTCTCTCGCTTCCCTTCTTGCAGCCACCACTCAAGTCTC 1320
1261 TGTGCTGCTGTGTGATCTCTCTCGCTTCCCTTCTTGCAGCCACCACTCAAGTCTC 1320
1321 CTGCTGCAACATCTTCTTAACTTCAACCAAGACATATTCGTGTGCAAGCTCAAGTTTA 1380
1321 CTGCTGCAACATCTTCTTAACTTCAACCAAGACATATTCGTGTGCAAGCTCAAGTTTA 1380
1381 TTTCAACCCAGAAAGCTCATTTTGTCTTCAACATGTGGAATTTCTGTCTACGCGACA 1440
1381 TTTCAACCCAGAAAGCTCATTTTGTCTTCAACATGTGGAATTTCTGTCTACGCGACA 1440
1441 ACAGAGGTTCTGCGAAGGAGATATGTAAGGCTGTGCTGTGTTGTTGCTTCAAGTT 1500
1441 ACAGAGGTTCTGCGAAGGAGATATGTAAGGCTGTGCTGTGTTGTTGCTTCAAGTT 1500
1501 CTTCAGGCAAAATCATCTGATCCCATGAAAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
1501 CTTCAGGCAAAATCATCTGATCCCATGAAAGACGCGGAAAGCCCTGCTCTTAAGATA 1560
1561 TCCATCTCTCTGGAACAAGAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
1561 TCCATCTCTCTGGAACAAGAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620

1561 TCCATCTCTCTGGAACAAGAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
1621 ATATGATGGGTCCAGAAACCGGACATAGCCCGTTTATTTGGTTCTTACAAATAGA 1677
1621 ATATGATGGGTCCAGAAACCGGACATAGCCCGTTTATTTGGTTCTTACAAATAGA 1677
RESULT 7
US-10-741-600-692
; Sequence 692, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 692
; LENGTH: 3256
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-692
Query Match 42.8%; Score 896; DB 21; Length 3256;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1646; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
67 TGTGAGCAAGCTGTGTGATCATGATTTTCTGCAATCTTCACTGATTAATGTAATCCGAT 126
160 TGTGAGCAAGCTGTGTGATCATGATTTTCTGCAATCTTCACTGATTAATGTAATCCGAT 219
127 AAGTATGACCTTAAACCGGAAACAGCTCTCTGTTGTTGTGTTTCTACACGGGACCC 186
220 AAGTATGACCTTAAACCGGAAACAGCTCTCTGTTGTTGTGTTTCTACACGGGACCC 219
187 GGAAGCCACCCGACACAGCCCGCAAGTTTGAAGAAATACAGAACCAACACTGCCG 246
280 GGAAGCCACCCGACACAGCCCGCAAGTTTGAAGAAATACAGAACCAACACTGCCG 339
247 GTTGATTTTCTTGTCTCACTGCGGTATGGTTTCTGAGTCTCGTGAATTCAGATCAACC 306
340 GTTGATTTTCTTGTCTCACTGCGGTATGGTTTCTGAGTCTCGTGAATTCAGATCAACC 399
307 TACTTTGCAATGGGGGAAATATTTGAATTAACGACTTCAAGAGCTTGAAGCCCGCAT 366
400 TACTTTGCAATGGGGGAAATATTTGAATTAACGACTTCAAGAGCTTGAAGCCCGCAT 459
367 TTCTATGACACTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426
460 TTCTATGACACTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 519
427 ATTGCTGACTCTGCGCAAGCCCTCAGAAAGCAATTTTAAGTCAAGAGAGAGAGAG 486
520 ATTGCTGACTCTGCGCAAGCCCTCAGAAAGCAATTTTAAGTCAAGAGAGAGAGAGAG 579
487 ATTAAGTGGCACTCCCGGTGGATCACTGATCTCTTGAAGACAGACCTTGAAGTCA 546
580 ATTAAGTGGCACTCCCGGTGGATCACTGATCTCTTGAAGACAGACCTTGAAGTCA 639
547 GAGCTGCTACATTTGAATCTCAAGTCAAGCTTCTGAGATTCGATGATTCAGGAAGAAAG 606
640 GAGCTGCTACATTTGAATCTCAAGTCAAGCTTCTGAGATTCGATGATTCAGGAAGAAAG 699
607 GATTCTGAGGTTTGAAGCAAAATGAGTGAACAGCAACCAATCCAAATGTTGAATTTGAA 666
700 GATTCTGAGGTTTGAAGCAAAATGAGTGAACAGCAACCAATCCAAATGTTGAATTTGAA 759
667 GACTTGAAGCTTCACTTACCCGTTGAGTACCCCACTCTCAAGAGCTTCTGAATATT 726
760 GACTTGAAGCTTCACTTACCCGTTGAGTACCCCACTCTCAAGAGCTTCTGAATATT 819


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QY 727 CCNGGTTTACCCCGAATATTTAAGATACATCTGACAGAGTCTTGGCCAGAGAA 786
DB 820 CCGGTTTACCCCGAATATTTAAGATACATCTGACAGAGTCTTGGCCAGAGAA 879
QY 787 AGCCAAATCTGTGATCTCAGAGATCCAGTTTTCAGTGGCAATTTCAAGGAGTT 846
DB 880 AGCCAAATCTGTGATCTCAGAGATCCAGTTTTCAGTGGCAATTTCAAGGAGTT 939
QY 847 CAATTTACTACGAATATGATGCAATTAACCACTCTGCTGTGATGATGCAATTTCAAT 906
DB 940 CAATTTACTACGAATATGATGCAATTAACCACTCTGCTGTGATGATGCAATTTCAAT 999
QY 907 ACAGACTTTTCTATGAGCTGGAGATGCTTCAAGGATGATCTGAGCTTAAAGTATTC 966
DB 1000 ACAGACTTTTCTATGAGCTGGAGATGCTTCAAGGATGATCTGAGCTTAAAGTATTC 1059
QY 967 GAGGTACAAAGCTTACTCCAAAGACTGACGTTGAAGATTAAGAGAGCACTGCTCTT 1026
DB 1060 GAGGTACAAAGCTTACTCCAAAGACTGACGTTGAAGATTAAGAGAGCACTGCTCTT 1119
QY 1027 TTGAATAATTAAGGACAGACCAAGAAAGAAAGAGTACTTACCCAGCATATACCTGG 1086
DB 1120 TTGAATAATTAAGGACAGACCAAGAAAGAAAGAGTACTTACCCAGCATATACCTGG 1179
QY 1087 GAGTGTCTCTCCAGTTCAATTTTACCTGCTGTCTGAATCCGAGCAATTCCTAATAAG 1146
DB 1180 GAGTGTCTCTCCAGTTCAATTTTACCTGCTGTCTGAATCCGAGCAATTCCTAATAAG 1239
QY 1147 GCATTTTTCGAGCCCTTGTGACATATACAGTGAAGTGTGAAAAGGCGACGCTACAG 1206
DB 1240 GCATTTTTCGAGCCCTTGTGACATATACAGTGAAGTGTGAAAAGGCGACGCTACAG 1299
QY 1207 GAGCTGTGACATTAACAAGGAGGAGCGATTAATAGCCGCTTTGTACGAGATGCTGTGCC 1266
DB 1300 GAGCTGTGACATTAACAAGGAGGAGCGATTAATAGCCGCTTTGTACGAGATGCTGTGCC 1359
QY 1267 TGCCTGTGAGATCTCTCTGCTGCTTCCCTTCTGACAGCACTCACTGCTCTGCTC 1326
DB 1360 TGCCTGTGAGATCTCTCTGCTGCTTCCCTTCTGACAGCACTCACTGCTCTGCTC 1419
QY 1327 GAACATCTTCTTAACTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTATTTAC 1386
DB 1420 GAACATCTTCTTAACTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTATTTAC 1479
QY 1387 CAGAGAAAGCTCCATTTTGTCTTCAATTTGTGAATTTCTGTCTACGCAACAAGAG 1446
DB 1480 CAGAGAAAGCTCCATTTTGTCTTCAATTTGTGAATTTCTGTCTACGCAACAAGAG 1539
QY 1447 GTTCTGCGGAAGGATATGTAACAGGCTGGCTGGCTTGTGTGCTTCACTTCTTCCAG 1506
DB 1540 GTTCTGCGGAAGGATATGTAACAGGCTGGCTGGCTTGTGTGCTTCACTTCTTCCAG 1599
QY 1507 CCAGAACATATGATGATCCCATGAAGACAGGAGGAAAGCCCTGCTCTTAAGATATCATC 1566
DB 1600 CCAGAACATATGATGATCCCATGAAGACAGGAGGAAAGCCCTGCTCTTAAGATATCATC 1659
QY 1567 TCTCTCGAACAACAATTTCTTCACTTACAGATGACCCCTCAATCCCATCATATATG 1626
DB 1660 TCTCTCGAACAACAATTTCTTCACTTACAGATGACCCCTCAATCCCATCATATATG 1719
QY 1627 GTGGGTTCAGAAACCGGACATAGCCCGTTTATTTGGGTTCTTCAACAATGAGAAATC 1686
DB 1720 GTGGGTTCAGAAACCGGACATAGCCCGTTTATTTGGGTTCTTCAACAATGAGAAATC 1779
QY 1687 CAAGAACACACCCAGATGGAATTTTGGAGCATGTGTT 1727
DB 1780 CAAGAACACACCCAGATGGAATTTTGGAGCATGTGTT 1820

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RESULT 8
US-10-741-600-693
; Sequence 693, Application US/10741600

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; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; NUMBER OF SEQ ID NOS: 2003-12-22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 693
; LENGTH: 3274
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-741-600-693

Query Match      42.8%; Score 896; DB 21; Length 3274;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1646; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 67 TGTGAGCAAGCTGTGTACATGATTTTCTGAGATCTTCACTGATTTAGTGAATCCGAT 126
DB 178 TGTGAGCAAGCTGTGTACATGATTTTCTGAGATCTTCACTGATTTAGTGAATCCGAT 237
QY 127 AAGTATGACCTAATAAACGAAACAGCTCTCTGTGTGTGTGTGTCTACACGAGCACC 186
DB 238 AAGTATGACCTAATAAACGAAACAGCTCTCTGTGTGTGTGTGTGTCTACACGAGCACC 297
QY 187 GAGAGCCCAACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACACTGCCG 246
DB 298 GAGAGCCCAACCCGACACAGCCCGCAAGTTTGTAAAGAAATACAGAACCAACACTGCCG 357
QY 247 GTTGAATTTCTTGTCTCACTCGGGGTATGAGGTATCTGGGTCTGGGTATCAAGATACAC 306
DB 358 GTTGAATTTCTTGTCTCACTCGGGGTATGAGGTATCTGGGTCTGGGTATCAAGATACAC 417
QY 307 TACTTTTGCATGGGGGGAAGATTAATGATTAACGACTCAAGAGCTTGAAGCCCGCAT 366
DB 418 TACTTTTGCATGGGGGGAAGATTAATGATTAACGACTCAAGAGCTTGAAGCCCGCAT 477
QY 367 TTCTATGACACTGACATGACATGATGATGATGATTTAGAACTTGTGTGTTAGCCGTGG 426
DB 478 TTCTATGACACTGACATGACATGATGATGATGATTTAGAACTTGTGTGTTAGCCGTGG 537
QY 427 ATTGCTGACCTGTGCGACGCTCTCAGAAAGCAATTTTATGATCAAGCAGAGACAAGAGAG 486
DB 538 ATTGCTGACCTGTGCGACGCTCTCAGAAAGCAATTTTATGATCAAGCAGAGACAAGAGAG 597
QY 487 ATTAAGTGGGCACTCCCGGTGGCATCACTGCAATCTTGAAGACAGACCTTGTGAAGTCA 546
DB 598 ATTAAGTGGGCACTCCCGGTGGCATCACTGCAATCTTGAAGACAGACCTTGTGAAGTCA 657
QY 547 GAGTGTCTACATTTGAATCTCAAGTGAAGCTTGTGAATTTCAAGATTTCAAGAAAG 606
DB 658 GAGTGTCTACATTTGAATCTCAAGTGAAGCTTGTGAATTTCAAGATTTCAAGAAAG 717
QY 607 GATTTGAGGTTTGAAGAAATGACATGAACACGACCAATCCATGTTGTATTTGA 666
DB 718 GATTTGAGGTTTGAAGAAATGACATGAACACGACCAATCCATGTTGTATTTGA 777
QY 667 GACTTTGAGTCCCACTTACCCGTTGCGTACCCCACTCTCAACAAGCTCTGTAATATT 726
DB 778 GACTTTGAGTCCCACTTACCCGTTGCGTACCCCACTCTCAACAAGCTCTGTAATATT 837
QY 727 CCTGGTTTACCCCGAATATTTAAGGTACATCTGACAGAGTCTTGGCCAGAGAA 786
DB 838 CCTGGTTTACCCCGAATATTTAAGGTACATCTGACAGAGTCTTGGCCAGAGAA 897
QY 787 AGCCAAATCTGTGATCTCAGAGATCCAGTTTTCAGTGGCAATTTCAAGGAGTT 846
DB 898 AGCCAAATCTGTGATCTCAGAGATCCAGTTTTCAGTGGCAATTTCAAGGAGTT 957
QY 847 CAATTTACTACGAATATGATGCAATTAACCACTCTGCTGTGATGATTTCAAT 906

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Db 958 CAACTTCTGAGATGATGCTATTAACCACTCTGCTGATGAAATTTGCAATTTCAAT 1017
Qy 907 ACAGACTTTTCTATAGAGCTTGAGATGCTTTCAGCGTGAATCTGCCCTAACAGTATTC 966
Db 1018 ACAGACTTTTCTATAGAGCTTGAGATGCTTTCAGCGTGAATCTGCCCTAACAGTATTC 1077
Qy 967 GAGGTCAAAAGCTTATCTCCAAAGATGAGCTTGAAGATTAAGAGAGCATGCTGCTT 1026
Db 1078 GAGGTCAAAAGCTTATCTCCAAAGATGAGCTTGAAGATTAAGAGAGCATGCTGCTT 1137
Qy 1027 TTGAAAAATAAAGGAGACACAAAGAAAGAGACTTACCTTACCCGACATATACCTGCG 1086
Db 1138 TTGAAAAATAAAGGAGACACAAAGAAAGAGACTTACCTTACCCGACATATACCTGCG 1197
Qy 1087 GAGTGTCTCTCAGATTGATTTTACCTGCTGCTTGAATTCGAGCAATTCCTAAAG 1146
Db 1198 GAGTGTCTCTCAGATTGATTTTACCTGCTGCTTGAATTCGAGCAATTCCTAAAG 1257
Qy 1147 GCATTTTGGAGAGCTTGTGAGATTAACAGTGAAGTGTGAAAAAGCCGAGCTTACAG 1206
Db 1258 GCATTTTGGAGAGCTTGTGAGATTAACAGTGAAGTGTGAAAAAGCCGAGCTTACAG 1317
Qy 1207 GAGCTGTGAGTAAACAAAGGGGAGCCGATTAAGCCGCTTGTGAAGATGCTGCTG 1266
Db 1318 GAGCTGTGAGTAAACAAAGGGGAGCCGATTAAGCTTGTGAAGATGCTGCTGCTG 1377
Qy 1267 TGCCTTGTGATCTCTCTGCTGCTTCCCTTGTGAGCAGCAGCTCAGTCTCTGCTC 1326
Db 1378 TGCCTTGTGATCTCTCTGCTGCTTCCCTTGTGAGCAGCAGCTCAGTCTCTGCTC 1437
Qy 1327 GAACATCTTCTTAACTTCAACCCAGACCATTTGCTGTGAGTGAAGTCAATTTTAC 1386
Db 1438 GAACATCTTCTTAACTTCAACCCAGACCATTTGCTGTGAGTGAAGTCAATTTTAC 1497
Qy 1387 CCAAGAAAGCTTCAATTTTGTCTTCAACATTTGGAATTTGCTGTGAGTGAAGTCA 1446
Db 1498 CCAAGAAAGCTTCAATTTTGTCTTCAACATTTGGAATTTGCTGTGAGTGAAGTCA 1557
Qy 1447 GTTCTGGAAGGAGATGATGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1506
Db 1558 GTTCTGGAAGGAGATGATGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1617
Qy 1507 CCAACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1566
Db 1618 CCAACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1677
Qy 1567 TCTCTCTGAAACAACAATTTCTTCACTTACAGATGAGCCCTCAATCCCATCATATG 1626
Db 1678 TCTCTCTGAAACAACAATTTCTTCACTTACAGATGAGCCCTCAATCCCATCATATG 1737
Qy 1627 GTGGGTTCAGAAACCGGATAGCCCGTTTATTTGGGTTCTTACAAATAGAGAAATC 1686
Db 1738 GTGGGTTCAGAAACCGGATAGCCCGTTTATTTGGGTTCTTACAAATAGAGAAATC 1797
Qy 1687 CAAGAACAACCAAGTGAATTTTGGAGCATGTGTT 1727
Db 1798 CAAGAACAACCAAGTGAATTTTGGAGCATGTGTT 1838

RESULT 9
US-10-029-386-6369
; Sequence 6369, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
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; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 6369
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008727.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.45
; OTHER INFORMATION: NT HIT: AF121205.1, EVALU0 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALU0 3.30e+00
; OTHER INFORMATION: EST_HUMAN HIT: AV132586.1, EVALU0 0.00e+00
US-10-029-386-6369

Query Match 15.8%; Score 330; DB 16; Length 591;
Best Local Similarity 99.7%; Pred. No. 1.7e-169;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 401 GTTTGAACCTTGTTGGTGGACCGGTGATGCTGGAATCTGGCCGACCTCAGAAAGCATT 460
Db 38 GTTTGAACCTTGTTGGTGGACCGGTGATGCTGGAATCTGGCCGACCTCAGAAAGCATT 97
Qy 461 TTAGGTCAAGCAGAGACAAAGAGAGATAGTGGCCACTCCCGGTGGATCAGCTGCAT 520
Db 98 TTAGGTCAAGCAGAGACAAAGAGAGATAGTGGCCACTCCCGGTGGATCAGCTGCAT 157
Qy 521 CTTGAGAGACAGCTTGTGAAGTCAAGCTGCTACATTTGATTTCAATGAGCTTGC 580
Db 158 CTTGAGAGACAGCTTGTGAAGTCAAGCTGCTACATTTGATTTCAATGAGCTTGC 217
Qy 581 TGAGATTCATGATTCAGAGAAAGAGATTCAGAGTTTGAAGCAAAATGACGTAGACA 640
Db 218 TGAGATTCATGATTCAGAGAAAGAGATTCAGAGTTTGAAGCAAAATGACGTAGACA 277
Qy 641 GCACCAATCAATGTTGTAATTAAGACTTGAAGTCTCACTTACCCGTTGCTGCTGCT 700
Db 278 GCACCAATCAATGTTGTAATTAAGACTTGAAGTCTCACTTACCCGTTGCTGCTGCT 337
Qy 701 CACTCTCAGAGCTCTGTAATATCTGCTTACCCCAAGAAATTTACAGTACATC 760
Db 338 CACTCTCAGAGCTCTGTAATATCTGCTTACCCCAAGAAATTTACAGTACATC 397
Qy 761 TGCAGAGTCTCTGGCCAGG 781
Db 398 TGCAGAGTCTCTGGCCAGG 418

RESULT 10
US-10-029-386-20100
; Sequence 20100, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20100
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008727.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.45
; OTHER INFORMATION: NT HIT: g114729757, EVALU0 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALU0 1.80e+00
; OTHER INFORMATION: EST_HUMAN HIT: AV132586.1, EVALU0 0.00e+00
US-10-029-386-20100
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Query Match 15.7%; Score 328; DB 16; Length 379;
Best Local Similarity 99.7%; Pred. No. 26-168;
Matches 378; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 402 TTAAAGCTTGTGTGAGCCGTGAGTGTGCTGAGCTTGGCCAGCCCTCAGAAAGCATTT 461
DB 1 TTAAAGCTTGTGTGAGCCGTGAGTGTGCTGAGCTTGGCCAGCCCTCAGAAAGCATTT 60
QY 462 TAGGTCAAGCAGAGCAGAGAGATTAAGTGGCCCATCTCCGGTGGCATTCCTGGATC 521
DB 61 TAGGTCAAGCAGAGCAGAGAGATTAAGTGGCCCATCTCCGGTGGCATTCCTGGATC 120
QY 522 CTGAGAGCAGACCTTGTGAAGTCAAGAGCTGCTACACATTGAATCTCAAGTGGATCTT 581
DB 121 CTGAGAGCAGACCTTGTGAAGTCAAGAGCTGCTACACATTGAATCTCAAGTGGATCTT 180
QY 582 GAGATTGATGATTCAGAGAAAGAGATTCAGAGTTTGAAGCAAAATGCAAGTGAACG 641
DB 181 GAGATTGATGATTCAGAGAAAGAGATTCAGAGTTTGAAGCAAAATGCAAGTGAACG 240
QY 642 CAACCAATCCAAATGTTGTAATGGAAGACTTTGAGTCTTCACTTACCCGTTGGTACCCC 701
DB 241 CAACCAATCCAAATGTTGTAATGGAAGACTTTGAGTCTTCACTTACCCGTTGGTACCCC 300
QY 702 ACTCTCAAGAGCTCTGGAATATTCCTGTTTACCCCGAATATTTACAGTACATCT 761
DB 301 ACTCTCAAGAGCTCTGGAATATTCCTGTTTACCCCGAATATTTACAGTACATCT 360
QY 762 GCAGAGTCTCTTGGCCAG 780
DB 361 GCAGAGTCTCTTGGCCAG 379

RESULT 11
US-10-029-386-1735
Sequence 1735, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 1735
LENGTH: 591
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC021609.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
OTHER INFORMATION: NT HIT: AF121205.1, EVALUE 0.00e+00
OTHER INFORMATION: EST HUMAN HIT: AU132586.1, EVALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUE 3.30e+00
US-10-029-386-1735

Query Match 13.3%; Score 279; DB 16; Length 591;
Best Local Similarity 99.5%; Pred. No. 1.6e-141;
Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGTGAGCCGTGAGTGTGCTGAGCTTGGCCAGCCCTCAGAAAGCATTT 460
DB 38 GTTTAGAACTTGTGTGAGCCGTGAGTGTGCTGAGCTTGGCCAGCCCTCAGAAAGCATTT 97

QY 461 TTAGGTCAAGCAGAGCAGAGAGATTAAGTGGCCCATCTCCGGTGGCATCCTGCAT 520
DB 98 TTAGGTCAAGCAGAGCAGAGAGATTAAGTGGCCCATCTCCGGTGGCATCCTGCAT 157
QY 521 CCTGAGAGCAGACCTTGTGAAGTCAAGAGCTGCTACACATTGAATCTCAAGTGGATCTT 580
DB 158 CCTGAGAGCAGACCTTGTGAAGTCAAGAGCTGCTACACATTGAATCTCAAGTGGATCTT 217
QY 581 TGAGATTGATGATTCAGAGAAAGAGATTCAGAGTTTGAAGCAAAATGCAAGTGAACA 640
DB 218 TGAGATTGATGATTCAGAGAAAGAGATTCAGAGTTTGAAGCAAAATGCAAGTGAACA 277
QY 641 GCAACCAATCCAAATGTTGTAATGGAAGACTTTGAGTCTTCACTTACCCGTTGGTACCCC 700
DB 278 GCAACCAATCCAAATGTTGTAATGGAAGACTTTGAGTCTTCACTTACCCGTTGGTACCCC 337
QY 701 CACTCTCAAGAGCTCTGGAATATTCCTGTTTACCCCGAATATTTACAGTACATC 760
DB 338 CACTCTCAAGAGCTCTGGAATATTCCTGTTTACCCCGAATATTTACAGTACATC 397
QY 761 TGCAGAGTCTCTTGGCCAG 781
DB 398 TGCAGAGTCTCTTGGCCAG 418

RESULT 12
US-10-029-386-15435
Sequence 15435, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 15435
LENGTH: 379
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC021609.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUE 1.80e+00
OTHER INFORMATION: EST HUMAN HIT: AU132586.1, EVALUE 0.00e+00
OTHER INFORMATION: NT HIT: g114729757, EVALUE 0.00e+00
US-10-029-386-15435

Query Match 13.2%; Score 277; DB 16; Length 379;
Best Local Similarity 99.5%; Pred. No. 1.9e-140;
Matches 377; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 TTAAAGCTTGTGTGAGCCGTGAGTGTGCTGAGCTTGGCCAGCCCTCAGAAAGCATTT 60
QY 462 TAGGTCAAGCAGAGCAGAGAGATTAAGTGGCCCATCTCCGGTGGCATTCCTGGATC 521
DB 61 TAGGTCAAGCAGAGCAGAGAGATTAAGTGGCCCATCTCCGGTGGCATTCCTGGATC 120
QY 522 CTGAGAGCAGACCTTGTGAAGTCAAGAGCTGCTACACATTGAATCTCAAGTGGATCTT 581
DB 121 CTGAGAGCAGACCTTGTGAAGTCAAGAGCTGCTACACATTGAATCTCAAGTGGATCTT 180

QY	Db	QY	Db	QY	Db	QY	Db	QY	Db		
582	GAGATTGCATGATTGAGGAAGAAGATTCGTAGGTTTGAAGCAAAATGCGATGAACG	641	181	GAGATTCATGATTTAGGAGAGAAAGGATTCGAGGTTTGAAGCAAAATGCGATGAACG	240	642	CAACCAATCCAATGTTGTATTTGAAGAATCTTGAGTCTCACTTACCCGTTGCGTACCCC	701	241	CAACCAATCCAATGTTGTATTTGAAGAATCTTGAGTCTCACTTACCCGTTGCGTACCCC	300
702	ACTCTCAACAAGCTCTCTGAATATTTCTCGTGTATTTACCCCGAATATTTACAGGTACATCT	761	301	ACTCTCAACAAGCTCTCTGAATATTTCTCGTGTATTTACCCCGAATATTTACAGGTACATCT	360	762	GCAGGAGTCTCTTTGGCCAG	780	361	GCAGGAGTCTCTTTGGCCAG	379

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: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.57
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.79
: OTHER INFORMATION: SWISSPROT HIT: O61608, EVALUE 4.00e-04
: OTHER INFORMATION: EST HUMAN HIT: AA085543.1, EVALUE 7.00e-94
: OTHER INFORMATION: NT HIT: g113325067, EVALUE 5.00e-94
US-10-029-386-14338

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Query Match	8.4%	Score 175	DB 16	Length 175
Best Local Similarity	100.0%	Pred. No. 1.7e-84		
Matches 175	Conservative 0	Mismatches 0	Indels 0	Gaps 0

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Db	1 75	AAAAGAGTCAGACATTTCTTAAGAGATGGAGTCTTAATCATCATGAAAGTTCTCTC	116
QY	1 827	AAGAGATGCTCTCTTGGGGAGAGAGAAAGCCCGACAAAGTATGTAACAAGACAATCCA	1886
Db	1 15	AAGAGATGCTCTCTTGGGGAGAGAGAGAGCCCGACAAAGTATGTAACAAGACAATCCA	56
QY	1 887	GCTTCATGCGCAGAGGTGCGAANAATCTCTCCAGAGGAACGCGCATATTAT	1941
Db	55	GCTTCATGCGCAGAGGTGCGAANAATCTCTCCAGAGGAACGCGCATATTAT	1

Search completed: August 27, 2005, 17:33:32
Job time : 902.113 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 23:18:31 ; Search time 4537.36 Seconds
(without alignments)
17558.328 Million cell updates/sec

Title: US-09-371-347A-47

Perfect score: 2093

Sequence: 1 atgaggaggttcgtctact.....ttcagatattcgtcaca 2093

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1288	61.5	3100	3	BC062577 Homo sapi
2	956	45.7	3143	3	BC035977 Homo sapi
3	719	34.4	908	5	BX348674 BX348674
4	689	32.9	874	4	BM801462 AGENCOURT
5	623	29.8	646	7	CN260357 CN260357
6	565	27.0	565	1	AU279788 AU279788
7	535	25.6	877	1	AU124440 AU124440
8	531	25.4	1661	5	BQ218755 AGENCOURT
9	517	24.7	826	4	BI772430 BI772430
10	512	24.5	776	6	CB997527 AGENCOURT
11	507	24.2	834	5	BU941078 AGENCOURT
12	455	21.7	822	1	AU132586 AU132586
13	448	21.4	591	2	AW965709 EST377782
14	446	21.3	818	6	CD559384 AGENCOURT
15	434	20.7	591	4	BI025283 RC5-MT025
16	431	20.6	974	5	BX375211 BX375211
17	406	19.4	710	5	BU570323 AGENCOURT
18	384	18.3	527	4	BI025277 RC5-MT025
19	374	17.9	579	7	CN260360 CN260360
20	368	17.6	852	5	BQ431497 AGENCOURT
21	361	17.2	692	7	CN260359 CN260359
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23	359	17.2	499	6	CD704108 EST20635
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25	341	16.3	395	4	BM838530
26	340	16.2	526	2	AW952883 EST364953
27	337	16.1	818	7	CF995233 AGENCOURT
28	335	16.0	413	2	BF810368 BF810368
29	335	16.0	413	2	BF810479 RC5-CI014
30	332	15.9	366	1	AA085543 AA085543
31	331	15.8	521	6	CB164340 CB164340
32	320	15.3	839	4	BG531787 BG531787
33	311	14.9	478	4	BM754488 BM754488
34	302	14.4	440	4	BG877205 BG877205
35	297	14.2	416	6	CB996520 CB996520
36	292	14.0	528	2	BE301292 BE301292
37	291	13.9	664	7	CR768694 CR768694
38	291	13.9	667	7	CR770923 CR770923
39	291	13.9	667	7	CR557482 CR557482
40	276	13.2	481	7	CR549172 CR549172
41	272	13.0	301	1	AL704780 AL704780
42	269	12.9	642	2	BF346446 BF346446
43	264	12.6	366	6	CB289831 CB289831
44	257	12.3	366	2	BF808461 BF808461
45	257	12.3	368	1	AA355001 AA355001

ALIGNMENTS

RESULT 1	BC062577	3100 bp	mRNA	linear	HTC 25-NOV-2003
LOCUS	BC062577				
DEFINITION	Homo sapiens cDNA clone IMAGE:5189058, containing frame-shift errors.				
ACCESSION	BC062577				
VERSION	BC062577.1	GI:38511756			
KEYWORDS	HTC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Strausberg, R., Peingold, R.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Schenker, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheffer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Datchenko, L., Marziani, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uebelin, T.B., Toshitani, S., Carninci, P., Prange, C., Rana, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mallory, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hilyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, U., Helton, E., Ketterman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Small, D.B., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
TITLE	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
JOURNAL	22388257				
MEDLINE	12477932				
PUBMED	2 (bases 1 to 3100)				
REFERENCE	Strausberg, R.				
AUTHORS	Direct Submission				
TITLE	Submitted (24-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,				
JOURNAL	USA NIH-MGC Project URL: http://mgc.nci.nih.gov				
REMARK	Contact: MGC help desk				
COMMENT	Email: cgabs-r@mail.nih.gov				
	Tissue Procurement: Life Technologies, Inc.				

CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Gatherburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgti.nih.gov
Ahner, N., Ayle, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.M., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Scantirpop, S., Thomas, P.D., Touchman, J.W.,
Teurisson, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAK Plate: 135 Row: e Column: 21
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA g1: 4505278
This clone has the following problem: frame shifted.

FEATURES

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1. 3100
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Best Local Similarity 99.6%; Pred. No. 0;
Matches 1808; Conservative 0; Mismatches 2; Indels 5; Gaps 2;
283 GGTCTCGGTGATTCAGATACACCTATTTGCAATGGGGGAGAGATATGATTAACGA 342
172 GGTCTCGGTGATTCAGATACACCTATTTGCAATGGGGGAGAGATATGATTAACGA 231
343 CTTCAAGAGCTTGAAGCCCGCATTTCTATGACACTGACATGACATGACATGCTGTAGT 402
232 CTTCAAGAGCTTGAAGCCCGCATTTCTATGACACTGACATGACATGACATGCTGTAGT 291
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292 TTGAACTTGTGTTGAGCGGTGATTTGCTGACCTGGCCAGCCCTCAGAAAGCATTTT 351
463 AGGTCAAGCAGAGCAGAGAGAGATTAAGTGGCGCACTCCCGGTGCGATCACTGCATCC 522
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703 CTCTCAAGAGCTTCTGAATATTCCTGTTTACCCCAAGATATTTTACAGGTACATCTG 762
592 CTCTCAAGAGCTTCTGAATATTCCTGTTTACCCCAAGATATTTTACAGGTACATCTG 651
763 CAGAGTCTCTTGGCAGAGAGAGAGAGAGATATCTGATCTTGAAGAGATCCAGTTT 822
652 CAGAGTCTCTTGGCAGAGAGAGAGAGAGATATCTGATCTTGAAGAGATCCAGTTT 711

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QY 1003 GATTAAG 1062
DB 892 GATTAAG 950
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DB 1011 GAAATCCGAGCAATTTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1070
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QY 1719 TGGTTGTTTGGCTGAG 1778
DB 1611 TGGTTGTTTGGCTGAG 1670
QY 1779 CATTTCTTAAG 1838
DB 1671 CATTTCTTAAG 1730
QY 1839 GTTGGGAG 1898
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QY 1959 AATATGGCCAGAGATGTACATGATGCTCTTGCCAAATATATAGCAAGAGGTTGAGATT 2018
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DB 1911 GAAAACTAGAGCAATGAAAAACCTGGCCACTTTAAAGAAAGAAAGCGTACCTTCAG 1970
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QY 2079 GATATTTGGTCATAA 2093
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DB 1971 GATATTTGGTCATAA 1985
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RESULT 2
LOCUS BC035977 3143 bp mRNA linear HTC 20-SEP-2002
DEFINITION BC035977 Homo sapiens, clone IMAGE:461253, mRNA.
ACCESSION BC035977
VERSION BC035977.1 GI:23243305
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3143)
Strausberg, R.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-ahgc.stanford.edu>
Contact: (Dickson, Mark) mdc@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAL Plate: 41 Row: g Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4505278
This clone has the following problem: frame shifted.
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QY 61 GAAATGTGTAGCAAGCTGTGTATCATGGAATTTCTGCAAGATCTTCACTGATTAAGTAA 120
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DB 112 GAAATGTGTAGCAAGCTGTGTATCATGGAATTTCTGCAAGATCTTCACTGATTAAGTAA 171
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QY 121 TCCGATTAAGTATGACTTAAACCGAAACAGCTCTCTTGTGTGTGTTCTACACAG 180
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DB 172 TCCGATTAAGTATGACTTAAACCGAAACAGCTCTCTTGTGTGTGTTCTACACAG 231
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DB 352 TACACCTACTTTTGCAATGCGGGGGAAGATATATTGATTAACGACTTCAGAGCC 411
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DB 472 CGGTGATTTGCTGACCTGCGCAGCCCTCAGAAAGCAATTTAGGTCAAGAGACAA 531
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DB 712 ATTGAAGACTTTGAGTCTCTCACTTACCCGTTGGTATACCCCACTCTCAGAGCTCTCTG 771
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QY 721 AATATTCCTGTTTACCCCGCAATATTTACAGGTACATCTGCAGAGATCTCTGGCCAG 780
| | | | |
DB 772 AATATTCCTGTTTACCCCGCAATATTTACAGGTACATCTGCAGAGATCTCTGGCCAG 831
| | | | |
QY 781 GAGGAAGCCAGTATCTGTGACTTCAGAGATCCAGTTTCAAGTGCATATTCAGAG 840
| | | | |
DB 832 GAGGAAGCCAGTATCTGTGACTTCAGAGATCCAGTTTCAAGTGCATATTCAGAG 891
| | | | |
QY 841 GCGATTCAACTTACTACGATGATGCCATTAACCACTCTGCTGTAGATTTGACATT 900
| | | | |
DB 892 GCGATTCAACTTACTACGATGATGCCATTAACCACTCTGCTGTAGATTTGACATT 951
| | | | |
QY 901 TCAATACAGACTTTTCTATAGCCTTGAGATGCTTCAAGCTGATCTGCCCTAACAT 960
| | | | |
DB 952 TCAATACAGACTTTTCTATAGCCTTGAGATGCTTCAAGCTGATCTGCCCTAACAT 1011
| | | | |
QY 961 GATTCTGAGTACAAAGCCTATCCAAAGACGTCAGCTTGAAGATTAAGAGACAGCTG 1020
| | | | |
DB 1012 GATTCTGAGTACAAAGCCTATCCAAAGACGTCAGCTTGAAGATTAAGAGACAGCTG 1071
| | | | |
QY 1021 GTCTTTTGAATTAAGGACAGACAAAGAGAAAGG 1058
| | | | |
DB 1072 GTCTTTTGAATTAAGGACAGACAAAGAGAAAGG 1109
| | | | |
RESULT 3
LOCUS BX348674 908 bp mRNA linear EST 08-APR-2004
BX348674

DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
BX348674 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DC010Y111 5-PRIME, mRNA sequence.	BX348674	BX348674.1	GI:30375301	EST.	Homo sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	1 (bases 1 to 908)	Li, W.B., Gruber, C., Jesse, J., and Polayes, D.	Full-length cDNA libraries and normalization unpublished (2001)	Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: secre@genoscope.cns.fr , Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3392.f

For more information about this cluster, see http://www.genoscope.cns.fr/cdna?b=CS0BAG006ZB02_CS00490_1&c=3392.f

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FEATURES
SOURCE
    location/Qualifiers
    1..908
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="CSODC010Y11.1"
    /tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
    /clone_id="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
    /note="First strand cDNA was primed with a NotI-oligo(dT)
    primer. Five prime end enriched, double-strand cDNA was
    digested with Not I and cloned into the Not I and EcoR V
    sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN

Query Match	Score	DB	5;	Length	908;
34.48;					

Matches 719; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

674 AGTCTCACTTACCCGTTGGTACCCCACTCTCACAGCCTCTGATATTCTGGTT 733

Db 28 AGTCCTCACTTACCCGTTGGTACCCCACTCTCAAGA CCTCTCTGAATATTCCTGTT 87

734 TACCCCGAATATTACAGGTACATCTGCAGAGTCTCTTGGCCAGGAGGAAGCCAAG 793

Db 88 TACCCCGAGATATTACAGGTACATCTGCAGAGTCTCTTGGCCAGAGGAAGCCAAG 147

QY 794 TATCTGCTTCAGCAGATCCAGTTTTCAGTGCCAATTCAAAGGCAGTTCACCTTA 853

Db 148 TATCTGTA CTTCAGCAGATCCAGTTT TCAAGTGCCAA TTTCA AAGGCA GTTCA ACTTA 207

854 CTACGAATGATGCCATAAAACCACTCTGCTGTGAGATTGGACATTCAATACAGACT 913

Db 208 CTACGAATGATGCCATAAAACCACCTCTGCTGCTAGAAATTGGACATTTCAAATACAGACT 267

914 TTTCCCTATCAGCCTGGAGATGCCCTTCAAGCGTGATCTGCCCTAACAGTGATTCTGAGGTAC 973

Db 268 TTTCTATCAGCCTGGAGATGCCTTCAGCGTGATCTGCCCTAACAGTGATTCTGAGGTAC 327

974 AAAGCTACTCCAAGACTGCAGCTTGAAGATAAAGAGAGCACTGCGTCTTTGAAA 1033

Db 328 AAAGCTACTCCAAAGACTGCAGCTTGAAGATAAAAGAGAGCACCTGCGTCTTTGAAA 387

1034 TAAAGCAGACACAAAGAAGAGCTACTTACCCAGCATATACCTGCGGATGT 1093

Db 388 TAAAGCAGACACAAAGAAGAGCTACTTACCCGAGCATATACCTGCGGATGTT 447

Db	448	CTCTCCAGTTCATTTTACTGCGTCTTGAATCCAGCAATTCCTAAAAAGCAATTTT	507
QY	1154	TGCGAGCCCTTTGTGACATATACAGATGACAGTGTGTAAGCCGAGCTACAGAGCTGT	1213
Db	508	TGCGAGCCCTTTGTGACATATACAGTACAGTGTGTAAGCCGAGCTACAGAGCTGT	567
QY	1214	GCACTAAACAAGGGGCGAGCCGATTAATGAGCCGCTTTGTACAGAGATGCTGTGCTGCTTGT	1273
Db	568	GCACTAAACAAGGGGCGAGCCGATTAATGAGCCGCTTTGTACAGAGATGCTGTGCTGCTTGT	627
QY	1274	TGATCTCTCTCTCTGCTTCCCTCTTGGCCAGCCAGCACTCAGTCTCTGTGCAATC	1333
Db	628	TGATCTCTCTCTCTGCTTCCCTCTTGGCCAGCCAGCACTCAGTCTCTGTGCAATC	687
QY	1334	TTCTTAACCTTCAACCCAGACCAATATTGATGTGCAAGCTCAAGTTTATTTCCACCAGGA	1392
Db	688	TTCTTAACCTTCAACCCAGACCAATATTGATGTGCAAGCTCAAGTTTATTTCCACCAGGA	746

RESULT 4
 BM801462
 LOCUS
 DEFINITION
 5', mRNA sequence.

874 bp mRNA linear EST 05-MAR-2002
 AGENCOURT_6459212 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5560477

VERSION	BM601462.1	GI:19118285
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
REFERENCE	1 (bases 1 to 874)	
AUTHORS	NH-MGC http://mgc.nci.nih.gov/ .	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Straubeberg, Ph.D.	

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation

found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAM12286 Row: 1 Column: 14

FEATURES

Location/Qualifiers

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/organism="Homo sapiens"
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/db_xref="taxon:9606"

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/tissue_type="duodenal adenocarcinoma, cell line"

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/clone_lib="NIH_MGC_88"
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Site_1: NoTI; Site_2: SaLI; Cloned unidirectionally;

enriched for full-length clones and constructed by Life

ORIGIN

Query Match	32.98;	Score 689;	DB 4;	Length 874;
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Matches 739; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 ATGAGGAGTTCTGTTACTATATGCTACACAGCAGGACAGGCAGAAGGCCATCGCAGAA 60

Db 50 ATGAGAGGTTTCTGTTACTATATGCTACACAGCAGGACAGGCAAGGCCATCGCAGAA 109

61 GAATGTGTGAGCAAGCTGTGGTACATGATTTTCTGCAGATCTTCACTGTATTAGTGA 120

Db 110 GAAATATGTGACCAAGCTGTGTGATGATGATTTCTGACATCTTCACTGATTTAGTGA 169
Qy 121 TCCGATTAAGTATGACTTAATAAACCAGAAAGGCTCCCTGTTGTTGTTGTTCTACAG 180
Db 170 TCCGATTAAGTATGACTTAATAAACCAGAAAGGCTCCCTGTTGTTGTTGTTCTACAG 229
Qy 181 GGCACCGGAGACCCACCCGACACAGCCGCAAGTTGTTAGGAATAACAGAACCAACA 240
Db 230 GGCACCGGAGACCCACCCGACACAGCCGCAAGTTGTTAGGAATAACAGAACCAACA 289
Qy 241 CTGCGGTTGATTTCTTCTGCTCACTGCGGTATGAGTTACTGGTCTCGGTATTCAGA 300
Db 290 CTGCGGTTGATTTCTTCTGCTCACTGCGGTATGAGTTACTGGTCTCGGTATTCAGA 349
Qy 301 TACACCTACTTTTGCAATGAGGAGGAAGATTAATTGATTAACGATTCAGAGCTTGAGCC 360
Db 350 TACACCTACTTTTGCAATGAGGAGGAAGATTAATTGATTAACGATTCAGAGCTTGAGCC 409
Qy 361 CGGCAATTTCTATGACACTGACATGACATGATGATGATGATTTAGAACTTGTTGAG 420
Db 410 CGGCAATTTCTATGACACTGACATGACATGATGATGATGATTTAGAACTTGTTGAG 469
Qy 421 CGGTGATTTCTGACACTGCGCAAGCTCTGAGAAACATTTTATGATGATGATGAT 480
Db 470 CGGTGATTTCTGACACTGCGCAAGCTCTGAGAAACATTTTATGATGATGATGAT 529
Qy 481 GAGGAGATTAAGTGGGCACTCCCGGTGATGATGATGATGATGATGATGATGATGAT 540
Db 530 GAGGAGATTAAGTGGGCACTCCCGGTGATGATGATGATGATGATGATGATGATGAT 589
Qy 541 AAGTCAGAGCTGCTACACATTTGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 590 AAGTCAGAGCTGCTACACATTTGATGATGATGATGATGATGATGATGATGATGATGAT 649
Qy 601 AGAAAGATTTCTGAGGTTTGAAGCAAAATGACATGACAGCAACCAATTCATTTGTA 660
Db 650 AGAAAGATTTCTGAGGTTTGAAGCAAAATGACATGACAGCAACCAATTCATTTGTA 709
Qy 661 ATTGAAGACTTTGAGTCTTCACTTACCCGTTGATGATGATGATGATGATGATGATGAT 720
Db 710 ATTGAAGACTTTGAGTCTTCACTTACCCGTTGATGATGATGATGATGATGATGATGAT 769
Qy 721 AATATTCCTGTTTACCCCT 740
Db 770 AATATTCCTGTTTACCCCT 789

RESULT 5
CN260357 646 bp mRNA linear EST 16-MAY-2004
LOCUS 17000424179730 GRN_BS Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN260357
ACCESSION CN260357.1 GI:47276771
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 646)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Muraue, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkoweki, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 646 Std Error: 0.00.

TITLE
JOURNAL
COMMENT

FEATURES
source

Location/Qualifiers
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ORIGIN

Query Match 29.8%; Score 623; DB 7; Length 646;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 987 AAGCTGACGCTTGAAGATTAAGAGAGACACTGCGCTTTTGAATAATTAAGGACAGAC 1046
Db 24 AAGCTGACGCTTGAAGATTAAGAGAGACACTGCGCTTTTGAATAATTAAGGACAGAC 83
Qy 1047 AAG 1106
Db 84 AAG 143
Qy 1107 TTTTACCTGCTGCTTGAAGATTCGAGCAATTCCTAATAAGGCAATTTTTCGAGCCCTGT 1166
Db 144 TTTTACCTGCTGCTTGAAGATTCGAGCAATTCCTAATAAGGCAATTTTTCGAGCCCTGT 203
Qy 1167 GAGCTATACAGTGAAGTGTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1226
Db 204 GAGCTATACAGTGAAGTGTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263
Qy 1227 GCGAGCCGATTATGACCGCTTTGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1286
Db 264 GCGAGCCGATTATGACCGCTTTGACAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 323
Qy 1287 GCGCTTCCCTTTGCGAGCCAGCACTGAGTCCGCTGCGAGCAATCTTCTTAACTTCA 1346
Db 324 GCGCTTCCCTTTGCGAGCCAGCACTGAGTCCGCTGCGAGCAATCTTCTTAACTTCA 383
Qy 1347 ACCGAGACCATTAATGCTGACAGTCAAGTTATTTTCAACCGAGAAAGCTCATTTGT 1406
Db 384 ACCGAGACCATTAATGCTGACAGTCAAGTTATTTTCAACCGAGAAAGCTCATTTGT 443
Qy 1407 CTTCAACATTTGTAATTTCTGTCTACTGCAACAAGAGTTCTGCGAGAGAGATATG 1466
Db 444 CTTCAACATTTGTAATTTCTGTCTACTGCAACAAGAGTTCTGCGAGAGAGATATG 503
Qy 1467 TACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1526
Db 504 TACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 563
Qy 1527 TGAAGACAGCGGAG 1586
Db 564 TGAAGACAGCGGAG 623
Qy 1587 TTTTCACTTACCAAGATGACCCCT 1609
Db 624 TTTTCACTTACCAAGATGACCCCT 646

RESULT 6
A0279788 565 bp mRNA linear EST 31-JUL-2003
LOCUS A0279788 CHONS2 Homo sapiens cDNA clone CHONS2001448 5', mRNA
DEFINITION A0279788
ACCESSION A0279788
VERSION A0279788.1 GI:28299015
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 565)
AUTHORS Imabayashi,H., Mori,T., Gojo,S., Kiyono,T., Sugiyama,T., Irie,R.,
Isogai,T., Hata,J., Tomoya,Y., and Umezawa,A.
TITLE Redifferentiation of dedifferentiated chondrocytes and
chondrogenesis of human bone marrow stromal cells via chondrosphere
formation with expression profiling by large-scale cDNA analysis
JOURNAL Exp. Cell Res. 288 (1), 35-50 (2003)
MEDLINE 22760698
PUBMED 12878157
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project, Sugiyama,T., Wakamatsu,A., Irie,R.,
Umezawa,A., Fukuma,M., Kusakari,S., Hata,J., Ishii,S., Yamamoto,J.,
Isogo,Y., Saito,K., Nakamura,Y., Masuko,Y., Nagai,K., Isogai,T.,
HRI human cDNA project; cDNA library construction & 5'-end one
pass sequencing: Helix Research Institute.
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ORIGIN
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Matches 565; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

819 TTTTCAAGTCCCAATTTCAAGGCACTTCACTTCAAGATGATGCTAAACAC 878
1 TTTTCAAGTCCCAATTTCAAGGCACTTCACTTCAAGATGATGCTAAACAC 60
879 TCGGCTGTAATGGAATTTGCAATTAAGACTTTTCTATCAGCTGAGATGCTT 938
61 TCGGCTGTAATGGAATTTGCAATTAAGACTTTTCTATCAGCTGAGATGCTT 120
939 CAGCGTATCGCTTCAAGATGATGTAAGAGCTTCAAGAGCTGAGCT 998
121 CAGCGTATCGCTTCAAGATGATGTAAGAGCTTCAAGAGCTGAGCT 180
999 TGAAGATTAAGAGAGAGAGCTGCTCTTTGAAATTAAGGCAAGAAAGG 1058
181 TGAAGATTAAGAGAGAGAGCTGCTCTTTGAAATTAAGGCAAGAAAGG 240
1059 AGCTACCTTACCCAGAGATATACCTGGGAGATGTTCTCAGTTATTTTAC 1118
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1119 TCTTGAATCCAGAGCAATTCCTAAAGCAATTTTTCGAGCCCTTGAGCTAT 1178
301 TCTTGAATCCAGAGCAATTCCTAAAGCAATTTTTCGAGCCCTTGAGCTAT 360
1179 TGAAGTGTGAAAGGCGAGGCTACAGAGCTGTGAGTAAACAGAGGCGAG 1238
361 TGAAGTGTGAAAGGCGAGGCTACAGAGCTGTGAGTAAACAGAGGCGAG 420
1239 TAGCGCTTTGTAGAAATGCTGTGCTGCTGTTGTAATCTCTCTGCTTTCC 1298
421 TAGCGCTTTGTAGAAATGCTGTGCTGCTGTTGTAATCTCTCTGCTTTCC 480
1299 TTGCGAGCAGCACTGAGTCTGCTGCAACATCTTCTTAACTTCAACCCAGAC 1358
481 TTGCGAGCAGCACTGAGTCTGCTGCAACATCTTCTTAACTTCAACCCAGAC 540

ORIGIN
Query Match 25.6%; Score 535; DB 1; Length 877;
Best Local Similarity 100.0%; Pred. No. 1.4e-282;
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1143 AAAGGATTTTTCGAGCCCTTGAGACTATACAGTGAAGGCAAGGAGGCT 1202
192 AAAGGATTTTTCGAGCCCTTGAGACTATACAGTGAAGGCAAGGAGGCT 251
1203 ACAGAGCTGTGAGTAACAGAGGCGAGCCGATTAAGCCGCTTTGTAAGAT 1262
252 ACAGAGCTGTGAGTAACAGAGGCGAGCCGATTAAGCCGCTTTGTAAGAT 311
1263 TGCCTGCTTTGAGATCTCTCTGCTTCCCTTTGTCGAGCCCACTCAGTCT 1322
312 TGCCTGCTTTGAGATCTCTCTGCTTCCCTTTGTCGAGCCCACTCAGTCT 371
1323 GCTCGAAGCATCTTCCAACTTCAACCGAGACATATGCTGCAAGCTCAAGTT 1382
372 GCTCGAAGCATCTTCCAACTTCAACCGAGACATATGCTGCAAGCTCAAGTT 431
1383 TCACCAGAGAAAGCTCATTTTGTCTTCAACATTTGTAATTTCTGTACTGCA 1442
432 TCACCAGAGAAAGCTCATTTTGTCTTCAACATTTGTAATTTCTGTACTGCA 491

QY 1443 AGAGGTTCTGCGAAGGAGATGTACAGGCTGCGCTTGTGTTGCTTCACTTCT 1502
 DB 492 AAGAGTTCTGCGAAGGAGATGTACAGGCTGCGCTTGTGTTGCTTCACTTCT 551
 QY 1503 TCAGCCAAATCATGATGATCCCATGAAGACAGCGGAAAGCCCTGCTTAAAGATATC 1562
 DB 552 TCAGCCAAATCATGATGATCCCATGAAGACAGCGGAAAGCCCTGCTTAAAGATATC 611
 QY 1563 CATCTCTCTCGAACAACAATTTCTTCCACTTACCAAGATAGACCCCTCAATCCCATCAT 1622
 DB 612 CATCTCTCTCGAACAACAATTTCTTCCACTTACCAAGATAGACCCCTCAATCCCATCAT 671
 QY 1623 AATGGTGGTCCGAAACCGGATAGCCCGTTTATTTGGTCTCTCAACATAGA 1677
 DB 672 AATGGTGGTCCGAAACCGGATAGCCCGTTTATTTGGTCTCTCAACATAGA 726
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 DEFINITION AGENCOURT_7565843 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6041670
 5', mRNA sequence.
 ACCESSION BQ218755
 VERSION BQ218755.1 GI:20400155
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1061)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 plate: LLAM13279 row: n column: 07
 High quality sequence stop: 518.
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 /clone_1lb="NIH_MGC_92"
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 Site 2: SalI. Cloned unidirectionally; oligo-dT primed.
 Average insert size 2.5 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."
 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 2.3e-280; Indels 0; Gaps 0;
 Matches 531; Conservative 0; Mismatches 0;

DB 121 GGATCTGAATCCGAGCAATTCCTAAAGGCAATTTTGGAGCCCTTGTGACTATA 180
 QY 1175 CCAAGTACAGTCTGTAAAGGCGCAGGCTACAGAGCTGTGAGTAAACAAGGGGCGCG 1234
 DB 181 CCAAGTACAGTCTGTAAAGGCGCAGGCTACAGAGCTGTGAGTAAACAAGGGGCGCG 240
 QY 1235 ATTATAGCGCTTGTGAGAGATGCGCTGTGCTGTTGTGATCTCTCTGCTTCC 1294
 DB 241 ATTATAGCGCTTGTGAGAGATGCGCTGTGCTGTTGTGATCTCTCTGCTTCC 300
 QY 1295 CTCTTCCAGCCACACACTCACTCTCTGCTGGAACATCTTCTTAACTCAACAC 1354
 DB 301 CTCTTCCAGCCACACACTCACTCTCTGCTGGAACATCTTCTTAACTCAACAC 360
 QY 1355 CATATCTGTGTGACAGCTCAATTTATTTACCCAGGAAGCTCCATTTGTCTTAACA 1414
 DB 361 CATATCTGTGTGACAGCTCAATTTATTTACCCAGGAAGCTCCATTTGTCTTAACA 420
 QY 1415 TTGTGGAATTTCTGTCTACGCAACAAGAGTTCTGCGAAGGAGATGTACAGGCT 1474
 DB 421 TTGTGGAATTTCTGTCTACGCAACAAGAGTTCTGCGAAGGAGATGTACAGGCT 480
 QY 1475 GGCTGGCTTGTGTGTTGCTTCACTTCAAGCCAAACATATGATGCC 1525
 DB 481 GGCTGGCTTGTGTGTTGCTTCACTTCAAGCCAAACATATGATGCC 531
 RESULT 9
 LOCUS B1772430 826 bp mRNA linear EST 25-SEP-2001
 DEFINITION 603055786F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5205285 5',
 mRNA sequence.
 ACCESSION B1772430
 VERSION B1772430.1 GI:15764008
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 826)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 plate: LLAM11514 row: 1 column: 22
 High quality sequence stop: 824.
 Location/Qualifiers
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 /clone="IMAGE:5205285"
 /lab_host="DH10B"
 /clone_1lb="NIH_MGC_122"
 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
 Site 1: NotI; Site 2: EcoRV (destroyed); RNA source
 anonymous pool of 24 week female lung, 16 week female
 spleen, and 20-22 week male spleens. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.4 kb; insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 026. Note:
 this is a NIH_MGC Library."
 FEATURES
 source

Db 688 AGAAGATCTGA 701

RESULT 11
BU941078
LOCUS
DEFINITION
AGENCOURT 10540067 NIH-MGC 128 Homo sapiens cDNA clone
IMAGE:6712893 5', mRNA_sequence.
BU941078
BU941078.1 GI:24129897
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 834)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNML at:
<http://image.llnl.gov>
Plate: L12CM3022 row: e column: 21
High quality sequence stop: 586.
Location/Qualifiers
1..834

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6712893"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (T1-phage-resistant)"
 /clone_1fb="NIH-MGC 128"
 /note="vector: pDNR-LIB; Site 1: 5'fl (ggccatcagccg);
 Site 2: 5'fl (ggccgcctccgcg); Double-stranded cDNA was
 prepared from a pool of 40 cell line polyA+ RNAs (bladder
 - 2%, blood - 33.4%, brain - 1.4%, eye - 1%, intestine -
 4%, connective tissue - 5.6%, breast - 12.5%, colon
 - 2.2%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
 salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
 adaptors were used in cloning as follows:
 5'-AAGCATGCTATCAAGCAGATGCGCATTCAGCGCG-3' and
 5'-ATTCTAGAGCGCGAGCGCGCGGCACATG-3' (30) NK-3'. Full-length
 enriched library was constructed using the Clontech
 Creator SMART kit and size-selected to contain the >2 kb
 size fraction (other fractions present in NIH-MGC 126 and
 NIH-MGC 127). Library created in the laboratory of T.
 Utsida, M.D., Ph.D. (NIH, NIH). Note: this is a NIH-MGC
 library."

[illegible]

Oy	ATTGAATCTGAAGTCAGAGCTTCTGAGATTGGAATTGAAATTCAGAGAAAGAAAGATTTCTGAGGTT	618
Db	ATTGAATCTGAAGTCAGAGCTTCTGAGATTGGAATTGAAATTCAGAGAAAGAAAGATTTCTGAGGTT	242
Oy	TTGAGGCAAAATGCAGTGAAACAGCAACCAATCCAAATGTGTAATTGAAAGCTTTGAGTCC	678
Db	TTGAGGCAAAATGCAGTGAAACAGCAACCAATCCAAATGTGTAATTGAAAGCTTTGAGTCC	302
Oy	TCACTTACCCGTTGGGTACCCCACTCCACAAACCTCTCGAATATTTCCGTGTTACCC	738
Db	TCACTTACCCGTTGGGTACCCCACTCCACAAACCTCTCGAATATTTCCGTGTTACCC	362
Oy	CCAGAAATTTTACAGGTACATCTGCAAGAGTCTCTTGAGCCAGAGAAAGCCAAGTATCT	798
Db	CCAGAAATTTTACAGGTACATCTGCAAGAGTCTCTTGAGCCAGAGAAAGCCAAGTATCT	422
Oy	GTGACTTCAGCAGATCCAGTCTTTCAAGTGCCAAATTTCAAAAGCAGTTCAACTTAACG	858
Db	GTGACTTCAGCAGATCCAGTCTTTCAAGTGCCAAATTTCAAAAGCAGTTCAACTTAACG	482
Oy	AATAGATGCATTAATAAACCACTGCTGCTGTAGAAATTGACATTTCAAAATACAGACTTTTCC	918
Db	AATAGATGCATTAATAAACCACTGCTGCTGTAGAAATTGACATTTCAAAATACAGACTTTTCC	542
Oy	TATCAGCCTGGAGATGCTTCAAGGTATCTGCCCTTAACAGTGAATTCTGAGGTCAAAAGC	978
Db	TATCAGCCTGGAGATGCTTCAAGGTATCTGCCCTTAACAGTGAATTCTGAGGTCAAAAGC	602
Oy	CTACTCCAA 987	
Db	CTACTCCAA 611	

	RESULT	12	
AU132586	LOCUS		
AU132586	DEFINITION	922 bp	mRNA linear EST 01-AUG-2002
AU132586 NT2RP4 Homo sapiens cDNA clone NT2RP4000141 5'			mRNA sequence.
AU132586	ACCESSION		
AU132586	VERSION		
AU132586.1 GI:10992940	KEYWORDS		
EST.	SOURCE		
Homo sapiens (human)	ORGANISM		
Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.. 1 (bases 1 to 822) Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Salto,K., Yamamoto,J., Nishikawa,T., Nakamura.Y., Negai,T., Sugano,S., Masuno,Y. and Isogai.T.	TITLE		
HRI human CDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Salto,K., Yamamoto,J., Nishikawa,T., Nakamura.Y., Negai,T., Sugoan,S., Masuno.Y., Isogai,T.) Unpublished (2000)	JOURNAL COMMENT		
Contact: Takao Isogai Genomics laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel.: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomcs@ri.co.jp HRI human CDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.			

FEATURES	SOURCE	Location/Qualifiers
1.	.832	
	/organism="Homo sapiens"	
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	/db_xref="taxon:9606"	
	/clone="NT2RP4000141"	
	/cell_type="LeierLocar carcinoma"	
	/cell_line="NT2"	

ORIGIN

/clone_11b="NT2RP4"
/note="Vector: pME18SFLJ, mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"

Query Match 21.7%; Score 455; DB 1; Length 822;

Best Local Similarity 99.6%; Pred. No. 1.8e-238; Indels 0; Gaps 0;

Matches 555; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 283 GGTCTCGGATTCAGAAATACACCTACTTTGGCAATGGGGGAGATTAATGATTAACGA 342
DB 182 GGTCTCGGATTCAGAAATACACCTACTTTGGCAATGGGGGAGATTAATGATTAACGA 241
QY 343 CTTCAGAGCTTGAGAGCCCGGCAATTTCTATGACATGACATGACATGCTGTAGGT 402
DB 242 CTTCAGAGCTTGAGAGCCCGGCAATTTCTATGACATGACATGACATGCTGTAGGT 301
QY 403 TTGAATCTGTGTGAGCCGCGGATTCGAGCTCTGGCCAGCCCTCAAGAAAGCAATTTT 462
DB 302 TTGAATCTGTGTGAGCCGCGGATTCGAGCTCTGGCCAGCCCTCAAGAAAGCAATTTT 361
QY 463 AGGTCAAGCAGAGAGAGAGATTAAGTGGGCACTCCCGGTGCATCAGCTGCATCC 522
DB 362 AGGTCAAGCAGAGAGAGAGATTAAGTGGGCACTCCCGGTGCATCAGCTGCATCC 421
QY 523 TTGAAGCAGAGCTTTGTGAAGTCAAGAGCTGCTACATTTGAATCTCAAGTGCATTCG 582
DB 422 TCAGAGCAGAGCTTTGTGAAGTCAAGAGCTGCTACATTTGAATCTCAAGTGCATTCG 481
QY 583 AGATTCATGATTCAGAGAAAGAGATTCGAGGTTTGAAGCAAAATGAGTGAACAGC 642
DB 482 AGATTCATGATTCAGAGAAAGAGATTCGAGGTTTGAAGCAAAATGAGTGAACAGC 541
QY 643 AACCAATCCAAATGTTGTAATGAAGCTTGAAGTCTCACTTACCCGTTGATACCCCA 702
DB 542 AACCAATCCAAATGTTGTAATGAAGCTTGAAGTCTCACTTACCCGTTGATACCCCA 601
QY 703 CTCTCAGAGCTCTCTGAATATTTCTGTGTTTACCCCAAGATTTTACAGGTACATCTG 762
DB 602 CTCTCAGAGCTCTCTGAATATTTCTGTGTTTACCCCAAGATTTTACAGGTACATCTG 661
QY 763 CAGAGCTCTTGGGCGAGAGAAAGCAAGTATCTGTGACTTCAGAGATTCAGATTTT 822
DB 662 CAGAGCTCTTGGGCGAGAGAAAGCAAGTATCTGTGACTTCAGAGATTCAGATTTT 721
QY 823 CAGAGCTCTTGGGCGAGAGAAAGCAAGTATCTGTGACTTCAGAGATTCAGATTTT 882
DB 722 CAGAGCTCTTGGGCGAGAGAAAGCAAGTATCTGTGACTTCAGAGATTCAGATTTT 781

RESULT 13
AM965709 591 bp mRNA linear EST 01-JUN-2000
LOCUS AM965709 MAGE resequencing, MAGI Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaepard, R., Gay, C.,
Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Quackenbush, J.
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208

Email: johng@tigr.org
Plate: 218
Seq primer: Reverse.
Location/Qualifiers
1..591

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_11b="MAGE resequencing, MAGI"
/note="Vector: pBluescriptSKm"

ORIGIN

Query Match 21.4%; Score 448; DB 2; Length 591;

Best Local Similarity 100.0%; Pred. No. 1.3e-234; Indels 0; Gaps 0;

Matches 448; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1192 AAGCGAGGCTACAGAGCTGTCAGTAAACAAGGGGAGCCGATTAATAGCCGCTTGTG 1251
DB 1 AAGCGAGGCTACAGAGCTGTCAGTAAACAAGGGGAGCCGATTAATAGCCGCTTGTG 60
QY 1252 CGAGATGCTGTGCTGCTGTGTGATCTCTCTGCTTCCCTTCTTCCAGCCACA 1311
DB 61 CGAGATGCTGTGCTGCTGTGTGATCTCTCTGCTTCCCTTCTTCCAGCCACA 120
QY 1312 CTGAGTCTGCTGTGCAACATCTTCTTAACTTCAACCCAGACATTTGTGTGCAAGC 1371
DB 121 CTGAGTCTGCTGTGCAACATCTTCTTAACTTCAACCCAGACATTTGTGTGCAAGC 180
QY 1372 TCAGATTTATTCACCGAGAAAGCTCAATTTGTCTTCAACATTTGTGAAATTTCTGT 1431
DB 181 TCAGATTTATTCACCGAGAAAGCTCAATTTGTCTTCAACATTTGTGAAATTTCTGT 240
QY 1432 ACTGCCAACAAGAGGTTCTGCGAAGGAGATATGTAACAGCTGAGCTTGTGTT 1491
DB 241 ACTGCCAACAAGAGGTTCTGCGAAGGAGATATGTAACAGCTGAGCTTGTGTT 300
QY 1492 GCTTCAGTTCTTACGCCAACAATCATGATCCCATGAAAGACAGCCGGAAGCCCTGCT 1551
DB 301 GCTTCAGTTCTTACGCCAACAATCATGATCCCATGAAAGACAGCCGGAAGCCCTGCT 360
QY 1552 CCTAGATATTCATCTCTCTGCAACAACAATTTCTTCACTTACAGATGACCCCTCA 1611
DB 361 CCTAGATATTCATCTCTCTGCAACAACAATTTCTTCACTTACAGATGACCCCTCA 420
QY 1612 ATCCCATCATTAATGAGGCTCCAGGA 1639
DB 421 ATCCCATCATTAATGAGGCTCCAGGA 448

RESULT 14
CD559384 818 bp mRNA linear EST 11-JUN-2003
LOCUS CD559384
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Garhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: Clontech Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/MLN at:
<http://image.jnl.gov>
 Plate: NDCM198 row: n column: 24
 High quality sequence stop: 484.
 Location/Qualifiers

FEATURES

1. 818
 /organism="Homo sapiens"
 /mol_type="rRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30409775"
 /issue_type="Pooled"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattagcc);
 Site 2: SfiI (ggcgccgcgcgc); Library is oligo-dT primed
 and directionally cloned. PBMC - Peripheral Blood
 Mononuclear Cells. RNA was pooled from 3/hour stimulation
 with PMA adn Ionomycin. 5' and 3' adaptors were used in
 cloning as follows: 5' adaptor sequence:
 5'-CACGCCCATTTATGCC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCCCGAGGCCCGCAGATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.69
 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH MGC Library."

ORIGIN

Query Match 21.3%; Score 446; DB 6; Length 818;

Best Local Similarity 99.6%; Pred. No. 1,7e-233;

Matches 546; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

425 GGATTGCTGAGCTCTGGCCAGCCCTCAGAAAGATTAGTCAACGAGAGCAAGAG 484
 3 GGATTGCTGAGCTCTGGCCAGCCCTCAGAAAGATTAGTCAACGAGAGCAAGAG 62
 485 AATTAAGTGGCGACCTCCGGTGGCATCCTCGATCCTTGAAGAGACGCTTGTAAT 544
 63 AATTAAGTGGCGACCTCCGGTGGCATCCTCGATCCTTGAAGAGACGCTTGTAAT 122
 545 CAGAGCTGCTACATTTGATCTCAAGTGAAGCTTCAAGATTCAGATTCAGAGAA 604
 123 CAGAGCTGCTACATTTGATCTCAAGTGAAGCTTCAAGATTCAGATTCAGAGAA 182
 605 AGGATTCGAGGTTTGAAGCAAAATGCAGTGAAGCAACCAATCAATGTTGTAAT 664
 183 AGGATTCGAGGTTTGAAGCAAAATGCAGTGAAGCAACCAATCAATGTTGTAAT 242
 665 AAGACTTGAAGTCTCACTTACCGTTCCGATCCCACTCTCAAGAGCTCTGTAAT 724
 243 AAGACTTGAAGTCTCACTTACCGTTCCGATCCCACTCTCAAGAGCTCTGTAAT 302
 725 TTCCTGGTTTACCCCGAATATTTACAGGTACATGAGAGAGCTCTTGGCAGAG 784
 303 TTCCTGGTTTACCCCGAATATTTACAGGTACATGAGAGAGCTCTTGGCAGAG 362
 785 AAGCCAGATCTGATCTGATCTGAGAGATTCAGATTTTCAAGTCCAAATTTCAA 844
 363 AAGCCAGATCTGATCTGATCTGAGAGATTCAGATTTTCAAGTCCAAATTTCAA 422
 845 TTCAACTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 904
 423 TTCAACTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 482
 905 ATACAGACTTTTCTTACAGCTGAGATGATGATGATGATGATGATGATGATGAT 964
 483 ATACAGACTTTTCTTACAGCTGAGATGATGATGATGATGATGATGATGATGAT 542
 965 CTGAGAGTA 972
 543 CTGAGAGTA 550

RESULT 15

BI025283

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AUTHORS

REFERENCE

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1. 591

/organism="Homo sapiens"

/mol_type="rRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_id="MT0259"

/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

High quality sequence stop: 590.

Location/Qualifiers

ORIGIN

Query Match 20.7%; Score 434; DB 4; Length 591;

Best Local Similarity 99.8%; Pred. No. 6.6e-227;

Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

525 GAGGACAGCCTTGAAGTCAAGCTGCTACATTTGAAGCAAAATGCAAGTGAAG 584
 102 GAGGACAGCCTTGAAGTCAAGCTGCTACATTTGAAGCAAAATGCAAGTGAAG 161
 585 ATTGATGATTCAGAGAAAGATTTGAGGTTTGAAGCAAAATGCAAGTGAAG 644
 162 ATTGATGATTCAGAGAAAGATTTGAGGTTTGAAGCAAAATGCAAGTGAAG 221
 645 CCAATTCATTTGTTGATTTGAAGATTTGAGGTTTGAAGCAAAATGCAAGTGAAG 704
 222 CCAATTCATTTGTTGATTTGAAGATTTGAGGTTTGAAGCAAAATGCAAGTGAAG 281
 705 CTCACAGGCTCTGGAATATTCCTGTTTACCCCGAATATTTACAGGTACATCTGA 764

Db	282	CTGACAAAGCCTCTCTGAATATTCCTGGTTTACCCCGAAATTTTACAGGTACATCTGCA	341
Qy	765	GGAATCTCTTGGCCAGGAGGAAAGCCAAATATCTGTGACTTTCAGCAGATCCAGTTTTC	824
Db	342	GGAATCTCTTGGCCAGGAGGAAAGCCAAATATCTGTGACTTTCAGCAGATCCAGTTTTC	401
Qy	825	AGTGCCTTTCAAAGGCACTTCACTTACTAGATGATGCCATTAATAACCACTCTGCT	884
Db	402	AGTGCCTTTCAAAGGCACTTCACTTACTAGATGATGCCATTAATAACCACTCTGCT	461
Qy	885	GATAGATTTGACATTTCAATACAGACTTTTCTATCAGCTGGAGATGCTTCAGCCT	944
Db	462	GATAGATTTGACATTTCAATACAGACTTTTCTATCAGCTGGAGATGCTTCAGCCT	521
Qy	945	GATCTGCCCTTACAGTATTTCTGAGTACAAAGCCTTCCAAAGACTGCGAGCTTGAGA	1004
Db	522	GATCTGCCCTTACAGTATTTCTGAGTACAAAGCCTTCCAAAGACTGCGAGCTTGAGA	581
Qy	1005	TAAAA 1009	
Db	582	TAAAA 586	

Search completed: August 27, 2005, 15:58:39
 Job time : 4539.36 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 19:17:21 ; Search time 5995.75 Seconds
(without alignments)
16914.771 Million cell updates/sec

Title: US-09-371-347A-47

Perfect score: 2093
Sequence: 1 atgaggaggttctgttact.....ttcagagatattggtcacaata 2093

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1793	85.7	3259	6	AR144976 Sequence
2	1793	85.7	3259	6	AX050463 Sequence
3	1793	85.7	3259	6	AF025794 Homo sapi
4	1793	85.7	3259	6	AF121214 Homo sapi
5	1691	80.8	3241	6	CQ726091 Sequence
6	1640	78.4	3310	9	BC054816 Homo sapi
7	1220	58.3	2933	11	BV177620 sqmm95800
8	1220	58.3	2933	11	BV178010 sqmm97986
9	386	18.4	330	6	BD077780 5' EST of
10	381	18.2	1353	9	AF121205 Homo sapi
11	330	15.8	109626	9	AC010346 Homo sapi
12	330	15.8	110756	9	AC025174 Homo sapi
13	279	13.3	158199	2	AC022921 Homo sapi
14	279	13.3	167237	2	AC021609 Homo sapi
15	279	13.3	17536	2	AC091945 Homo sapi
16	189	9.0	1156	9	AF121210 Homo sapi
17	188	9.0	1034	9	AF121212 Homo sapi
18	188	9.0	167237	2	AC021609 Homo sapi
19	188	9.0	177596	2	AC091945 Homo sapi

c	20	183	8.7	1432	9	AF121208 Homo sapi
	21	161	7.7	158199	2	AC022921 Homo sapi
	22	158	7.5	1256	9	AF121208S02
	23	158	7.5	2475	6	AR454615 Sequence
	24	158	7.5	2475	6	AX375651 Sequence
	25	155	7.4	2011	9	AF121208S06
	26	146	7.0	2214	9	AF121208S12
	27	129	6.2	4506	9	AF121208S01
	28	125	6.0	969	9	AF121208S05
	29	121	5.8	1119	9	AF121208S10
	30	119	5.7	1200	9	AF121208S03
	31	78	3.7	244	6	BD204284 5' EST and
	32	63	3.0	63	6	AX611833 Sequence
	33	60	2.9	60	6	CO539377 Sequence
	34	54	2.6	54	6	AX611839 Sequence
	35	54	2.6	54	6	AX611843 Sequence
c	36	51	2.4	51	6	AX162161 Sequence
	37	48	2.3	48	6	AX611835 Sequence
	38	48	2.3	48	6	AX611841 Sequence
	39	47	2.2	183	6	CO670532 Sequence
	40	44	2.1	650	9	AF121208S08
	41	41	2.0	41	6	AX611845 Sequence
	42	38	1.8	38	6	AX611837 Sequence
	43	38	1.8	63	6	AX611834 Sequence
c	44	32	1.5	238720	2	AC095949 Rattus no
	45	32	1.5	271339	2	AC131637 Rattus no

ALIGNMENTS

RESULT 1	AR144976	3259 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	AR144976	Sequence 23 from patent US 6210950.			
DEFINITION	AR144976				
ACCESSION	AR144976.1	GI:15106843			
VERSION					
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 3259)				
AUTHORS	Johnson, W.G. and Stemroos, R.Scott.				
TITLE	Methods for diagnosing, preventing, and treating developmental disorders due to a combination of genetic and environmental factors				
JOURNAL	Patent: US 6210950-A 23 03-Apr-2001;				
FEATURES	Location/Qualifiers				
source	1..3259				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
ORIGIN					
Query Match	85.7%;	Score 1793;	DB 6;	Length 3259;	
Best Local Similarity	99.8%;	Pred. No. 0;			
Matches 2093;	Conservative	0;	Mismatches	0;	Indels 4; Gaps 1;
QY	1	ATGAGGAGGTTTCTGTACTATATGTATACACGACGAGCAAGCCAAAGCCATCCGAGAA	60		
DB	80	ATGAGGAGGTTTCTGTACTATATGTATACACGACGAGCAAGCCAAAGCCATCCGAGAA	139		
QY	61	GAATGTGTAGCAAGCTGTGTATCATGATATTTTGTGAGATCTTCATCGTATTAAGTAA	120		
DB	140	GAATGTGTAGCAAGCTGTGTATCATGATATTTTGTGAGATCTTCATCGTATTAAGTAA	199		
QY	121	TCGATTAAGTATGACCTTAAACCGAAGAGCTCTTGTGTGTGGTTTCTACACG	180		
DB	200	TCGATTAAGTATGACCTTAAACCGAAGAGCTCTTGTGTGTGGTTTCTACACG	259		
QY	181	GGACCGGAGACCCACCCGACAGCCGCCAAGTTTGTAAAGAAATTAAGAACCAACA	240		
DB	260	GGACCGGAGACCCACCCGACAGCCGCCAAGTTTGTAAAGAAATTAAGAACCAACA	319		
QY	241	CTGCCGTTGATTTTCTGCTACCTGCGGTATGGGTACTGGGTCTCGGTATTCAGAA	300		

D	b		320	CTGCCGGTGAATTTCTTTGCTCACCCTGGGTATGGGTTACTGGGTCCTCGTGATTCCAGAA	379
Q	y		301	TACACCTAATTTTTGCATATGGGGGAGAATAATTGATTAACGACTTCAAGACTTGGAGCC	360
D	b		380	TACACTACTTTTCCAATGGGGGAGATTAATTGATTAACGACTTCAAGACTTGGAGCC	439
Q	y		361	CGGATTTCTATGACCTGGACATGTCGATGCACTGTGTAGAGTTTAGAATTGTGGTTGAG	420
D	b		440	CGGATTTCTATGACCTGGACATGTCGATGCACTGTGTAGAGTTTAGAATTGTGGTTGAG	499
Q	y		421	CCGTGATATGTGCACTCTGSCCAGACCCTCAGAAAGCATTTTATAGTCAAGCAGAGACA	480
D	b		500	CCGTGATATGTGCACTCTGSCCAGACCCTCAGAAAGCATTTTATAGTCAAGCAGAGACA	559
Q	y		481	GAGAGATTAATGAGCGCATCTCCGGTGGCATCACCTGCATCTTGAAGACAGACTTGTG	540
D	b		560	GAGAGATTAATGAGCGCATCTCCGGTGGCATCACCTGCATCTTGAAGACAGACTTGTG	619
Q	y		541	AAGTCAGAGCTGCTACACATTTGAATCTCTAATCCAGCTTCTGAAGATTCGATTTACAGA	600
D	b		620	AAGTCAGAGCTGCTACACATTTGAATCTCTAATCCAGCTTCTGAAGATTCGATTTACAGA	679
Q	y		601	AGAAAGATTTCTAGAGTTTGAAGCAAAATCAGTGAACAGCAACCAATCCAAATGTTGTA	660
D	b		680	AGAAAGATTTCTAGAGTTTGAAGCAAAATCAGTGAACAGCAACCAATCCAAATGTTGTA	739
Q	y		661	ATTGAAGACTTTGAGTCTCTCACTTACCCGTTGSGTACCCCACCTCTCAAGACCTCTCTG	720
D	b		740	ATTGAAGACTTTGAGTCTCTCACTTACCCGTTGSGTACCCCACCTCTCTCAAGACCTCTCTG	799
Q	y		721	AATATCTCTGTTTACCCCCAGAAATATTACAGGTACATCTGCAGAGTCTCTTGGCCAG	780
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D	b		980	TCAAAATACAGCTTTTCTATACGCTTGAGATGCTTCAGCGTATGTGCTTCAACGT	1039
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RESULT 3
AF025794 3259 bp mRNA linear PRI 26-MAR-1998
LOCUS Homo sapiens methionine synthase reductase (MTRR) mRNA, complete
DEFINITION
ACCESSION AF025794
VERSION AF025794.1 GI:2981302
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 (bases 1 to 3259)
Leclerc, D., Wilson, A., Dumas, R., Gafuick, C., Song, D., Watkins, D.,
Heng, H.H.Q., Rommens, J.M., Scherer, S.W., Rosenblatt, D.S. and
Gravel, R.A.
Cloning and mapping of a cDNA for methionine synthase reductase, a
flavoprotein defective in patients with homocystinuria
Proc. Natl. Acad. Sci. U.S.A. 95 (6), 3059-3064 (1998)
MEDLINE
PUBMED 9501215
REFERENCE
1 (bases 1 to 3259)
Leclerc, D.
Direct Submission
Submitted (19-SEP-1997) Human Genetics, McGill University -
Montreal Children's Hospital Research Institute, 4060 Ste-Catherine
West, Montreal, Que H3Z 2Z3, Canada
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Leclerc, D.
Direct Submission
Submitted (12-NOV-1997) Human Genetics, McGill University -
Montreal Children's Hospital Research Institute, 4060 Ste-Catherine
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ORIGIN
Query Match 85.7%; Score 1793; DB 9; Length 3259;
Best Local Similarity 99.8%; Pred. No. 0;
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LOCUS Homo sapiens methionine synthase reductase (MTRR) mRNA, complete
DEFINITION cdb.
ACCESSION AF121214
VERSION AF121214.1 GI:6561338
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 3291)
Leclerc,D., Odievre,M., Wu,Q., Wilson,A., Huizenga,J.U., Rozen,R.,
Scherer,S.W. and Gravel,R.A.
Molecular cloning, expression and physical mapping of the human
methionine synthase reductase gene
Gene 240 (1), 75-88 (1999)
JOURNAL MEDLINE
20033550
PUBMED 10564814
2 (bases 1 to 3291)
Leclerc,D., Odievre,M.-H., Wu,Q., Wilson,A., Huizenga,J.U.,
Johns,T., Shoubiridge,E.A., Rosenblatt,D.S., Scherer,S.W., Rozen,R.
and Gravel,R.A.
Direct Submission
Submitted (18-JAN-1999) Human Genetics, Montreal Children's
Hospital, 4060 Ste-Catherine West, Montreal, Quebec H3Z 2Z3, Canada
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ORIGIN

Query Match 85.7%; Score 1793; DB 9; Length 3291;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

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RESULT 5

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 VERSION CQ726091.1 GI:42288134
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 REFERENCE
 AUTHORS 1
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RESULT 6
BC054816 3310 bp mRNA linear PRI 16-SEP-2003

LOCUS BC054816
DEFINITION Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase reductase, mRNA (CDNA clone IMAGE:5205285), partial cds.

VERSION BC054816
KEYWORDS BC054816.1 GI:33392775

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 3310)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Denge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Urdin, T.B., Tomihyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Vallalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.B., Schneringer, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-rt@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gatherburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgr.nih.gov

Akhter, N., Ayale, K., Beckstrom-Stenberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCluskey, J.C., McDowell, J., Pearson, R., Stantiron, S., Thomas, P.J., Touchman, J.W., Tsung, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.lnl.gov>
Series: IRAC Plate: 115 Row: d Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4505278.

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VERSION BVL77620.1 GI:48013757
KEYWORDS STS.

SOURCE Homo sapiens (human)
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 REFERENCE 1 (bases 1 to 2933)
 AUTHORS Nelson,R.M., Marnellloe,G., Kammerer,S., Hoyal,C.R., Shi,M.M., Cantor,C.R. and Braun,A.
 TITLE Large-Scale Validation of Single Nucleotide Polymorphisms in Gene Regions
 JOURNAL Genome Res. (2004) In press
 COMMENT Contact: Andreas Braun
 Pharmaceuticals division
 Sequenom, Inc.
 3595 John Hopkins Court, San Diego, CA 92121, USA
 Tel: 18582029018
 Fax: 18582029020
 Email: abraun@sequenom.com
 Primer A: No primer sequence submitted
 Primer B: No primer sequence submitted
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 Db 1706 GAAAGGATATGTACAGGCTGCTGCTGCTTGTGTTGTTCTTCAAGTTCTTCAAGCAAACT 1647
 Qy 1515 ACATGATCCCATGAAGACA 1534
 Db 1646 ACATGATCCCATGAAGACA 1627

RESULT 8
 BV178010/c 2933 bp DNA linear STS 10-JUN-2004
 LOCUS eqm97986 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
 DEFINITION tagged site.
 ACCESSION BV178010
 VERSION BV178010.1 GI:48014252
 KEYWORDS STS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2933)
 AUTHORS Nelson,R.M., Marnellloe,G., Kammerer,S., Hoyal,C.R., Shi,M.M., Cantor,C.R. and Braun,A.
 TITLE Large-Scale Validation of Single Nucleotide Polymorphisms in Gene Regions
 JOURNAL Genome Res. (2004) In press
 COMMENT Contact: Andreas Braun
 Pharmaceuticals division
 Sequenom, Inc.
 3595 John Hopkins Court, San Diego, CA 92121, USA
 Tel: 18582029018
 Fax: 18582029020
 Email: abraun@sequenom.com
 Primer A: No primer sequence submitted

Primer B: No primer sequence submitted
STS size: 2933.
Location/Qualifiers
1..2933
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_11b="Human DNA (Sequencem)"
<1..>2933

STS

Query Match 58.3%; Score 1220; DB 11; Length 2933;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 315 CAATGGGGGAGATTAATGATTAACGACTTCAAGGCTTGAAGCCCGCATTTCTATGA 374
DB 2846 CAATGGGGGAGATTAATGATTAACGACTTCAAGGCTTGAAGCCCGCATTTCTATGA 2787
QY 375 CACTGGACATGAGATGACGTGTAGTGTAGAACTTGTGTGAGCCGATGATGCTGG 434
DB 2786 CACTGGACATGAGATGACGTGTAGTGTAGAACTTGTGTGAGCCGATGATGCTGG 2727
QY 435 ACTCTGGCAGCCCTCAGAAAGCATTTTGTGTGACAGAGACAAGAGATTAAGTG 494
DB 2726 ACTCTGGCAGCCCTCAGAAAGCATTTTGTGTGACAGAGACAAGAGATTAAGTG 2667
QY 495 CGCATCTCCGGTGGCATCACTGTCATCTTGAAGACAGACCTTGTGAGTCAAGCTGCT 554
DB 2666 CGCATCTCCGGTGGCATCACTGTCATCTTGAAGACAGACCTTGTGAGTCAAGCTGCT 2607
QY 555 ACACATTAATCAAGTGAAGCTTGTGATTCATGATTAAGAGAAAGGATTTCTGA 614
DB 2606 ACACATTAATCAAGTGAAGCTTGTGATTCATGATTAAGAGAAAGGATTTCTGA 2547
QY 615 GGTTTGAAGCAAAATGACAGTAACCAACCAATGTTGTAATTGAAGACTTTGA 674
DB 2546 GGTTTGAAGCAAAATGACAGTAACCAACCAATGTTGTAATTGAAGACTTTGA 2487
QY 675 GTCTCATTACCCGTTGGTATCCGCCACTCTGACAAGCCTCTGTAATATTCCTGTTT 734
DB 2486 GTCTCATTACCCGTTGGTATCCGCCACTCTGACAAGCCTCTGTAATATTCCTGTTT 2427
QY 735 ACCCCCAAAATATTTACAGTATATCTGACAGAGTCTTTGGCCAGAGAAAGCCAACT 794
DB 2426 ACCCCCAAAATATTTACAGTATATCTGACAGAGTCTTTGGCCAGAGAAAGCCAACT 2367
QY 795 ATCTGATCTTCAAGATCAAGTTTTCAGAGCAATTTCAAGGAGGATTTCAACTTAC 854
DB 2366 ATCTGATCTTCAAGATCAAGTTTTCAGAGCAATTTCAAGGAGGATTTCAACTTAC 2307
QY 855 TACGAATGATGCCATTAATAACACTGCTGTGTGATTAAGATTTCAATTAACAGACTT 914
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QY 915 TTCTTATCAAGCTTGAAGATCTTCAAGCTGATCTGCTTAACAGATTTCTGAGTACA 974
DB 2246 TTCTTATCAAGCTTGAAGATCTTCAAGCTGATCTGCTTAACAGATTTCTGAGTACA 2187
QY 975 AAGCTACTTCAAAAGCTGAGCTTGAAGATAAAGAGAGACCTGCGTCTTTTGAATAAT 1034
DB 2186 AAGCTACTTCAAAAGCTGAGCTTGAAGATAAAGAGAGACCTGCGTCTTTTGAATAAT 2127
QY 1035 AAAGGACACACAAAGAAAGAGAGCTTACCCAGACATATACCTGCGGAGATGTT 1094
DB 2126 AAAGGACACACAAAGAAAGAGAGCTTACCCAGACATATACCTGCGGAGATGTT 2067
QY 1095 TCTTCAGTTCATTTTAACTGTGTCTTGAATCCAGCAATTCCTTAAAGAGCATTTT 1154
DB 2066 TCTTCAGTTCATTTTAACTGTGTCTTGAATCCAGCAATTCCTTAAAGAGCATTTT 2007
QY 1155 GCAGAGCCTTGTGACATATCAAGTGAAGTGTGAAGAGCGAGCTACAGAGCTGTG 1214

DB 2006 GCGAGCCCTTGTGACATATACAGTGAAGTGTGAAAAAGCGAGCTACAGAGCTGTG 1947
QY 1215 CAGTAAACAAAGGGAGAGCGGATTAATAGCGCTTGTGAGAGATGCTGTGCTGTT 1274
DB 1946 CAGTAAACAAAGGGAGAGCGGATTAATAGCGCTTGTGAGAGATGCTGTGCTGTT 1887
QY 1275 GGATCTCTCTCTGCTGCTTCCCTTCTTGGCAGGCAACCACTGCTCTGCTGAACATCT 1334
DB 1886 GGATCTCTCTCTGCTGCTTCCCTTCTTGGCAGGCAACCACTGCTCTGCTGAACATCT 1827
QY 1335 TCTTAACTTCAACCCAGACATATTCGTGTGCAAGCTCAAGTTATTTACCCAGAAA 1394
DB 1826 TCTTAACTTCAACCCAGACATATTCGTGTGCAAGCTCAAGTTATTTACCCAGAAA 1767
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QY 1455 GAAGGAGATATGACAGCTGAGCTGCTGCTTGTGTGCTTCAAGTTCTTCAACCAACAT 1514
DB 1706 GAAGGAGATATGACAGCTGAGCTGCTGCTTGTGTGCTTCAAGTTCTTCAACCAACAT 1647
QY 1515 ACATGCATCCCATGAAGACA 1534
DB 1646 ACATGCATCCCATGAAGACA 1627

RESULT 9
BD077780
LOCUS BD077780 390 bp DNA linear PAT 27-AUG-2002
DEFINITION 5'EST of secretory proteoin in brain.
ACCESSION BD077780
VERSION BD077780.1 GI:22623383
KEYWORDS JP 2001512015-A/65.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 390)
AUTHORS Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
TITLE 5'EST of secretory protein in brain
JOURNAL Patent: JP 2001512015-A 65 21-AUG-2001;
GENSET

COMMENT OS Homo sapiens (human)
PN JP 2001512015-A/65
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505293
PR 01-AUG-1997 US 08/905223
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLERT,BRUNO PI
LACROIX
PC C12N15/09,C07K14/47,C12M1/00,C12P21/02,C12O1/68,C12N15/00 CC
Von Heijne matrix
CC score 6.9
CC seq SLSLASHSVSC/SN
FH Key Location/Qualifiers
FT sig_peptide 289..357.
Location/Qualifiers
1..390
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
source

ORIGIN

Query Match 18.4%; Score 386; DB 6; Length 390;
Best Local Similarity 100.0%; Pred. No. 8.7e-199;
Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 970 GTACAAAGCTTCTCAAGATGACGCTTGAAGATTAAGAGAGACGCGCTTTTG 1029
DB 3 GTACAAAGCTTCTCAAGATGACGCTTGAAGATTAAGAGAGACGCGCTTTTG 62
QY 1030 AAAATTAAGGACACAAAGAAAGAGAGCTTACCCAGCATATACCTGCGGGA 1089

Db 63 AAAATAAGGACACACAAAGAAAGAGCTACCTTACCACGATATACCTGCGGGA 122
QY 1090 TGTCTCTCAGTTCATTTTACCTGTGTCTTGAATCCGAGCAATTCCTAAAGGCA 1149
Db 123 TGTCTCTCAGTTCATTTTACCTGTGTCTTGAATCCGAGCAATTCCTAAAGGCA 182
QY 1150 TTTTGGAGCCCTTGTGAGCTATACAGTGAAGTGTCTGAAAAAGCCAGCTTACAGAG 1209
Db 183 TTTTGGAGCCCTTGTGAGCTATACAGTGAAGTGTCTGAAAAAGCCAGCTTACAGAG 242
QY 1210 CTGTGACGTAAACAAAGGGGAGCGATTTATAGCCGCTTTGTACAGATGCTGTGCTGC 1269
Db 243 CTGTGACGTAAACAAAGGGGAGCGATTTATAGCCGCTTTGTACAGATGCTGTGCTGC 302
QY 1270 TTGTGGATCTGAA 1329
Db 303 TTGTGGATCTGAA 362
QY 1330 CATCTTCTTAACTTCAACCCAGACC 1355
Db 363 CATCTTCTTAACTTCAACCCAGACC 388

RESULT 10
F121202804 1353 bp DNA linear PRI 14-DEC-1999
LOCUS Homo sapiens methionine synthase reductase (MTRR) gene, exon 5.
ACCESSION AF121205
VERSION AF121205.1 GI:6572530
KEYWORDS
SEGMENT 4 of 12
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Leclerc,D., Odievre,M., Wu,Q., Wilson,A., Huizenga,J.J., Rozen,R.,
Scheer,S.W. and Gravel,R.A.
TITLE Molecular cloning, expression and physical mapping of the human
methionine synthase reductase gene
JOURNAL Gene 240 (1), 75-88 (1999)
MEDLINE 20033550
PUBMED 10564814
REFERENCE 2 (bases 1 to 1353)
AUTHORS Leclerc,D.
TITLE Direct Submission
JOURNAL Submitted (20-JAN-1999) Human Genetics, Montreal Children's
Hospital, 4060 Ste-Catherine West, Montreal, Quebec H3Z 2Z3, Canada

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
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358..736
/gene="MTRR"
/number=5

ORIGIN

Query Match 18.2%; Score 381; DB 9; Length 1353;
Best Local Similarity 100.0%; Pred. No. 4.2e-196;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 401 GTTTAAGACTTGTTGAGCCGTGATTTGCTGAGCTTGGCCAGCCCTCAGAAAGCAAT 460
Db 357 GTTTAAGACTTGTTGAGCCGTGATTTGCTGAGCTTGGCCAGCCCTCAGAAAGCAAT 416
QY 461 TTAGGTCAAGCAGACGACAAAGAGAGATTAAGTGGCGCACTCCCGGTGGCAATCCTGCAT 520
Db 417 TTAGGTCAAGCAGACGACAAAGAGAGATTAAGTGGCGCACTCCCGGTGGCAATCCTGCAT 476
QY 521 CTTGAGGACGACCTTGTGAAGTCAAGCTGTACACATTGAATTCGAAGTCAAGCTTC 580

Db 477 CCTTGGAGCAGACCTTGTGAAGTCAAGCTGTACATTAATCTCAAGTCAAGCTTC 536
QY 581 TGAATTCGATGATTCAGAGAAAGAGATTCGAGTTTGAAGCAAAATGAGTGAACA 640
Db 537 TGAATTCGATGATTCAGAGAAAGAGATTCGAGTTTGAAGCAAAATGAGTGAACA 596
QY 641 GCAACCATTCGAATGTTGATTAATTGAAGACTTTGAGTCTTCATCTTACCCGTGGTACCCC 700
Db 597 GCACCAATTCGAATGTTGATTAATTGAAGACTTTGAGTCTTCATCTTACCCGTGGTACCCC 656
QY 701 CACTTCACAAGCTCTCTGAATATCTGTGTTTACCCCGAGAAATTTACAGAGTATC 760
Db 657 CACTTCACAAGCTCTCTGAATATCTGTGTTTACCCCGAGAAATTTACAGAGTATC 716
QY 761 TGCAGAGTCTCTTGGCCAGG 781
Db 717 TGCAGAGTCTCTTGGCCAGG 737

RESULT 11
AC010346 109626 bp DNA linear PRI 10-NOV-2000
LOCUS Homo sapiens chromosome 5 clone CITB-H1_2018B2, complete sequence.
ACCESSION AC010346
VERSION AC010346.6 GI:11136705
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Unpublished
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 109626)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Nov 10, 2000 this sequence version replaced gi:9256196.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
STS Content:
WI-9255 G05749.

FEATURES

source

Location/Qualifiers
1..109626
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CITB-H1_2018B2"

ORIGIN

Query Match 15.8%; Score 330; DB 9; Length 109626;
Best Local Similarity 99.7%; Pred. No. 2.2e-168;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 401 GTTTAAGACTTGTTGAGCCGTGATTTGCTGAGCTTGGCCAGCCCTCAGAAAGCAAT 460
Db 88571 GTTTAAGACTTGTTGAGCCGTGATTTGCTGAGCTTGGCCAGCCCTCAGAAAGCAAT 88630
QY 461 TTAGGTCAAGCAGACGACAAAGAGAGATTAAGTGGCGCACTCCCGGTGGCAATCCTGCAT 520
Db 88631 TTAGGTCAAGCAGACGACAAAGAGAGATTAAGTGGCGCACTCCCGGTGGCAATCCTGCAT 88690

QY 521 CCTTGAGGACAGACCTTGTGAAGTCAAGCTGCTACACATTTGAATCTCAAGTCAGCTTC 580
 Db 88691 CCTCGAGGACAGACCTTGTGAAGTCAAGCTGCTACACATTTGAATCTCAAGTCAGCTTC 88750
 QY 581 TGAATTCATGATTCAGAGAGAAAGAGATTCAGAGTTTGAAGCAAAAATGCAAGTGAACA 640
 Db 88751 TGAATTCATGATTCAGAGAGAAAGAGATTCAGAGTTTGAAGCAAAAATGCAAGTGAACA 88810
 QY 641 GCAACCAATCCAAATGTTGTAATTTGAAGACTTTGAGTCTCACTTACCCTGCGTACCCC 700
 Db 88811 GCAACCAATCCAAATGTTGTAATTTGAAGACTTTGAGTCTCACTTACCCTGCGTACCCC 88870
 QY 701 CACTCTCACAAGCTCTCGAATATTCGTTTACCCCAAGATTTTACAGGTACATC 760
 Db 88871 CACTCTCACAAGCTCTCGAATATTCGTTTACCCCAAGATTTTACAGGTACATC 88930
 QY 761 TGCAGAGTCTCTTGGCCAGG 781
 Db 88931 TGCAGAGTCTCTTGGCCAGG 88951

RESULT 12
 AC025174 110756 bp DNA linear PRI 28-MAR-2002
 LOCUS Homo sapiens chromosome 5 clone CTD-2072124, complete sequence.
 DEFINITION AC025174
 AC025174.5 GI:19774456
 VERSION HTG.
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITLE 1 (bases 1 to 110756)
 JOURNAL DOB Joint Genome Institute and Stanford Human Genome Center.
 REFERENCE
 AUTHORS Unpublished
 TITLE 2 (bases 1 to 110756)
 JOURNAL DOB Joint Genome Institute.
 REFERENCE
 AUTHORS Direct Submission
 TITLE Submitted (07-MAR-2002) Production Sequencing Facility, DOB Joint
 JOURNAL Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 3 (bases 1 to 110756)
 REFERENCE
 AUTHORS DOB Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAR-2002) Production Sequencing Facility, DOB Joint
 REFERENCE
 AUTHORS Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 4 (bases 1 to 110756)
 JOURNAL DOB Joint Genome Institute and Stanford Human Genome Center.
 REFERENCE
 AUTHORS Direct Submission
 TITLE Submitted (28-MAR-2002) DOB Joint Genome Institute, 2800 Mitchell
 JOURNAL Drive, Walnut Creek, CA 94598, USA
 On Mar 28, 2002 this sequence version replaced gi:19224767.
 COMMENT Draft Sequence Produced by DOB Joint Genome Institute
 www.jgi.doe.gov
 FINISHING Completed at Stanford Human Genome Center
 www.shgc.stanford.edu
 Quality: Phrap Quality >=40 100% of Sequence;
 Estimated Total Number of Errors is 0.
 Location/Qualifiers
 1. 110756
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="5"
 /clone="CTD-2072124"

ORIGIN

Query Match 15.8%; Score 330; DB 9; Length 110756;
 Best Local Similarity 99.7%; Pred. No. 2.2e-168;
 Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 GTTAGAATCTTGTTGAGCCGCTGATTCCTGAGACTCTGCGACGCTTCAAGAAAGATT 460

Db 20040 GTTAGAATCTTGTTGAGCCGCTGATTCCTGAGACTCTGCGACGCTTCAAGAAAGATT 20099
 QY 461 TTAGGTCAAGGAGAGAGAGAGATTAATGAGGCGCACTCCCGGTGGATCACTGATC 520
 Db 20100 TTAGGTCAAGGAGAGAGAGATTAATGAGGCGCACTCCCGGTGGATCACTGATC 20159
 QY 521 CCTTGAGGACAGACCTTGTGAAGTCAAGCTGCTACACATTTGAATCTCAAGTCAGCTTC 580
 Db 20160 CCTCGAGGACAGACCTTGTGAAGTCAAGCTGCTACACATTTGAATCTCAAGTCAGCTTC 20219
 QY 581 TGAATTCATGATTCAGAGAGAAAGAGATTCAGAGTTTGAAGCAAAAATGCAAGTGAACA 640
 Db 20220 TGAATTCATGATTCAGAGAGAAAGAGATTCAGAGTTTGAAGCAAAAATGCAAGTGAACA 20279
 QY 641 GCAACCAATCCAAATGTTGTAATTTGAAGACTTTGAGTCTCACTTACCCTGCGTACCCC 700
 Db 20280 GCAACCAATCCAAATGTTGTAATTTGAAGACTTTGAGTCTCACTTACCCTGCGTACCCC 20339
 QY 701 CACTCTCACAAGCTCTCGAATATTCGTTTACCCCAAGATTTTACAGGTACATC 760
 Db 20340 CACTCTCACAAGCTCTCGAATATTCGTTTACCCCAAGATTTTACAGGTACATC 20399
 QY 761 TGCAGAGTCTCTTGGCCAGG 781
 Db 20400 TGCAGAGTCTCTTGGCCAGG 20420

RESULT 13
 AC022921 158199 bp DNA linear HTG 12-MAR-2000
 LOCUS Homo sapiens clone RP11-138P20, WORKING DRAFT SEQUENCE, 12
 DEFINITION AC022921
 AC022921.2 GI:7229868
 VERSION HTG; HTGS PHASB1; HTGS_DRAFT.
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITLE 1 (bases 1 to 158199)
 JOURNAL Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 REFERENCE
 AUTHORS Homo sapiens, clone RP11-138P20
 JOURNAL Unpublished
 TITLE 2 (bases 1 to 158199)
 JOURNAL Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
 Boguslavsky, L., Bouckgalter, B., Brown, A., Burkett, G., Castle, A.,
 Choesel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
 DeRellano, K., Dewar, K., Domingo, M., Doyle, M., Feneator, J.,
 Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galsgan, J.,
 Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
 Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
 Landers, T., Lehocsky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
 Macdonald, P., Margulis, N., McKernan, P., McGurk, A., McKernan, K.,
 McPheters, R., Meldrum, J., Menus, L., Morrow, J., Naylor, J.,
 Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, T.M., Peterson, K.,
 Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Kochman, D.,
 Roy, A., Santos, R., Severy, P., Spencer, R., Stange-Thomann, N.,
 Stojanovic, N., Subramanian, A., Talamas, J., Testfaye, S., Theodore, J.,
 Tirelli, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
 Zimmer, A. and Zody, M.

COMMENT
 JOURNAL
 TITLE
 Direct Submission
 Submitted (07-FEB-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 12, 2000 this sequence version replaced gi:5921909.
 All repeats were identified using RepeatMasker:
 Smit, A.P.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu

```

Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: I6314
Center clone name: I38_P_20
----- Summary Statistics -----
Sequencing vector: M13; M77815; 100% of reads
Strategy: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 152636 bases at least Q40
Consensus quality: 155474 bases at least Q30
Consensus quality: 156388 bases at least Q20
Insert size: 178000; agarose-fp
Insert size: 157099; sum-of-contigs
Quality coverage: 4.4 in Q20 bases; agarose-fp
Quality coverage: 5.0 in Q20 bases; sum-of-contigs
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NOTE: This is a 'working draft' sequence. It currently
consists of 12 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
1
1284      1283: contig of 1283 bp in length
1384      4203: contig of 2820 bp in length
4204      4303: gap of 100 bp
4304      6786: contig of 2483 bp in length
6787      6886: gap of 100 bp
6887      9683: contig of 2797 bp in length
9684      9783: gap of 100 bp
9784      12902: contig of 3119 bp in length
12903     13002: gap of 100 bp
13003     16429: contig of 3427 bp in length
16430     16529: gap of 100 bp
16530     25301: contig of 8672 bp in length
25301     25301: gap of 100 bp
25302     36759: contig of 11458 bp in length
25302     36760: gap of 100 bp
36760     53921: contig of 17062 bp in length
53921     53922: gap of 100 bp
54022     72054: contig of 18033 bp in length
72055     72154: gap of 100 bp
72155     102527: contig of 30373 bp in length
102528    102527: gap of 100 bp
102628    158199: contig of 55572 bp in length.
FEATURES
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Location/Qualifiers
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/mol_type="genomic DNA"
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/clone_lib="RP11-138P20"
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1384..4203
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4304..6786
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6887..9683
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9784..12902
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ORIGIN	Query Match	13.3%; Score 279; DB 2; Length 158199;
	Best Local Similarity 99.5%; Pred. No. 1,7e-140;	
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misc_feature	/note="assembly_fragment" 54022..72054	
misc_feature	/note="assembly_fragment" 72155..102527	
misc_feature	/note="assembly_fragment" 102628..158199	
	/note="assembly_fragment"	
QY	401 GTTTAGAACTTGTGTGTAGCCCGTGAATTCCTGACTCTTGCCAGCCCTCAGAAAGCATT 460	
DB	3446 GTTTAGAACTTGTGTGTAGCCCGTGAATTCCTGACTCTTGCCAGCCCTCAGAAAGCATT 3505	
QY	461 TTTAGGTCAACAGAGAGCAAGAGAGAGTAGTGGCCGACCTCCGGTGGCATCACTTGCAT 520	
DB	3506 TTAGGTCAACAGAGAGCAAGAGAGTAGTGGCCGACCTCCGGTGGCATCACTTGCAT 3565	
QY	521 CCTTGAG 580	
DB	3566 CCTTGAG 3625	
QY	581 TGAGATTGATGATTCAG 640	
DB	3626 TGAGATTGATGATTCAG 3685	
QY	641 GCAACCAATCCATCTTTGTAATTTGAAGACTTTGAGTCTTCACTTACCCGTTGGTACCC 700	
DB	3686 GCAACCAATCCATCTTTGTAATTTGAAGACTTTGAGTCTTCACTTACCCGTTGGTACCC 3745	
QY	701 CACTTCAG 760	
DB	3746 CACTTCAG 3805	
QY	761 TGCAGAGATCTCTTGGCCAGG 781	
DB	3806 TGCAGAGATCTCTTGGCCAGG 3826	
RESULT 14		
AC021609	167237 bp DNA linear HTG 12-MAR-2000	
LOCUS	Homo sapiens clone RP11-259D10, WORKING DRAFT SEQUENCE, 6 unordered	
DEFINITION	pieces.	
ACCESSION	AC021609	
VERSION	AC021609.3 GI:7230210	
KEYWORDS	HTG; HTGS PHASE1; HTGS_DRAFT.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Euteleostomi; Primates; Catarrhini; Homnidae; Homo.	
TITLE	1 (bases 1 to 167237)	
JOURNAL	Bitren,B., Linton,L., Nusbaum,C. and Lander,E.	
REFERENCE	Unpublished	
AUTHORS	2 (bases 1 to 167237)	
	Bitren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,	
	Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Bede,F.,	
	Boguslavsky,L., Bouhgalter,B., Brown,A., Bukhet,G., Castle,A.,	
	Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,	
	DeKrellano,K., Dewar,K., Domino,M., Doyle,M., Fenebor,J.,	
	Ferreira,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J.,	
	Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,	
	Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,	
	Landers,T., Lehoczkv,J., Levine,R., Liu,C., Liu,G., Locke,K.,	
	Mcdonald,P., Margulis,N., McEwan,P., McGuck,A., McKernan,K.,	
	McHeaters,R., Melgrim,T., Menesius,L., Morrow,J., Naylor,J.,	
	Norman,C.H., O'Connor,T., O'Donnell,P., Oliver,T.M., Peterson,K.,	

TITLE

JOURNAL

COMMENT

Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talama, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliou, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmer, A., and Zody, M.

Submitted (16-JUN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Garden Street, Cambridge, MA 02141, USA

On Mar 12, 2000 this sequence version replaced gi:689697.

All repeats were identified using RepeatMasker:

Smith, A. P. A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center: MIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L5818

Center clone name: 259 D 10

Summary Statistics

Sequencing vector: M13, M7815, 100% of reads

Chemistry: Dye-terminator Big Dye, 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 16183 bases at least Q40

Consensus quality: 164380 bases at least Q30

Consensus quality: 165590 bases at least Q20

Insert size: 164000; agarose-fp

Insert size: 166737; sum-of-contigs

Quality coverage: 5.1 in Q20 bases; agarose-fp

Quality coverage: 5.0 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 3656: contig of 3656 bp in length
* 3657 3756: gap of 100 bp
* 3757 9436: contig of 5680 bp in length
* 9437 9536: gap of 100 bp
* 9537 27768: contig of 18232 bp in length
* 27769 27868: gap of 100 bp
* 27869 52058: contig of 24190 bp in length
* 52059 52158: gap of 100 bp
* 52159 80100: contig of 27942 bp in length
* 80101 80200: gap of 100 bp
* 80201 167237: contig of 87037 bp in length.

FEATURES

Source

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/note="assembly_fragment"

clone end: T7

vector side: left"

misc_feature

/note="assembly_fragment"

9537. 27768

/note="assembly_fragment"

clone end: SP6

misc_feature

/note="assembly_fragment"

52159. 80100

/note="assembly_fragment"

misc_feature

80201. 167237

/note="assembly_fragment"

Query Match 13.3%; Score 279; DB 2; Length 167237;
Best Local Similarity 99.5%; Pred. No. 1.7e-140;
Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

401 GTTTGAACTTGTGGTGGACCGTGAATGCTGGAATGCGGACGCTCAGAAACATT 460
62083 GTTTGAACTTGTGGTGGACCGTGAATGCTGGAATGCGGACGCTCAGAAACATT 62142
461 TTAGTCAAGCAGAGACAGAGAGATTAAGTGGCGCACTCCGCTGGCATCCTGCAT 520
62143 TTAGTCAAGCAGAGACAGAGAGATTAAGTGGCGCACTCCGCTGGCATCCTGCAT 62202
521 CCTTGAAGCAGACCTTGTGAAGTCAAGCTCTACATTTAATCTCAAGTCGACTTC 580
62203 CCTTGAAGCAGACCTTGTGAAGTCAAGCTCTACATTTAATCTCAAGTCGACTTC 62262
581 TGAGATTCATGATTCAGAGAAAGATTCAGAGTTTGAAGCAAAATGACATGAACA 640
62263 TGAGATTCATGATTCAGAGAAAGATTCAGAGTTTGAAGCAAAATGACATGAACA 62322
641 GCAACCAATCCATGTTGTAATGAAGACTTTGAGTCTCACTTACCCGTTCCGTAACCC 700
62323 GCAACCAATCCATGTTGTAATGAAGACTTTGAGTCTCACTTACCCGTTCCGTAACCC 62382
701 CACTCTCAGAACCTCTCGATATTTCTGTTTACCCCAAAATTTTACAGTATCATC 760
62383 CACTCTCAGAACCTCTCGATATTTCTGTTTACCCCAAAATTTTACAGTATCATC 62442
761 TGCAGAGTCTCTTGGCCAGG 781
62443 TGCAGAGTCTCTTGGCCAGG 62463

RESULT 15

AC091945

LOCUS

DEFINITION

AC091945

AC091945

AC091945

AC091945

AC091945

AC091945

AC091945

AC091945

AC091945

AC091945

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AC091945

AC091945

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AC091945

AC091945

Quality coverage: 10.01 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 1207: contig of 1207 bp in length
* 1208 1307: gap of unknown length
* 1308 3385: contig of 2078 bp in length
* 3386 3485: gap of unknown length
* 3486 5553: contig of 2068 bp in length
* 5554 5653: gap of unknown length
* 5654 7030: contig of 1377 bp in length
* 7031 7130: gap of unknown length
* 7131 9068: contig of 1939 bp in length
* 9070 9169: gap of unknown length
* 9170 11452: contig of 2283 bp in length
* 11453 11552: gap of unknown length
* 11553 16002: contig of 4450 bp in length
* 16003 16102: gap of unknown length
* 16103 21083: contig of 4981 bp in length
* 21084 21183: gap of unknown length
* 21184 26893: contig of 5710 bp in length
* 26894 26993: gap of unknown length
* 26994 29987: contig of 2994 bp in length
* 29988 30087: gap of unknown length
* 30088 32949: contig of 2862 bp in length
* 32950 33049: gap of unknown length
* 33050 38757: contig of 5708 bp in length
* 38758 38857: gap of unknown length
* 38858 45202: contig of 6345 bp in length
* 45203 45302: gap of unknown length
* 45303 50911: contig of 5609 bp in length
* 50912 51011: gap of unknown length
* 51012 55880: contig of 4869 bp in length
* 55881 55980: gap of unknown length
* 55981 63189: contig of 7209 bp in length
* 63190 63289: gap of unknown length
* 63290 69632: contig of 6343 bp in length
* 69633 69732: gap of unknown length
* 69733 76377: contig of 6645 bp in length
* 76378 76477: gap of unknown length
* 76479 83051: contig of 6574 bp in length
* 83052 83151: gap of unknown length
* 83152 94929: contig of 11778 bp in length
* 94930 95029: gap of unknown length
* 95030 104346: contig of 9317 bp in length
* 104347 104446: gap of unknown length
* 104447 115275: contig of 10829 bp in length
* 115276 115375: gap of unknown length
* 115376 123488: contig of 8113 bp in length
* 123489 123588: gap of unknown length
* 123589 133172: contig of 9584 bp in length
* 133173 133272: gap of unknown length
* 133273 145495: contig of 12223 bp in length
* 145496 145595: gap of unknown length
* 145596 160270: contig of 14675 bp in length
* 160271 160370: gap of unknown length
* 160371 177596: contig of 17226 bp in length.

FEATURES

source
1. 177596
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone_lib="RP11-35616"
/clone_lib="RP11-35616" human BAC library 11"

ORIGIN

Query Match 13.3%; Score 279; DB 2; Length 177596;

Best Local Similarity 99.5%; Pred. No. 1.7e-140; Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTTAGAACCTTGGTGGTGGCCGTGATTTGCTGCACTTGGCCAGCCCTCAGAAACATT 460
Db 83524 GTTTAGAACCTTGGTGGTGGCCGTGATTTGCTGCACTTGGCCAGCCCTCAGAAACATT 83583
QY 461 TTAGGTCAAGCAGAGGACAAAGAGATTAAGTGGCGCACTCCCGTGGCATCCAT 520
Db 83584 TTAGGTCAAGCAGAGGACAAAGAGATTAAGTGGCGCACTCCCGTGGCATCCAT 83643
QY 521 CCTTGAAGACAGACCTTGGTGAAGTCAAGCTGTACACTTGAATTCATAGTGAAGTTC 580
Db 83644 CCTGAGGACAGACCTTGGTGAAGTCAAGCTGTACACTTGAATTCATAGTGAAGTTC 83703
QY 581 TGAGATTGATGATTCAGGAGAAAGATTTCTAGGTTTGAAGCAAAATGCAGTGAACA 640
Db 83704 TGAGATTGATGATTCAGGAGAAAGATTTCTAGGTTTGAAGCAAAATGCAGTGAACA 83763
QY 641 GCAACCAATCCAAATGTTGTAATTGAAGACTTGAAGTCTTCACTTACCCGTTGGTACCCC 700
Db 83764 GCAACCAATCCAAATGTTGTAATTGAAGACTTGAAGTCTTCACTTACCCGTTGGTACCCC 83823
QY 701 CACTTCACAGGCTCTTGAATATTCCTGCTTACCCCAAGATTTTACAGGTACATC 760
Db 83824 CACTTCACAGGCTCTTGAATATTCCTGCTTACCCCAAGATTTTACAGGTACATC 83883
QY 761 TGCAGAGTCTCTTGGSCAGG 781
Db 83884 TGCAGAGTCTCTTGGSCAGG 83904

Search completed: August 27, 2005, 09:39:04
Job time : 5999.75 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 13:32:20 ; Search time 732.091 Seconds
(without alignment)
16924.161 Million cell updates/sec

Title: US-09-371-347A-47

Perfect score: 2093

Sequence: 1 atgagggaggttcctgtact.....ttcagatatttgcataca 2093

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneeqn1980s:*\n2: geneeqn1990s:*\n3: geneeqn2000s:*\n4: geneeqn2001as:*\n5: geneeqn2001bs:*\n6: geneeqn2002as:*\n7: geneeqn2002bs:*\n8: geneeqn2003as:*\n9: geneeqn2003bs:*\n10: geneeqn2003cs:*\n11: geneeqn2003ds:*\n12: geneeqn2004as:*\n13: geneeqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1970	94.1	2091	11	ADM43214 Human met
2	1793	85.7	3259	5	AA65070 DNA encod
3	1793	85.7	3259	5	AA65070 DNA encod
4	1793	85.7	3259	11	AA65070 DNA encod
5	1793	85.5	2094	11	ADM43206 Human tui
6	1739	83.1	2094	11	ADM43208 Human wll
7	1739	83.1	2094	11	ADM43212 Human met
8	1691	80.8	3259	3	AA58935 DNA encod
9	1677	80.1	2091	11	ADM43216 Human met
10	1640	78.4	3270	13	ADQ87538 Human tum
11	1595	76.2	3256	3	AA58976 A human m
12	1544	73.8	3255	3	AA58976 A human m
13	956	45.7	3189	13	ACH42470 Human dia
14	879	42.0	3256	13	ADQ39029 Human SNP
15	879	42.0	3274	13	ADQ39030 Human SNP
16	501	23.9	1986	4	AA641064 Human enco
17	386	18.4	390	2	AA641064 Human enco
18	330	15.8	591	12	ACH73174 Human Gen
19	328	15.7	379	12	ACH86905 Human Gen
20	317	15.1	1663	4	AA641602 cDNA enco

21	279	13.3	591	12	ACH68540 Human gen
22	277	13.2	379	12	ACH82240 Human gen
23	225	10.8	503	5	AA65069 DNA encod
24	188	9.0	525	12	ACH67438 Human gen
25	175	8.4	175	12	ACH81143 Human gen
26	158	7.5	2475	6	AD32365 Human lun
27	157	7.5	2475	13	AD32365 Human lun
28	137	6.5	525	12	ACH73117 Human gen
29	124	5.9	175	12	ACH86848 Human gen
30	78	3.7	244	3	AA242736 Human 5'
31	60	2.9	60	6	AB36264 Human sp1
32	51	2.4	51	4	AA178548 Human b11
33	38	1.8	1835	5	AA65071 DNA encod
34	30	1.4	1681	11	AD131127 Human CDN
35	26	1.2	26	3	AA58955 PCR prime
36	26	1.2	26	3	AA58955 PCR prime
37	26	1.2	26	6	ABX09549 Arterioscl
38	26	1.2	26	6	AA143713 Pregerat
39	26	1.2	26	11	ADM43205 Human met
40	26	1.2	26	11	ADM43189 Human met
41	25	1.2	25	3	AA58952 PCR prime
42	25	1.2	25	3	AA58937 PCR prime
43	25	1.2	25	3	AA58947 PCR prime
44	25	1.2	25	11	ADM43187 Human met
45	25	1.2	25	11	ADM43202 Human met

ALIGNMENTS

RESULT 1		
ADM43214		
ID	ADM43214	standard; cDNA; 2091 BP.
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AC	ADM43214;	
XX		
DT	03-JUN-2004	(first entry)
XX		
DE	Human methionine synthase reductase CDS del 1675-1678 variant.	
XX		
KM	Human; ss; Methionine synthase reductase polypeptide; HAMTRR; cancer	
KW	cardiovascular disease; neural tube defect; hyperhomocysteinemia;	
XX	chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.	
XX		
OS	Homo sapiens.	
XX		
FN	Key	Location/Qualifiers
FT	CDS	1..2091
FT		/*tag= a
FT		/product= "HAMTRRdelR559"
FT		/partial
FT		/note= "No stop codon shown"
FT	variation	replace(66,A)
FT		/*tag= b
FT		/standard_name= "Single_nucleotide polymorphism"
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FT		/*tag= c
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FT	variation	replace(1675,AGAG)
FT		/*tag= d
FN	US2003082676-A1.	
XX		
PD	01-MAY-2003.	
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PF	10-AUG-1999;	99US-00371347.
XX		
PR	16-JAN-1998;	98US-0071622P.
PR	15-JAN-1999;	99US-00232028.
XX		
PA	(GRAV/) GRAVEL R A.	
PA	(ROZE/) ROZEN R.	
PA	(LECL/) LECLERC D.	

PA (WILE/) WILSON A.
 PA (ROSE/) ROSENBLATT D.
 PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
 XX PFI: 2003-576610/54.
 XX P-PSDB; ADM43215.
 DR
 XX
 XX
 PT New substantially pure nucleic acid encoding a mammalian methionine
 PT synthase reductase polypeptide, useful for diagnosing, preventing or
 PT treating conditions associated with altered methionine synthase activity,
 PT e.g. cancer.
 PS
 PS Disclosure; SEQ ID NO 47; 26pp; English.
 CC
 CC The invention relates to a substantially pure nucleic acid that encodes a
 CC mammalian methionine synthase reductase polypeptide, hEmTR, or that
 CC hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
 CC ADM43209. Also included are a non-human animal where one or both genetic
 CC alleles encoding the methionine synthase reductase polypeptide are
 CC mutated, an antibody that specifically binds the above methionine
 CC synthase reductase polypeptide, a method of detecting the presence of the
 CC above polypeptide, a method for detecting sequence variants for
 CC methionine synthase reductase in a mammal, methods of treating or
 CC preventing cancer (or cardiovascular disease or neural tube defects) in a
 CC subject, methods of screening for a compound that modulates methionine
 CC synthase reductase biological activity and a method for detecting an
 CC increased risk of developing a neural tube defect in a mammalian embryo
 CC or foetus. The nucleic acid is useful in diagnosing, preventing or
 CC treating conditions associated with altered methionine synthase activity,
 CC such as cancer, cardiovascular disease or neural tube defects, or in
 CC screening for a compound that modulates methionine synthase reductase
 CC biological activity. Naturally occurring variants of the polypeptide are
 CC also associated with hyperhomocysteinaemia. The gene for hEmTR is
 CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
 CC sequence of a variant human hEmTR cDNA.
 CC
 XX
 XX Sequence 2091 BP; 589 A; 489 C; 480 G; 533 T; 0 U; 0 Other;
 SQ
 Query Match 94.1%; Score 1970; DB 11; Length 2091;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2090; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 421 CCGTGGATTGCTGGACTCTGGCCAGCCCTCAGAAAGCATTTTAAAGTCAAGCAGAGCA 480
 Qy 481 GAGAGATAAGTGGCCACTCCCGTGGCATCACTGCATCTTGAAGCAGACCTTGTG 540
 Db 481 GAGGATATAAGTGGCCACTCCCGTGGCATCACTGCATCTTGAAGCAGACCTTGTG 540
 Qy 541 AAGTCAGAGCTGCTACACATTGAATTCAAAGTCAGCTTCTGAGATTCCATGATTCAGGA 600
 Db 541 AAGTCAGAGCTGCTACACATTGAATTCAAAGTCAGCTTCTGAGATTCCATGATTCAGGA 600
 Qy 601 AGAAGAGATTCGAGGTTTGAAGCAAAATGCAGTAACAGCAACCAATCCAAATGTTGA 660
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 Db 661 ATTGAAGCTTTGAGTCTCACTTACCCGTCGGTACCCCACTCTCACAGCCTCTCTG 720
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 Qy 781 GAGGAAGCCAGATATCTGTGACTTTCAGAGATCCAGTTTTCAGTGCATTTGAAG 840
 Db 781 GAGGAAGCCAGATATCTGTGACTTTCAGAGATCCAGTTTTCAGTGCATTTGAAG 840
 Qy 841 GCAGTTCACCTTACTACGATGATGCAATTAACAACCACTCTGCTGATAGATTGACATT 900
 Db 841 GCAGTTCACCTTACTACGATGATGCAATTAACAACCACTCTGCTGATAGATTGACATT 900
 Qy 901 TCAATATACAGACTTTTCTATCAGCTGATGCTTCAAGCTGATCTGCTTAAACAGT 960
 Db 901 TCAATATACAGACTTTTCTATCAGCTGATGCTTCAAGCTGATCTGCTTAAACAGT 960
 Qy 961 GATTCGAGGTCAAGGCTTACCTCAAGATCGACCTTGAAGATTAAGAGAGACCTGC 1020
 Db 961 GATTCGAGGTCAAGGCTTACCTCAAGATCGACCTTGAAGATTAAGAGAGACCTGC 1020
 Qy 1021 GTCTCTTTGAAATTAAGGACAGACAAAGAAAGAGACTTACCTTACCCGACATATA 1080
 Db 1021 GTCTCTTTGAAATTAAGGACAGACAAAGAAAGAGACTTACCTTACCCGACATATA 1080
 Qy 1081 CCGCGGAGATGTTCTCTCCAGTTCAATTTTCTGCTGTTTGAATTCGAGCAATTCCT 1140
 Db 1081 CCGCGGAGATGTTCTCTCCAGTTCAATTTTCTGCTGTTTGAATTCGAGCAATTCCT 1140
 Qy 1141 AAAAAGCAATTTTGGAGAGCCCTGTGGAATAACAGAGACAGTGTGAAAAGCCAGG 1200
 Db 1141 AAAAAGCAATTTTGGAGAGCCCTGTGGAATAACAGAGACAGTGTGAAAAGCCAGG 1200
 Qy 1201 CTACAGAGCTGTGACATTAACAAAGGGGACGCCGATTAAGCCGTTTGTACAGATGCC 1260
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 Qy 1261 TGTGCTGCTGTTGGATCTCTCTGCTGCTTTCCTTTCGACAGCACACTCACTCTC 1320
 Db 1261 TGTGCTGCTGTTGGATCTCTCTGCTGCTTTCCTTTCGACAGCACACTCACTCTC 1320
 Qy 1321 CTGCTGGAACATCTTCTTAACTTCAACCAAGCAATATTCGATGCAAGCTCAAGTTTA 1380
 Db 1321 CTGCTGGAACATCTTCTTAACTTCAACCAAGCAATATTCGATGCAAGCTCAAGTTTA 1380
 Qy 1381 TTTCAACCAAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTTGTCTACTGCA 1440
 Db 1381 TTTCAACCAAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTTGTCTACTGCA 1440
 Qy 1441 ACAAGAGTTCTGCGGAAGGAGATATTAAGGCTGCTGCTTGTGTTGCTTCACTT 1500
 Db 1441 ACAAGAGTTCTGCGGAAGGAGATATTAAGGCTGCTGCTTGTGTTGCTTCACTT 1500
 Qy 1501 CTTCAAGCAAAATATATGATATCCCATGAAAGCAGGAGGAAAGCCCTGAGCTTAAAGAT 1560
 Db 1501 CTTCAAGCAAAATATATGATATCCCATGAAAGCAGGAGGAAAGCCCTGAGCTTAAAGAT 1560

QY 1561 TCCATCTCTCGAACAACAATTCCTTCACTTACAGATGACCCCTCAATCCCATC 1620
XX |||||
PS 1561 TCCATCTCTCTCGAACAACAATTCCTTCACTTACAGATGACCCCTCAATCCCATC 1620
CC |||||
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostic as expressed sequence tags for identifying expressed
CC genes. (II) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX |||||
SQ Sequence 3259 BP; 944 A; 695 C; 674 G; 946 T; 0 U; 0 Other;
Query Match 85.7%; Score 1793; DB 5; Length 3259;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservativity 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 1ATGAGAGAGGTTCTGTATATATGCTACACAGACGAGGACGAGCAAGCCATCGAGAA 60
DB 80 ATGAGAGAGGTTCTGTATATATGCTACACAGACGAGGACGAGCAAGCCATCGAGAA 139
QY 61 GAATGTGTAGACCAAGCTGTGTATATGCTACACAGACGAGGACGAGCAAGCCATCGAGAA 120
DB 140 GAATGTGTAGACCAAGCTGTGTATATGCTACACAGACGAGGACGAGCAAGCCATCGAGAA 199
QY 121 TCGATATATATGCTACACAGACGAGGACGAGCAAGCCATCGAGAA 180
DB 200 TCGATATATATGCTACACAGACGAGGACGAGCAAGCCATCGAGAA 259
QY 181 GGACCGGAGACCCACCGACACAGCCCGGAGTTGTTAAGAAATACAGACCAACA 240
DB 260 GGACCGGAGACCCACCGACACAGCCCGGAGTTGTTAAGAAATACAGACCAACA 319
QY 241 CTGCGGTTGATTTCTTCTCACTGCGGTATGCGTTACTGCGTCTCGGTATTCAGAA 300
DB 320 CTGCGGTTGATTTCTTCTCACTGCGGTATGCGTTACTGCGTCTCGGTATTCAGAA 379
QY 301 TACACCTACTTTTTCAGATGCGGAGAAATATATGATTAACGACTTCAAGAGCTTGAGCC 360
DB 380 TACACCTACTTTTTCAGATGCGGAGAAATATATGATTAACGACTTCAAGAGCTTGAGCC 439
QY 361 CGGATTTCTATGACATGAGCATGAGATGACTGTGTAGGTTTAAAGCTTGAGGTTAG 420
DB 440 CGGATTTCTATGACATGAGCATGAGATGACTGTGTAGGTTTAAAGCTTGAGGTTAG 499
QY 421 CCGTGATTTCTGACATCTGCGCAGCCCTCAGAAAGCATTTTAAAGTCAAGACAGAGCAA 480
DB 500 CCGTGATTTCTGACATCTGCGCAGCCCTCAGAAAGCATTTTAAAGTCAAGACAGAGCAA 559
QY 481 GAGGAGATTAAGTGGCCACTCCCGGTGATCATCTGATCTTGTAGAGACAGACTTTG 540
DB 560 GAGGAGATTAAGTGGCCACTCCCGGTGATCATCTGATCTTGTAGAGACAGACTTTG 619
QY 541 AAGTCAGAGCTGACATGATGATCAAGTCAAGCTTCTGAGATTCAGATTCAGGA 600
DB 620 AAGTCAGAGCTGACATGATGATCAAGTCAAGCTTCTGAGATTCAGATTCAGGA 679
QY 601 AGAAAGATTCGAGGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCCATGTTTGA 660

RESULT 2
AAS65070
ID AAS65070 standard; cDNA; 3259 BP.
XX
AC AAS65070;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #874.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001MO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR P-PSDB; ABG00883.
XX
PT WPI; 2001-639362/73.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnosis, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

Db 680 AGAAGATTCTGAGTTTGAAGCAAAATGACGTGAACGAAACCAATCCAAATGTTGA 739
Qy 661 ATTGAAGACTTTGAGTCTCCTACCTTACCCGTTGGTACCCCACTCTCAAGCCTCTG 720
Db 740 ATTGAAGACTTTGAGTCTCCTACCTTACCCGTTGGTACCCCACTCTCAAGCCTCTG 739
Qy 721 AATATTCTGTTTACCCCAAGATATTACAGGTACATCTGAGAGAGTCTTTGGCAG 780
Db 800 AATATTCTGTTTACCCCAAGATATTACAGGTACATCTGAGAGAGTCTTTGGCAG 859
Qy 781 GAGGAAGCCAGATCTGTGATCTTGAGAGATCAGTCTTTTCAAGGCCAATTTCAAG 840
Db 860 GAGGAAGCCAGATCTGTGATCTTGAGAGATCAGTCTTTTCAAGGCCAATTTCAAG 919
Qy 841 GCAATTCATCTTACAGAAATGATCCATAAAACACTGCTGTGTAGAAATGACAT 900
Db 920 GCAATTCATCTTACAGAAATGATCCATAAAACACTGCTGTGTAGAAATGACAT 979
Qy 901 TCAAAATCAGACTTTTCTTATCAGCTGTGAGATGCTTCAAGCTGATCTGCTAACAGT 960
Db 980 TCAAAATCAGACTTTTCTTATCAGCTGTGAGATGCTTCAAGCTGATCTGCTAACAGT 1039
Qy 961 GATTCTGAGGTACAAAGCCTACTCCAAAGA CTGAGCTTGAAGATAAAGAGAGACTGC 1020
Db 1040 GATTCTGAGGTACAAAGCCTACTCCAAAGACTGAGCTTGAAGATAAAGAGAGACTGC 1099
Qy 1021 GTCTTTTGAATAATTAAGGAGACACAAAGAAAGAGACTACTTACCCAGCATATA 1080
Db 1100 GTCTTTTGAATAATTAAGGAGACACAAAGAAAGAGACTACTTACCCAGCATATA 1159
Qy 1081 CTGCGGGAGTGTCTCTCAGCTTCAATTTTAACTGTGTCTTGAAATCCAGACATTCCT 1140
Db 1160 CTGCGGGAGTGTCTCTCAGCTTCAATTTTAACTGTGTGTGAAATCCAGACATTCCT 1219
Qy 1141 AAAAAGGCAATTTTGGAGGCGCTGTGAGCATATCCAGTGAAGTGTGAAAAGCGCAGG 1200
Db 1220 AAAAAGGCAATTTTGGAGGCGCTGTGAGCATATCCAGTGAAGTGTGAAAAGCGCAGG 1279
Qy 1201 CTACAGAGCTGTGACAGTAAACAAGGAGCGCATATTATAGCCGCTTTGTACAGAGATGCC 1260
Db 1280 CTACAGAGCTGTGACAGTAAACAAGGAGCGCATATTATAGCCGCTTTGTACAGAGATGCC 1339
Qy 1261 TGTGCTGCTTTGTGATCTCTCTCTGCTTCTCTTCCCTTCCAGCCACACATCAGTCTC 1320
Db 1340 TGTGCTGCTTTGTGATCTCTCTCTGCTTCTCTTCCCTTCCAGCCACACATCAGTCTC 1399
Qy 1321 CTGCTCGAATCTTCTCTTAACTCAACCCAGACATATTCGTGTGCAAGCTCAAGTTTA 1380
Db 1400 CTGCTCGAATCTTCTCTTAACTCAACCCAGACATATTCGTGTGCAAGCTCAAGTTTA 1459
Qy 1381 TTTCACCCAGAAAAGCTCAATTTGTCTTCAACATTTGTGAAATTTCTGTCTACGCCACA 1440
Db 1460 TTTCACCCAGAAAAGCTCAATTTGTCTTCAACATTTGTGAAATTTCTGTCTACGCCACA 1519
Qy 1441 ACAGAGTGTCTGCGGAAAGGAGATATGACAGCTGCTGCTGCTTTGTGTTGCTTCAAGTT 1500
Db 1520 ACAGAGTGTCTGCGGAAAGGAGATATGACAGCTGCTGCTGCTTTGTGTTGCTTCAAGTT 1579
Qy 1501 CTTCAGGCAAAATACATGATCCATGAAAGACAGCGGAAAGCCGTGGCTCCTAAGATA 1560
Db 1580 CTTCAGGCAAAATACATGATCCATGAAAGACAGCGGAAAGCCGTGGCTCCTAAGATA 1639
Qy 1561 TCCATCTCTCTCTGAAACAACAAATCTTTTCCACTTACAGATGACCCCTCAATCCCATC 1620
Db 1640 TCCATCTCTCTCTGAAACAACAAATCTTTTCCACTTACAGATGACCCCTCAATCCCATC 1699
Qy 1621 ATTAATGTTGGTCCAGAGACCGGATATGCCCCGTTTATTTGGGTTCTTACACAT---AG 1676
Db 1700 ATTAATGTTGGTCCAGAGACCGGATATGCCCCGTTTATTTGGGTTCTTACACATAGAGAG 1759
Qy 1677 AAATCTCAAGAAACAACCCAGATGAAATTTTGAACAAATGTGTTTGTGTTGGCTGC 1736
Db 1760 AAATCTCAAGAAACAACCCAGATGAAATTTTGAACAAATGTGTTTGTGTTGGCTGC 1819

Qy 1737 AGGCATMAAGATAGGATTAATCTATTCAAGAAAAGACTCAGACATTTCTTAAAGCATGGG 1796
Db 1820 AGGCATMAAGATAGGATTAATCTATTCAAGAAAAGACTCAGACATTTCTTAAAGCATGGG 1879
Qy 1797 ATCTTAATCTATCTAAAGGTTTCTTCTCTCAAGAGATGCTCTGTGGGAGAGAGAAAGCC 1856
Db 1880 ATCTTAATCTATCTAAAGGTTTCTTCTCTCAAGAGATGCTCTGTGGGAGAGAGAAAGCC 1939
Qy 1857 CCAGCAAGATATGTAACAACAACATCCAGCTTCATGGCCAGAGAGGTGGCAGAAATCTCTC 1916
Db 1940 CCAGCAAGATATGTAACAACAACATCCAGCTTCATGGCCAGAGAGGTGGCAGAAATCTCTC 1999
Qy 1917 CTTCAGAGAAACGGCCATATTTATGTGTGTGAGATGCAAGAAATATGGCCAAAGATGTA 1976
Db 2000 CTTCAGAGAAACGGCCATATTTATGTGTGTGAGATGCAAGAAATATGGCCAAAGATGTA 2059
Qy 1977 CATGATGCCCTTGTGCAATTAATTAACCAAGAGTGTGAGCTGAAATCATAGAGCAATG 2036
Db 2060 CATGATGCCCTTGTGCAATTAATTAACCAAGAGTGTGAGCTGAAATCATAGAGCAATG 2119
Qy 2037 AAAACCTGGCCACTTTAAAGAAAGAAACGCTACCTTCAGAGATATTGTGTCATTA 2093
Db 2120 AAAACCTGGCCACTTTAAAGAAAGAAACGCTACCTTCAGAGATATTGTGTCATTA 2176

RESULT 3
AAC91226
ID AAC91226 standard; DNA; 3259 BP.
XX
AC AAC91226;
XX
DT 20-MAR-2001 (first entry)
XX
DE Human schizophrenia related gene SHQ ID NO: 23.
XX
KW Human; schizophrenia; developmental disorder; spina bifida cystica;
KW Tourette's syndrome; bipolar illness; autism; conduct disorder;
KW attention deficit disorder; obsessive compulsive disorder;
KW chronic multiple tic syndrome; learning disorder; polymorphism; ds.
XX
OS Homo sapiens.
XX
PN MO200071754-A1.
XX
PD 30-NOV-2000.
XX
PF 24-MAY-2000; 2000MC-US014354.
XX
PR 25-MAY-1999; 99US-00318448.
XX
PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX
PI Johnson WG, Stenroos ES;
XX
DR MPI; 2001-025174/03.
XX
PT Diagnosing a developmental disorder, e.g. schizophrenia, by forming
PT datasets (DS) of genetic (e.g. genotypes of folate metabolism alleles)
PT and environmental variables affecting an individual and then comparing
PT these DS with reference DS.
XX
PS Disclosure; Page 142-143; 156pp; English.
XX
CC The present invention provides a novel method of estimating the
CC susceptibility of an individual to a developmental disorder using genetic
CC and environmental variables. The method can be used in the diagnosis,
CC prevention and treatment of disorders such as schizophrenia, spina bifida
CC cystica, Tourette's syndrome, bipolar illness, autism, conduct disorders,
CC attention deficit disorder, obsessive compulsive disorder, chronic
CC multiple tic syndrome and learning disorders such as dyslexia
XX
SQ Sequence 3259 BP; 944 A; 695 C; 674 G; 946 T; 0 U; 0 Other;

Query Match 85.7%; Score 1793; DB 5; Length 3259;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

1 ATGAGAGGTTCTGTACTATATGTCTACACAGCAGGAGCAGGCAAGGCCATTCGAGAA 60
80 ATGAGAGGTTCTGTACTATATGTCTACACAGCAGGAGCAGGCAAGGCCATTCGAGAA 139
61 GAAATGTGTAGACAGCTGTGTACATGTGATTTTCTGCGATCTTCACTGTATTATGTA 120
140 GAAATGTGTAGACAGCTGTGTACATGTGATTTTCTGCGATCTTCACTGTATTATGTA 199
121 TCCGATTAAGTATGACCTTAACAAACCGAAGAGCTCTCTGTGTGTGTGTTCTACAG 180
200 TCCGATTAAGTATGACCTTAACAAACCGAAGAGCTCTCTGTGTGTGTGTTCTACAG 259
181 GGCACCGAGAGCCACCCGACACAGCCCGAAGTTGTTAAGAAATACAGAACCAACA 240
260 GGCACCGAGAGCCACCCGACACAGCCCGAAGTTGTTAAGAAATACAGAACCAACA 319
241 CTGCGGTGATTTCTTGTCTACCTGCGGTATGGGTACTGGGTCTCGGTATTCAGAA 300
320 CTGCGGTGATTTCTTGTCTACCTGCGGTATGGGTACTGGGTCTCGGTATTCAGAA 379
301 TACACCTACTTTTGGCAATGGGGGGAGATTAATTGATTAACGACTTCAAGAGCTTGAG 360
380 TACACCTACTTTTGGCAATGGGGGGAGATTAATTGATTAACGACTTCAAGAGCTTGAG 439
361 CGGCAATTTCTATGACACTGAGACATGACATGATGTGATGATTTAGACTTGTGTGAG 420
440 CGGCAATTTCTATGACACTGAGACATGACATGATGTGATGATTTAGACTTGTGTGAG 499
421 CCGTGATGCTGTGACCTGTGGCCAGCCCTCAGAAAGCATTTTATGTCAGAGAGACA 480
500 CCGTGATGCTGTGACCTGTGGCCAGCCCTCAGAAAGCATTTTATGTCAGAGAGACA 559
481 GAGGAGATTAAGTGGGCGCACTCCCGGTGGATCACTGCAATCTTGGAGACAGACTTGG 540
560 GAGGAGATTAAGTGGGCGCACTCCCGGTGGATCACTGCAATCTTGGAGACAGACTTGG 619
541 AAGTCAGAGCTGTACACATTTGATCTCAAGTCAGACTTCTGAGATTCAGATTCAGAA 600
620 AAGTCAGAGCTGTACACATTTGATCTCAAGTCAGACTTCTGAGATTCAGATTCAGAA 679
601 AAGAAAGATTTCTGAGGTTTGAAGAAATGACGTGAACAGCAACCAATTCATGTTGTA 660
680 AAGAAAGATTTCTGAGGTTTGAAGAAATGACGTGAACAGCAACCAATTCATGTTGTA 739
661 ATTGAAGACTTTGAGTCTCACTTACCCGTGGTACCCCACTCTCAAGAGCTTCTG 720
740 ATTGAAGACTTTGAGTCTCACTTACCCGTGGTACCCCACTCTCAAGAGCTTCTG 799
721 AATATCTGTGTTTACCCCGAGAAATTTTACAGGTACATCTGAGAGATCTTGTGCGCAG 780
800 AATATCTGTGTTTACCCCGAGAAATTTTACAGGTACATCTGAGAGATCTTGTGCGCAG 859
781 GAGGAAAGCCAGATCTGTGACTTCAAGAGATTCAGGTTTTCAGTGCATTTCAAG 840
860 GAGGAAAGCCAGATCTGTGACTTCAAGAGATTCAGGTTTTCAGTGCATTTCAAG 919
841 GCGATTCACCTTACGATGATGATGCAATTAACCACTCTGCTGTGATTTGAGCAAT 900
920 GCGATTCACCTTACGATGATGATGCAATTAACCACTCTGCTGTGATTTGAGCAAT 979
901 TCAATATACAGACTTTTCTATGAGCTGTGAGATGCTTCAAGCTGTATCTGCTTACAG 960
980 TCAATATACAGACTTTTCTATGAGCTGTGAGATGCTTCAAGCTGTATCTGCTTACAG 1039
961 GATTTGAGGTACAAAGCTTACTCAAGACTGACAGCTTGAAGATTAAGAGAGCACTGC 1020
1040 GATTTGAGGTACAAAGCTTACTCAAGACTGACAGCTTGAAGATTAAGAGAGCACTGC 1099

1021 GTCTTTTGAATAAAGCAGACAAAGAAAGAGACTTACCTTACCCAGCATATA 1080
1100 GTCTTTTGAATAAAGCAGACAAAGAAAGAGACTTACCTTACCCAGCATATA 1159
1081 CTTGCGGATGTTCTCTCAGTTCAATTTTACCTGTGTCTTGAATCCGAGCAATTCCT 1140
1160 CTTGCGGATGTTCTCTCAGTTCAATTTTACCTGTGTCTTGAATCCGAGCAATTCCT 1219
1141 AAAAGGCAATTTTGGAGCCCTGTGACATTAACAGTACAGTGTGAAAAGGCGAG 1200
1220 AAAAGGCAATTTTGGAGCCCTGTGACATTAACAGTACAGTGTGAAAAGGCGAG 1279
1201 CTACAGAGCTGTGACATTAACAGAGGCGAGCTTATAGCCGCTTGTATGAGATGCC 1260
1280 CTACAGAGCTGTGACATTAACAGAGGCGAGCTTATAGCCGCTTGTATGAGATGCC 1339
1261 TGTGCTGTGTGTGATCTCTCTCGTTTCCCTTCTTGGCAGCAGCACTCAGTCTC 1320
1340 TGTGCTGTGTGTGATCTCTCTCGTTTCCCTTCTTGGCAGCAGCACTCAGTCTC 1399
1321 CTGCTCGAATCTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 1380
1400 CTGCTCGAATCTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 1459
1381 TTTCAACCCAGAAAGCTCCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 1440
1460 TTTCAACCCAGAAAGCTCCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 1519
1441 ACAAGGTTCTGCGAAGGAGATATGACAGCTGAGCTGAGCTTGTGTGCTTCACTT 1500
1520 ACAAGGTTCTGCGAAGGAGATATGACAGCTGAGCTGAGCTTGTGTGCTTCACTT 1579
1501 CTTGAGCCAAAT 1560
1580 CTTGAGCCAAAT 1639
1561 TCCATCTCTCTCGAACAACAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
1640 TCCATCTCTCTCGAACAACAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1699
1621 ATATATGTTGTTTCAAGAAACCGGCAATAGCCCGTTTATGTTTCTTCAACAT---AG 1676
1700 ATATATGTTGTTTCAAGAAACCGGCAATAGCCCGTTTATGTTTCTTCAACATAGAGAG 1759
1677 AAATCTCAAGAAACAACCCCAATATATATATATATATATATATATATATATATATAT 1736
1760 AAATCTCAAGAAACAACCCCAATATATATATATATATATATATATATATATATATAT 1819
1737 AAGCATTAAGATAGGAT 1796
1820 AAGCATTAAGATAGGAT 1879
1797 ATCTTAATCTTAAGGTTTCTTCTCAAGATGCTCTGTGTGGAGAGAGAGGCC 1856
1880 ATCTTAATCTTAAGGTTTCTTCTCAAGATGCTCTGTGTGGAGAGAGAGGCC 1939
1857 CAGCAAGAT 1916
1940 CAGCAAGAT 1999
1917 CTCCAGAGAGAGGCGCATTTATATATATATATATATATATATATATATATATATATAT 1976
2000 CTCCAGAGAGAGGCGCATTTATATATATATATATATATATATATATATATATATATAT 2059
1977 CATGATGCTCTTGTGCAATTAATAGCAAGAGTTGAGTTGAAAATCTAAGAGCAATG 2036
2060 CATGATGCTCTTGTGCAATTAATAGCAAGAGTTGAGTTGAAAATCTAAGAGCAATG 2119
2037 AAAACCTTGGCCACTTTAAAGAAAGAAAGCTTCAAGATATTTTGTCTATTA 2093
2120 AAAACCTTGGCCACTTTAAAGAAAGAAAGCTTCAAGATATTTTGTCTATTA 2176

RESULT 4
ADM43206
ID ADM43206 standard; cDNA; 3259 BP.
XX
AC ADM43206;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human full length cDNA encoding methionine synthase reductase.
XX
KM Human; ss; gene; Methionine synthase reductase polypeptide; HAMTR; cancer; cardiovascular disease; neural tube defect;
KM hyperhomocysteinemia; chromosome 5p15.2-p15.3; SNP;
KM single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 80..2176
FT /*tag= a
FT /product= "hamTRR"
FT replace(145, A)
FT /*tag= b
FT /standard_name= "Single_nucleotide_polymorphism"
FT replace(189, A)
FT /*tag= c
FT /standard_name= "Single_nucleotide_polymorphism"
XX
PN US2003082676-A1.
XX
PD 01-MAY-2003.
XX
PF 10-AUG-1999; 99US-00371347.
XX
PR 16-JAN-1998; 98US-0071622P.
XX 15-JAN-1999; 99US-00232028.
XX
PA (GRAY/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
XX
PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX
DR WPI, 2003-576610/54.
DR P-PSDB; ADM43207.
XX
PT New substantially pure nucleic acid encoding a mammalian methionine
PT synthase reductase polypeptide, useful for diagnosing, preventing or
PT treating conditions associated with altered methionine synthase activity,
PT e.g. cancer.
XX
PS Example 2; SEQ ID NO 24; 26pp; English.
XX
CC The invention relates to a substantially pure nucleic acid that encodes a
CC mammalian methionine synthase reductase polypeptide, HAMTR, or that
CC hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
CC ADM43209. Also included are a non-human animal where one or both genetic
CC alleles encoding the methionine synthase reductase polypeptide are
CC mutated, an antibody that specifically binds the above methionine
CC synthase reductase polypeptide, a method of detecting the presence of the
CC above polypeptide, a method for detecting sequence variants for
CC methionine synthase reductase in a mammal, methods of treating or
CC preventing cancer (or cardiovascular disease or neural tube defects) in a
CC subject, methods of screening for a compound that modulates methionine
CC synthase reductase biological activity and a method for detecting an
CC increased risk of developing a neural tube defect in a mammalian embryo
CC or foetus. The nucleic acid is useful in diagnosing, preventing or
CC treating conditions associated with altered methionine synthase activity,
CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are

CC also associated with hyperhomocysteinemia. The gene for HAMTR is
CC located on chromosome 5p15.2-p15.3. The present sequence is full length
CC sequence of the wild-type human hamTRR cDNA.
XX
SQ Sequence 3259 BP; 944 A; 695 C; 674 G; 946 T; 0 U; 0 Other;
Query Match 85.7%; Score 1793; DB 11; Length 3259;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 ATGAGAGGTTTCTGTACTATATGTCTACACAGCAGGACAGGCAAGCCATCGAGAA 60
DB 80 ATGAGAGGTTTCTGTACTATATGTCTACACAGCAGGACAGGCAAGCCATCGAGAA 139
QY 61 GAAATGTGTAGCAGACTGTGTACATGATTTTCTGCAGATCTTCACTGATTAAGTAA 120
DB 140 GAAATGTGTAGCAGACTGTGTACATGATTTTCTGCAGATCTTCACTGATTAAGTAA 199
QY 121 TCCGATTAAGTAACTTAAATACCGAAACAGCTCCCTTGTGTGTGTTTCTACACG 180
DB 200 TCCGATTAAGTAACTTAAATACCGAAACAGCTCCCTTGTGTGTGTTTCTACACG 259
QY 181 GGCACCGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGGAATACAGAACCAACA 240
DB 260 GGCACCGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGGAATACAGAACCAACA 319
QY 241 CTGCCGGTGAATTTCTTGTCTACCTTGGGATGAGTTTCTGGGTTCTCGGATTCAGAA 300
DB 320 CTGCCGGTGAATTTCTTGTCTACCTTGGGATGAGTTTCTGGGTTCTCGGATTCAGAA 379
QY 301 TACACCTACTTTTGAATGGGGGAGATTAATGATTAACGACTTCAAGCGTTGAGCC 360
DB 380 TACACCTACTTTTGAATGGGGGAGATTAATGATTAACGACTTCAAGCGTTGAGCC 439
QY 361 CGGCATTTCTATGACACTGACATGACATGACTGTGTAGAGTTTGAACCTTGTGTGAG 420
DB 440 CGGCATTTCTATGACACTGACATGACATGACTGTGTAGAGTTTGAACCTTGTGTGAG 499
QY 421 CCGTGATTTCTGACACTTGGCCAGCTTCAGAAAGCATTTTATGTCAGAGAGACAA 480
DB 500 CCGTGATTTCTGACACTTGGCCAGCTTCAGAAAGCATTTTATGTCAGAGAGACAA 559
QY 481 GAGGATATAGGGGCGCACTCCCGTGGCATCCGATCCCTTGGAGACAGACTTGTG 540
DB 560 GAGGATATAGGGGCGCACTCCCGTGGCATCCGATCCCTTGGAGAGAGACTTGTG 619
QY 541 AAGTCAGAGCTGTACACATTTGATCTCAAGTCGACCTTCTGAGATTCGATTCAGGA 600
DB 620 AAGTCAGAGCTGTACACATTTGATCTCAAGTCGACCTTCTGAGATTCGATTCAGGA 679
QY 601 AGAAGGATTTCTGAGTTTGAAGCAAAATGCAGTAAACAGCAACCAATCCAAATGTTGA 660
DB 680 AGAAGGATTTCTGAGTTTGAAGCAAAATGCAGTAAACAGCAACCAATCCAAATGTTGA 739
QY 661 ATTGAAGCTTTGAGTCCTCACTTACCCGTTGGTATCCCACTTCACAAGCTCTCG 720
DB 740 ATTGAAGCTTTGAGTCCTCACTTACCCGTTGGTATCCCACTTCACAAGCTCTCG 799
QY 721 AATATTCCTGTGTTTACCCCAAGATATTTTACAGAGTCACTGAGAGAGTCTTGGCCAG 780
DB 800 AATATTCCTGTGTTTACCCCAAGATATTTTACAGAGTCACTGAGAGAGTCTTGGCCAG 859
QY 781 GAGGAAAGCAAGATATCTGTGACTTCAGAGATCCAGTTTTCAGTGCCAATTTCAAG 840
DB 860 GAGGAAAGCAAGATATCTGTGACTTCAGAGATCCAGTTTTCAGTGCCAATTTCAAG 919
QY 841 GCAGTCACTTACTATGCAATGATGCAATTAACCAAGCTGTGTAGATTTGACATTT 900
DB 920 GCAGTCACTTACTATGCAATGATGCAATTAACCAAGCTGTGTAGATTTGACATTT 979
QY 901 TCAATATCAGACTTTTCTATCAGCTTGAAGATGCTTGAAGCTTGAAGCTTGAAGCTT 960
DB 980 TCAATATCAGACTTTTCTATCAGCTTGAAGATGCTTGAAGCTTGAAGCTTGAAGCTT 1039

QY 961 GATCTGAGGTACAAAGCTACTCCAAAGACTGACCTTGAAGATTAAGAGAGCACTGC 1020
 DB 1040 GATTCGAGGTACAAAGCTACTCCAAAGACTGACCTTGAAGATTAAGAGAGCACTGC 1099
 QY 1021 GTCTTTGAAAAATTAAGGACGACAAAGAAAGAAAGAGCTACTTACCCTCCAGCATATA 1080
 DB 1100 GTCTTTGAAAAATTAAGGACGACAAAGAAAGAAAGAGCTACTTACCCTCCAGCATATA 1159
 QY 1081 CCGCGGGGATGTTCTCTCCAGTTCATTTTACCTGGTGTCTGAATCCGAGCAATTCCT 1140
 DB 1160 CCGCGGGGATGTTCTCTCCAGTTCATTTTACCTGGTGTCTGAATCCGAGCAATTCCT 1219
 QY 1141 AAAAAGGCAATTTTGGAGCCCTTGTGAGCTATACAGTGAAGCTGTGAAAAGGACAGG 1200
 DB 1220 AAAAAGGCAATTTTGGAGCCCTTGTGAGCTATACAGTGAAGCTGTGAAAAGGACAGG 1279
 QY 1201 CTACAGAGCTGTGAGTAACAAAGGGGACCGGATTAAGCCGCTTTGTACGAGATGCC 1260
 DB 1280 CTACAGAGCTGTGAGTAACAAAGGGGACCGGATTAAGCCGCTTTGTACGAGATGCC 1339
 QY 1261 TGTGCTGCTGTGTGGATCTCTCTGCTTTCCTTTCGAGCCACACTCACTCTC 1320
 DB 1340 TGTGCTGCTGTGTGGATCTCTCTGCTTTCCTTTCGAGCCACACTCACTCTC 1399
 QY 1321 CTGCTGGAACATCTTCTAACTTCAACCCAGACATATTGCTGACAGCTCAAGTTTA 1380
 DB 1400 CTGCTGGAACATCTTCTAACTTCAACCCAGACATATTGCTGACAGCTCAAGTTTA 1459
 QY 1381 TTTCAACCAAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTCTGTCTACCTGCACA 1440
 DB 1460 TTTCAACCAAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTCTGTCTACCTGCACA 1519
 QY 1441 ACAAGGTTCTGGGAGGAGATGTACAGCTGGCTGGCTTGTGTGTTCTTCACTT 1500
 DB 1520 ACAAGGTTCTGGGAGGAGATGTACAGCTGGCTGGCTTGTGTGTTCTTCACTT 1579
 QY 1501 CTTACGCAAAACATATGATGATCCCATGAGACAGGGGAAAGCCCTGGCTCTTAAGATA 1560
 DB 1580 CTTACGCAAAACATATGATGATCCCATGAGACAGGGGAAAGCCCTGGCTCTTAAGATA 1639
 QY 1561 TCCATCTCTCTCGAACCAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
 DB 1640 TCCATCTCTCTCGAACCAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1699
 QY 1621 ATATGTTGGGTCACAGAACCGGCATAGCCCGTTATTGGGTTCTTACAACT---AG 1676
 DB 1700 ATATGTTGGGTCACAGAACCGGCATAGCCCGTTATTGGGTTCTTACAACTAGAGAG 1759
 QY 1677 AAATCTCAAGAAACAACACCCAGATGGAATTTTGGAGCAATGTGTGTTTTTGGCTGC 1736
 DB 1760 AAATCTCAAGAAACAACACCCAGATGGAATTTTGGAGCAATGTGTGTTTTTGGCTGC 1819
 QY 1737 AGGCAATAGGATAGGATTAATCTAATCAGAAAAGACTCAGACATTTCTTAAGCATGGG 1796
 DB 1820 AGGCAATAGGATAGGATTAATCTAATCAGAAAAGACTCAGACATTTCTTAAGCATGGG 1879
 QY 1797 ATCTTAATCTAATAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGAGAGAGAGCC 1856
 DB 1880 ATCTTAATCTAATAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGAGAGAGAGCC 1939
 QY 1857 CCAAGCAAGATATTAAGACAAATCCAGCTTCAATGAGGAGAGAGAGAGAGAGAGAGAG 1916
 DB 1940 CCAAGCAAGATATTAAGACAAATCCAGCTTCAATGAGGAGAGAGAGAGAGAGAGAGAG 1999
 QY 1917 CTCACAGAGAACGGCCATATTTATGTGTGTGAGATGCAAGAAATATGCGCAAGATGTA 1976
 DB 2000 CTCACAGAGAACGGCCATATTTATGTGTGTGAGATGCAAGAAATATGCGCAAGATGTA 2059
 QY 1977 CATGATGCTTGTGTGCAATATTAAGCAAGAGGTTGAGTTGAAAACTAGAGCAATG 2036
 DB 2060 CATGATGCTTGTGTGCAATATTAAGCAAGAGGTTGAGTTGAAAACTAGAGCAATG 2119

QY 2037 AAAACCTGGCCACTTTAAAGAGAAAAAGCCTTACTTACAGATATTTGTCTATTA 2093
 DB 2120 AAAACCTGGCCACTTTAAAGAGAAAAAGCCTTACTTACAGATATTTGTCTATTA 2176
 RESULT 5
 ID ADM43208
 ID ADM43208 standard; cDNA; 2094 BP.
 XX
 AC ADM43208;
 XX
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Human wild-type methionine synthase reductase CDS.
 XX
 KW Human; ss; Methionine synthase reductase polypeptide; hsmTRR; cancer;
 KW cardiovascular disease; neural tube defect; hyperhomocysteinemia;
 KW chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.
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 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2094
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 FT /partial
 FT /note= "No stop codon shown"
 FT replace(66,A)
 FT /*tag= b
 FT /standard_name= "single_nucleotide_polymorphism"
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 EN US2003082676-A1.
 XX
 PD 01-MAY-2003.
 XX
 XX 10-AUG-1999; 99US-00371347.
 XX
 XX 16-JAN-1998; 98US-0071622P.
 PR 15-JAN-1999; 99US-00232028.
 XX
 XX (GRAY/) GRAVEL R. A.
 PA (ROZE/) ROZEN R. A.
 PA (DECL/) LECLEERC D.
 PA (WILS/) WILSON A.
 PA (ROSE/) ROSENBLATT D.
 XX
 PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
 XX
 XX WPI; 2003-576610/54.
 DR P-PSDB; ADM43207.
 XX
 XX
 PT New substantially pure nucleic acid encoding a mammalian methionine
 PT synthase reductase polypeptide, useful for diagnosis, preventing or
 PT treating conditions associated with altered methionine synthase activity,
 PT e.g. cancer.
 XX
 PS Claim 3; SEQ ID NO 1; 26pp; English.
 XX
 CC The invention relates to a substantially pure nucleic acid that encodes a
 CC mammalian methionine synthase reductase polypeptide, hsmTRR, or that
 CC hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
 CC ADM43209. Also included are a non-human animal where one or both genetic
 CC alleles encoding the methionine synthase reductase polypeptide are
 CC mutated, an antibody that specifically binds the above methionine
 CC synthase reductase polypeptide, a method of detecting the presence of the
 CC above polypeptide, a method for detecting sequence variants for
 CC methionine synthase reductase in a mammal, methods of treating or
 CC preventing cancer (or cardiovascular disease or neural tube defects) in a
 CC subject, methods of screening for a compound that modulates methionine
 CC synthase reductase biological activity and a method for detecting an

CC increased risk of developing a neural tube defect in a mammalian embryo
CC or foetus. The nucleic acid is useful in diagnosing, preventing or
CC treating conditions associated with altered methionine synthase activity,
CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are
CC also associated with hyperhomocysteinaemia. The gene for HmTR is
CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
CC sequence of the wild-type human hsmTRR cDNA.

XX Sequence 2094 BP; 591 A; 489 C; 481 G; 533 T; 0 U; 0 Other;

Query Match 85.54; Score 1790; DB 11; Length 2094;

Best Local Similarity 99.84; Pred. No. 0; Mismatches 0; Indels 4; Gaps 1;

Matches 2090; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 ATGAGAGGTTTCTGTACTATATGCTACACAGAGGACAGGCAAGCCATCGAGAA 60
DB 1 ATGAGAGGTTTCTGTACTATATGCTACACAGAGGACAGGCAAGCCATCGAGAA 60
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DB 61 GAAATGTGAGCAAGCTGTGTACATGATTTTCTGAGATCTTCACTGTATTAGTAA 120
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DB 121 TCCGATPAGATGACCTTAAACCGAAACAGCTCCCTTGTGTGTGTTTCTACACG 180
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DB 181 GGCAACCGAAGCCACCGACACAGCCCGAGATTGTTAAGAAATACAGAACCAACA 240
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DB 241 CTGCGGTTGATTTCTTGTCTCACCTGCGGTATGGTTTACGGGTCTCGGTGATTGAA 300
QY 301 TACACCTACTTTTGGCAATGGGGGGAATTAATTGATTAACACTTCAAGAGCTTGAAGC 360
DB 301 TACACCTACTTTTGGCAATGGGGGGAATTAATTGATTAACACTTCAAGAGCTTGAAGC 360
QY 361 CGGCAATTTCTATGACACTGACATGACATGATGATGATGATGATGATGATGATGAT 420
DB 361 CGGCAATTTCTATGACACTGACATGACATGATGATGATGATGATGATGATGATGAT 420
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DB 421 CCGTGATTTGCTGAGCTCTGCGCAGCCCTCAAGAAAGATTTAGTCAACAGAGGCAA 480
QY 481 GAGGAGTAAGTGGCGACTCCGGGTGGCATCACTGCACTCTTGAAGGACAGACCTTGG 540
DB 481 GAGGAGTAAGTGGCGACTCCGGGTGGCATCACTGCACTCTTGAAGGACAGACCTTGG 540
QY 541 AAGTCAGAGCTGTACACATTTGAATCTCAAGTGTGATGATGATGATGATGATGATGAT 600
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DB 601 AGAAAGATTTCTGAGTTTGAAGCAAAATGACAGTGAACAGCAACCAATCAATGTTGTA 660
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DB 1141 AAAAAGGCAATTTTGTGAGACCTTGTGACTATACAGTGAACAGTCTGAAAAAGGCAAG 1200
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QY 1261 TGTGCTGTGTGTGATCT 1320
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DB 1321 CTGCTGGAACATCTTCTTAACTTGAACCCACATATTCGTTGACAGTCAAGTTTA 1380
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QY 1857 CCAGCAAAGTATGTAACAACAACATCTGAGCTTCAATGCGCAAGAGTGGCGAATCTTC 1916
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QY 1861 CCAGCAAAGTATGTAACAACAACATCTGAGCTTCAATGCGCAAGAGTGGCGAATCTTC 1920
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QY 1917 CTCAGAGAGAGGCGCATTTTATGTGTGAGATGCAAGAAATAGGCAAGATGTA 1976

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Db	1981	CATGATGCCCTTGTGCAGAAATATATAGCAGAGGTTGGAGTTGAAAACTAGAAAGCAATG	2040
Qy	2037	AAACCCCTGGCATTATTAAGAGAAAAAGCGTACCTTCAGGATATTTGGTCA	2090
Db	2041	AAACCCCTGGCATTATTAAGAGAAAAAGCGTACCTTCAGGATATTTGGTCA	2094
RESULT 6			
ADM43212	ID	ADM43212 standard; cDNA; 2094 BP.	
XX	AC	ADM43212;	
XX	DT	03-JUN-2004 (first entry)	
DE	DE	Human methionine synthase reductase CDS G110A variant.	
XX	XX	Human; ss; Methionine synthase reductase polypeptide; HsMTRR; cancer;	
KW	KW	cardiovascular disease; neural tube defect; hyperhomocysteinemia;	
KM	KM	chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.	
XX	OS	Homo sapiens.	
XX	FT	Key	location/Qualifiers
FT	FT	CDS	1..2094
FT	FT		/*tag= a
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FT	FT		/partial
FT	FT		/note= "No stop codon shown"
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FT	FT	variation	/standard_name= "Single_nucleotide_polymorphism"
FT	FT		replace(110,G)
FT	FT		/*tag= c
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XX	PD	01-MAY-2003.	
XX	PF	10-AUG-1999;	99US-00371347.
XX	PR	16-JAN-1998;	98US-0071622P.
XX	PR	15-JAN-1999;	99US-00232028.
XX	PA	(GRAV// GRAVEL R A.	
PA	PA	(ROZE// ROZEN R.	
PA	PA	(LECL// LECLERC D.	
PA	PA	(WILS// WILSON A.	
PA	PA	(ROSE// ROSENBLATT D.	
PI	PI	Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;	
XX	XX	MP1, 2003-576610/54.	
DR	DR	P-P8DB; ADM43213.	
XX	XX		
PT	PT	New substantially pure nucleic acid encoding a mammalian methionine	
PT	PT	synthase reductase polypeptide, useful for diagnosing, preventing or	
PT	PT	treating conditions associated with altered methionine synthase activity,	
PT	PT	e.g. cancer.	
PS	PS	Disclosure; SEQ ID NO 43; 26pp; English.	
CC	CC	The invention relates to a substantially pure nucleic acid that encodes a	
CC	CC	mammalian methionine synthase reductase polypeptide, HsMTRR, or that	
CC	CC	hybridises at high stringency to a nucleic acid appearing as ADM43208 or	
CC	CC	ADM43209. Also included are a non-human animal where one or both genetic	
CC	CC	alleles encoding the methionine synthase reductase polypeptide are	
CC	CC	mutated, an antibody that specifically binds the above methionine	

CC	synthase reductase polypeptide, a method of detecting the presence of the
CC	above polypeptide, a method for detecting sequence variants for
CC	methionine synthase reductase in a mammal, methods of treating or
CC	preventing cancer (or cardiovascular disease or neural tube defects) in a
CC	subject, methods of screening for a compound that modulates methionine
CC	synthase reductase biological activity and a method for detecting an
CC	increased risk of developing a neural tube defect in a mammalian embryo
CC	or foetus. The nucleic acid is useful in diagnosing, preventing or
CC	treating conditions associated with altered methionine synthase activity,
CC	such as cancer, cardiovascular disease or neural tube defects, or in
CC	screening for a compound that modulates methionine synthase reductase
CC	biological activity. Naturally occurring variants of the polypeptide are
CC	also associated with hyperhomocysteinaemia. The gene for hMTRR is
CC	located on chromosome 5p15.2-p15.3. The present sequence is the coding
CC	sequence of a variant human hMTRR cDNA.
XX	
SQ	Sequence 2094 BP; 592 A; 489 C; 480 G; 533 T; 0 U; 0 Other;
Query Match	83.1%; Score 1739; DB 11; Length 2094;
Best Local Similarity	99.8%; Pred. No. 0;
Matches 2089; Conservative	0; Mismatches 1; Indels 4; Gaps 1;
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DG	181 GGACACCGGAGACCCACCGCACAGCCCGAAGTTGTTAAGAAATACAGAACCAACA 240
OY	241 CTGCCGGTGAATTTCTTGTGCTCACCCTGGCATGTGGTACTGGGTCTCGGTGATTCAGA 300
DG	241 CTGCCGGTGAATTTCTTGTGCTCACCCTGGCATGTGGTACTGGGTCTCGGTGATTCAGA 300
OY	301 TACACCTTACTTTTGCAATGGGGGAGATAATTGATTAACGACTTCAAGAGCTTGGAGCC 360
DG	301 TACACCTTACTTTTGCAATGGGGGAGATAATTGATTAACGACTTCAAGAGCTTGGAGCC 360
OY	361 CGGCAATTTCTATGACATGAGCATGCAATGACATGATGAGTTTAGAATTGTGGTTAG 420
DG	361 CGGCAATTTCTATGACATGAGCATGCAATGACATGATGAGTTTAGAATTGTGGTTAG 420
OY	421 CGGTGATTTGCTGACCTCTGGCAGGCCCTCAGAAAGCAATTTTAGTCAAGCAGAGACA 480
DG	421 CGGTGATTTGCTGACCTCTGGCAGGCCCTCAGAAAGCAATTTTAGTCAAGCAGAGACA 480
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OY	541 AAGTGAAGCTGCTACATATTGAATCTCAAGTCGAGTTCTGAGATTGAGATTCACAGA 600
DG	541 AAGTGAAGCTGCTACATATTGAATCTCAAGTCGAGTTCTGAGATTGAGATTCACAGA 600
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DG	601 AGAAAGATTTGAGGTTTGAAGCAAAATGACATGAGAACCAATCCAATGTTGTA 660
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DG	661 ATTGAAGACTTGAAGTCTCACTTACCCGTTCCGTAACCCCACTCTCAAGACCTCTCTG 720
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DG	721 AATATATCTCGGTTTACCCCCAGAAATTTTACAGATACATTCGACAGAGATCTTGGCCAG 780

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Db 781 GAGAAAGCCAAAGATCTGTGACTTCAGCAGATCCAGTTTTCAGAGTCCAAATTTCCAAAG 840
QY 841 GCAGTTCACTTACTAGCAATGATGCAATTAACCACTCTGCTGGTGAATTTGACATTT 900
Db 841 GCAGTTCACTTACTAGCAATGATGCAATTAACCACTCTGCTGGTGAATTTGACATTT 900
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Db 1021 GTCCCTTTTGAATTAAGGAGACACAAAGAAAGAAAGACTCTCCCTTACCCAGCATATA 1080
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Db 1081 CCTGCGGAGATGTTCTCTCAGATTCATTTTACCTGCTGTGAAATCCGAGCAATTCCT 1140
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Db 1321 CTGCTGGAACATCTTCTTAACTTCAACCCAGACCATATTTGTGTGCAAGCTCAAGTTTA 1380
QY 1381 TTTTCAACCCAGAAAGCCCAATTTTGTCTGATCAATTTGTGAAATTTGTCTTACTGCGACA 1440
Db 1381 TTTTCAACCCAGAAAGCCCAATTTTGTCTGATCAATTTGTGAAATTTGTCTTACTGCGACA 1440
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Db 1441 ACAGAGGTTCTGCGGAGAGGAGATATGACAGCTGCTGCTGTGTGTGCTTCACTT 1500
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QY 1677 AAACTCCAAAGAACACCCAGATGAAATTTTGGAGCAATGTGTGTTTGTGCTGC 1736
Db 1677 AAACTCCAAAGAACACCCAGATGAAATTTTGGAGCAATGTGTGTTTGTGCTGC 1736
QY 1737 AGGATTAAGATGAGGATTAATCTATTCAGAAAGAGTCAACATTTCTTAAAGCATGG 1796
Db 1737 AGGATTAAGATGAGGATTAATCTATTCAGAAAGAGTCAACATTTCTTAAAGCATGG 1796
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Db 1741 AGGATTAAGATGAGGATTAATCTATTCAGAAAGAGTCAACATTTCTTAAAGCATGG 1800
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QY 1801 ATCTTAATCATCTTAAAGGTTTCTTCTCAAGAGATCTCTGTGTGGGAGAGAAAGCC 1860
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QY 1857 CCAGCAAGTATGATACAGAACATCCAGCTTCATGCCCCAGGAGGTGGCAGAAATCTTC 1916
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QY 2041 AAAACCTGGCCACTTTTAAAGAAAGAAACGCTTACCTTCAGATATTTTGCTCA 2094
Db 2041 AAAACCTGGCCACTTTTAAAGAAAGAAACGCTTACCTTCAGATATTTTGCTCA 2094
RESULT 7
ADM43209
ID ADM43209 standard; cDNA; 2094 BP.
XX
AC ADM43209;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human methionine synthase reductase CDS G66A variant.
XX
KW Human; ss; Methionine synthase reductase polypeptide; HsMTTR; cancer;
KW cardiovascular disease; neural tube defect; hypochromic/spherocytosis;
KW chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2094
FT /tag= a
FT /product= "HsMTTR"
FT /partial
FT /note= "No stop codon shown"
FT variation
FT /tag= b
FT /tag= d
FT /standard name= "single_nucleotide polymorphism"
FT /replace (110,A)
FT /tag= c
FT /standard_name= "single_nucleotide polymorphism"
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XX
PD 01-MAY-2003.
XX
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PR 16-JAN-1998; 98US-0071622P.
PR 15-JAN-1999; 99US-00232026.
XX
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
XX
PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX
DR WPI; 2003-576610/54.
XX
DR P-PDB; ADM43211.
XX
PT New substantially pure nucleic acid encoding a mammalian methionine
PT synthase reductase polypeptide, useful for diagnosing, preventing or
PT treating conditions associated with altered methionine synthase activity,
PT e.g. cancer.
XX
PS Claim 3; SEQ ID NO 41; 26bp; English.
XX

The invention relates to a substantially pure nucleic acid that encodes a mammalian methionine synthase reductase polypeptide, hSMTR, or that hybridizes at high stringency to a nucleic acid appearing as AD43208 or AD43209. Also included are a non-human animal where one or both genetic alleles encoding the methionine synthase reductase polypeptide are mutated, an antibody that specifically binds the above methionine synthase reductase polypeptide, a method of detecting the presence of the above polypeptide, a method for detecting sequence variants for methionine synthase reductase in a mammal, methods of treating or preventing cancer (or cardiovascular disease or neural tube defects) in a subject, methods of screening for a compound that modulates methionine synthase reductase biological activity and a method for detecting an increased risk of developing a neural tube defect in a mammalian embryo or foetus. The nucleic acid is useful in diagnosing, preventing or treating conditions associated with altered methionine synthase activity, such as cancer, cardiovascular disease or neural tube defects, or in screening for a compound that modulates methionine synthase reductase biological activity. Naturally occurring variants of the polypeptide are also associated with hyperhomocysteinaemia. The gene for hSMTR is located on chromosome 5p15.2-p15.3. The present sequence is the coding sequence of a variant human hSMTR cDNA.

Sequence 2094 BP; 592 A; 489 C; 480 G; 533 T; 0 U; 0 Other;

Query Match 83.1%; Score 1739; DB 11; Length 2094;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2089; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

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DB 1 ATGAGAGAGTTCTGTATCTATATGCTACAGACAGGAGCAGGCAAAAGCCATTCGAGAA 60
QY 61 GAAATGTGTGAGCAAGCTGTGTACATGATTTTCTGCGATCTTCACTGTATTAGTAA 120
DB 61 GAAATGTGTGAGCAAGCTGTGTACATGATTTTCTGCGATCTTCACTGTATTAGTAA 120
QY 121 TCCGATTAAGTATGACCTTAAACCCGAAACAGCTCTCTGTGTGTGTGTTCTACACAG 180
DB 121 TCCGATTAAGTATGACCTTAAACCCGAAACAGCTCTCTGTGTGTGTGTTCTACACAG 180
QY 181 GGCACCGGAGACCCAGCCGACAGAGCCGCAAGTTGTTAGAAATACAGAACCAACA 240
DB 181 GGCACCGGAGACCCAGCCGACAGAGCCGCAAGTTGTTAGAAATACAGAACCAACA 240
QY 241 CTGCGCGTGTATTTCTTTGCTCACTGCGGTATGCGTTACTGGTCTCGGTATTCAGAA 300
DB 241 CTGCGCGTGTATTTCTTTGCTCACTGCGGTATGCGTTACTGGTCTCGGTATTCAGAA 300
QY 301 TACACCTACTTTTGCAATGGGGGGAAGATTAATTGAATTAACGACTTCAGAGCTGGAGCC 360
DB 301 TACACCTACTTTTGCAATGGGGGGAAGATTAATTGAATTAACGACTTCAGAGCTGGAGCC 360
QY 361 CGGCAATTTCTATGACATGAGCATGAGTGACTGTAGTTTGAAGCTTGTGTTGAG 420
DB 361 CGGCAATTTCTATGACATGAGCATGAGTGACTGTAGTTTGAAGCTTGTGTTGAG 420
QY 421 CCGTGTATGCTGACCTGCGCCAGCCCTCAGAAAGCATTTTAAAGTCAAGAGAGCAA 480
DB 421 CCGTGTATGCTGACCTGCGCCAGCCCTCAGAAAGCATTTTAAAGTCAAGAGAGCAA 480
QY 481 GAGGAGATTAAGTGGGCACTCCGGTGGATCACTGCACTCTTGAGGACAGACTTGTG 540
DB 481 GAGGAGATTAAGTGGGCACTCCGGTGGATCACTGCACTCTTGAGGACAGACTTGTG 540
QY 541 AAGTCAGAGCTCTACATGATTAATCTCAAGTCAAGCTTCTGAGATTCGATATTCAGGA 600
DB 541 AAGTCAGAGCTCTACATGATTAATCTCAAGTCAAGCTTCTGAGATTCGATATTCAGGA 600
QY 601 AAGAAAGATTCGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATTCGATTTGTA 660
DB 601 AAGAAAGATTCGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATTCGATTTGTA 660
QY 661 ATTGAAGACTTGAAGTCTCACTTACCGTTCGTTACCCCACTTCACAGAGCTTCTG 720
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DB 661 ATTGAAGACTTGAAGTCTCACTTACCGTTCGTTACCCCACTTCACAGAGCTTCTG 720
QY 721 AATATTCCTGCTTTACCCCAAGAAATATTACAGATCAATTCGAGAGCTTCTGCGCAG 780
DB 721 AATATTCCTGCTTTACCCCAAGAAATATTACAGATCAATTCGAGAGCTTCTGCGCAG 780
QY 781 GAGAAAGCAAGTATCTGTGACTTCAGAGATTCAGATTTTCAAGTGCATTTCAAG 840
DB 781 GAGAAAGCAAGTATCTGTGACTTCAGAGATTCAGATTTTCAAGTGCATTTCAAG 840
QY 841 GCAAGTTCAACTTACTAGATGATGATCCATTAACCACTCTGCTGTAGATTTGACATT 900
DB 841 GCAAGTTCAACTTACTAGATGATGATCCATTAACCACTCTGCTGTAGATTTGACATT 900
QY 901 TCAATATCAGACTTTTCTATGAGCTGAGATGCTTCAAGGTATCTGCTTAACT 960
DB 901 TCAATATCAGACTTTTCTATGAGCTGAGATGCTTCAAGGTATCTGCTTAACT 960
QY 961 GATTCTGAGTACAAAGCTTACTCCAAAGACTGACAGCTTGAAGATTAAGAGACATG 1020
DB 961 GATTCTGAGTACAAAGCTTACTCCAAAGACTGACAGCTTGAAGATTAAGAGACATG 1020
QY 1021 GTCTTTTGAATAAAGGACAGACAAAGAAAGAGACTTACCTTACCCGACATATA 1080
DB 1021 GTCTTTTGAATAAAGGACAGACAAAGAAAGAGACTTACCTTACCCGACATATA 1080
QY 1081 CCGCGGAGATGTTCTCTCAAGTTCAATTTTACCTGTGTCTTGAATCCGACATTTCT 1140
DB 1081 CCGCGGAGATGTTCTCTCAAGTTCAATTTTACCTGTGTCTTGAATCCGACATTTCT 1140
QY 1141 AAAAAGGATTTTGGAGCCCTGTGAGCTATACAGTACAGTGTGTAAGAAAGGCGAG 1200
DB 1141 AAAAAGGATTTTGGAGCCCTGTGAGCTATACAGTACAGTGTGTAAGAAAGGCGAG 1200
QY 1201 CTACAGAGCTGTGAGTAAACAGAGGCGACGCGATTAAGCCGCTTGTACAGATGCG 1260
DB 1201 CTACAGAGCTGTGAGTAAACAGAGGCGACGCGATTAAGCCGCTTGTACAGATGCG 1260
QY 1261 TGTGCTGCTGTGTGATGATCTCTCTCGTTCCCTTCTGCGACGACACTCGATCTC 1320
DB 1261 TGTGCTGCTGTGTGATGATCTCTCTCGTTCCCTTCTGCGACGACACTCGATCTC 1320
QY 1321 CTGCTCGAATCTTCTCTTAAATTTCAACCCAGACATTAAGTGTGCAAGCTCAAGTTA 1380
DB 1321 CTGCTCGAATCTTCTCTTAAATTTCAACCCAGACATTAAGTGTGCAAGCTCAAGTTA 1380
QY 1381 TTTCAACCGAGAAAGCTCAATTTGTCTTCAACATTTGTGGAATTTCTGTCTACGACA 1440
DB 1381 TTTCAACCGAGAAAGCTCAATTTGTCTTCAACATTTGTGGAATTTCTGTCTACGACA 1440
QY 1441 ACAAGAGTTCTGCGAAGGAGATATGACAGCTGAGCTGAGCTTGTGAGTCTTCACTG 1500
DB 1441 ACAAGAGTTCTGCGAAGGAGATATGATGACAGCTGAGCTGAGCTTGTGAGTCTTCACTG 1500
QY 1501 CTTGAGCCAAATATCATGATCCCATGAAAGCAACCGGAAAGCCCTGAGCTCTTAAGATA 1560
DB 1501 CTTGAGCCAAATATCATGATCCCATGAAAGCAACCGGAAAGCCCTGAGCTCTTAAGATA 1560
QY 1561 TCCATCTCTCTCGAACAACAATTTCTTCACTTACAGATGAGCCCTCAATCCCATC 1620
DB 1561 TCCATCTCTCTCGAACAACAATTTCTTCACTTACAGATGAGCCCTCAATCCCATC 1620
QY 1621 ATTAATGTGGGTCAAGAAACCGGATAGCCCGTTTATTTGGTCTTCAACAT---AG 1676
DB 1621 ATTAATGTGGGTCAAGAAACCGGATAGCCCGTTTATTTGGTCTTCAACAT---AG 1676
QY 1677 AAATCGAAGAAACAACCGAGATGGAATTTTGAAGCAATGTGATTTTGGCTGC 1736
DB 1677 AAATCGAAGAAACAACCGAGATGGAATTTTGAAGCAATGTGATTTTGGCTGC 1736
QY 1681 AAATCGAAGAAACAACCGAGATGGAATTTTGAAGCAATGTGATTTTGGCTGC 1740
DB 1681 AAATCGAAGAAACAACCGAGATGGAATTTTGAAGCAATGTGATTTTGGCTGC 1740
QY 1737 AGGCATTAAGATGAGATTAATCTATTCAGAAAGAGCTCAGACATTTCTTAAAGATGAG 1796
```

Db 1741 AGGCATAGAGATGGGATTTATCTTATTCAGAAAAAGCTCAGACATTTCTTAAAGCATGGG 1800
Qy 1797 ATCTTAATCATCTAAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1856
Cc 1801 ATCTTAATCATCTAAAGGTTTCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1860
Qy 1857 CCAGCAAGATATATACAGCAACATTCAGCTTCATGCGCCAGAGAGGTGGGAGATCTTC 1916
Db 1861 CCAGCAAGATATATACAGCAACATTCAGCTTCATGCGCCAGAGAGGTGGGAGATCTTC 1920
Qy 1917 CTCGAGAGAGAGCCATATTTATGTGTGTGAGATGCAAGAAATATGCGCAAGATGTA 1976
Db 1921 CTCGAGAGAGAGCCATATTTATGTGTGTGAGATGCAAGAAATATGCGCAAGATGTA 1980
Qy 1977 CATGATGCTCTTGTGCAATATATAGCAAGAGTTGAGTTGAAAACTAGAGCAATG 2036
Db 1981 CAGATGCTCTTGTGCAATATATAGCAAGAGTTGAGTTGAAAACTAGAGCAATG 2040
Qy 2037 AAAACCTGGCCCTTTTAAAGAAAGAAACGCTACCTTCAAGATATTGTGTCA 2090
Db 2041 AAAACCTGGCCCTTTTAAAGAAAGAAACGCTACCTTCAAGATATTGTGTCA 2094

RESULT 8
AAAS8935
ID AAAS8935 standard; DNA; 3259 BP.
XX
AC AAAS8935;
XX
DT 07-NOV-2000 (first entry)
XX
DE DNA encoding a human methionine synthase reductase polypeptide.
XX
KM Human: methionine synthase reductase; MTRR; Cancer;
KM cardiovascular disease; Down's Syndrome; neural tube defect;
KM prematurity coronary artery disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 80..2176
FT /tag= a
FT /product= "methionine synthase reductase"
XX
XX MO200042196-A2.
XX
PD 20-JUL-2000.
XX
PF 14-JAN-2000; 2000MO-IB000209.
XX
PR 15-JAN-1999; 99US-00232028.
PR 10-AUG-1999; 99US-00371347.
XX
XX (UYMC-) UNIV MCGILL.
XX
PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
DR MPI; 2000-46131/40.
DR P-PSDB; AAB07591.
XX
PT Mammalian methionine synthase reductase nucleic acid used for detecting
PT an increased risk of developing a neural tube defect. Down's Syndrome or
PT cardiovascular disease in a mammalian embryo or fetus.
XX
PS Claim 3; Fig 3; 85pp; English.
XX
Cc The present sequence encodes a human methionine synthase reductase (MTRR)
Cc polypeptide. Inhibitors of MTRR polypeptide and polynucleotide are used
Cc for treating or preventing cancer, cardiovascular disease, Down's
Cc Syndrome or neural tube defects in a subject. The cardiovascular disease
Cc is premature coronary artery disease. The compounds are detected by
Cc methods which screen for modulators of MTRR biological activity. MTRR
Cc polypeptide or nucleic acid is examined for the presence of a

Cc polymorphism in the parents or the embryo or foetus, and the information
Cc used for detecting an increased risk of an embryo or foetus developing
Cc cancer, cardiovascular disease, Down's Syndrome or neural tube defects
XX
SQ Sequence 3259 BP; 944 A; 706 C; 663 G; 946 T; 0 U; 0 Other;

Query Match 80.8%; Score 1691; DB 3; Length 3259;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2091; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

Qy 1 ATGAGAGAGGTTCTGTATCATATATGCTACACAGAGGAGCAGGCAAGGCCATTCGAGAA 60
Db 80 ATGAGAGAGGTTCTGTATCATATATGCTACACAGAGGAGCAGGCAAGGCCATTCGAGAA 139
Qy 61 GAATGTGTGAGCAAGCTGTGTAATGATTTTCTGAGATCTTCACTGATTAAGTGA 120
Db 140 GAATGTGTGAGCAAGCTGTGTAATGATTTTCTGAGATCTTCACTGATTAAGTGA 199
Qy 121 TCGATTAAGTATGACTTAAACCCGAAACAGCTCTCTGTTGTTGTTGTTTCTACAG 180
Db 200 TCGATTAAGTATGACTTAAACCCGAAACAGCTCTCTGTTGTTGTTGTTTCTACAG 259
Qy 181 GGCACCGAGAGACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAAC 240
Db 260 GGCACCGAGAGACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAAC 319
Qy 241 CTGCGGTTGATTTCTTTGCTCACTGCGGTATGGGTTA CTGGTCTCGGTATTCAGAA 300
Db 320 CTGCGGTTGATTTCTTTGCTCACTGCGGTATGGGTTA CTGGTCTCGGTATTCAGAA 379
Qy 301 TACACCTACTTTTGCAATGGGGGGAAGATTAATGATTAACGATTCGAAGCTTGAAGCC 360
Db 380 TACACCTACTTTTGCAATGGGGGGAAGATTAATGATTAACGATTCGAAGCTTGAAGCC 439
Qy 361 CGGCATTTCTATGACACTGACATGACATGACTGTGAGTTTGAACCTTGTTGAG 420
Db 440 CGGCATTTCTATGACACTGACATGACATGACTGTGAGTTTGAACCTTGTTGAG 499
Qy 421 CCGTGAATGCTGACTGTGCGCAGCCCTCAGAAAGCATTTTAAAGTCAAGAGAGACAA 480
Db 500 CCGTGAATGCTGACTGTGCGCAGCCCTCAGAAAGCATTTTAAAGTCAAGAGAGACAA 559
Qy 481 GAGGATTAAGTGGCGCACTCCCGGTGGCATCACTGCAATCTTGAAGACAGACCTTGTG 540
Db 560 GAGGATTAAGTGGCGCACTCCCGGTGGCATCACTGCAATCTTGAAGACAGACCTTGTG 619
Qy 541 AAGTCAGAGCTGACATGCAATGCAATCTCAAGTGAAGCTTCTGAGATTCGATTCAGGA 600
Db 620 AAGTCAGAGCTGACATGCAATGCAATCTCAAGTGAAGCTTCTGAGATTCGATTCAGGA 679
Qy 601 AGAAGGATTTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCAAATGTTGA 660
Db 680 AGAAGGATTTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATCCAAATGTTGA 729
Qy 661 ATTGAAGACTTTGAGTCTTCACTTACCCGTTGGTACCCCACTTCAAGGCTCTCG 720
Db 740 ATTGAAGACTTTGAGTCTTCACTTACCCGTTGGTACCCCACTTCAAGGCTCTCG 799
Qy 721 AATATTCCTGTTTACCCCGAGAAATTTTACAGGTACATCTGAGAGAGTCTTGGCCAG 780
Db 800 AATATTCCTGTTTACCCCGAGAAATTTTACAGGTACATCTGAGAGAGTCTTGGCCAG 859
Qy 781 GAGGAAAGCCAAATATCTGACTTCAGCAGATTCAGGTTTCAAGTCCCAATTTCAAG 840
Db 860 GAGGAAAGCCAAATATCTGACTTCAGCAGATTCAGGTTTCAAGTCCCAATTTCAAG 919
Qy 841 GCGATTCACTTACGAGATGATGCAATTAACCACTCTGCTGTAAGTATGACATT 900
Db 920 GCGATTCACTTACGAGATGATGCAATTAACCACTCTGCTGTAAGTATGACATT 979
Qy 901 TCAATATGACATTTTCTATGAGCTGGAGATGCTTGAAGCTGATCTGCTTAACAGT 960
Db 980 TCAATATGACATTTTCTATGAGCTGGAGATGCTTGAAGCTGATCTGCTTAACAGT 1039

QY 961 GATCTGAGGTACAAAGCCTACTCAAAGACGTGACGTTGAAGATAAAAGAGAGACTGC 1020
DB 1040 GATTCTGAGGTACAAAGCCTACTCAAAGACGTGACGTTGAAGATAAAAGAGAGACTGC 1099
QY 1021 GTCTCTTTGAAAAATAAAGGACAGACAAAGAAAGAAAGAGCTTACCTCCAGCATATA 1080
DB 1100 GTCTCTTTGAAAAATAAAGGACAGACAAAGAAAGAAAGAGCTTACCTCCAGCATATA 1159
QY 1081 CTTGCGGAGATGTTCTCTCCAGTTGATTTTACCTGCTGCTGAAATCCGAGCAATTCCT 1140
DB 1160 CTTGCGGAGATGTTCTCTCCAGTTGATTTTACCTGCTGCTGAAATCCGAGCAATTCCT 1219
QY 1141 AAAAAGGCAATTTTGGAGCCCTTGAGACTATACAGAGACAGTCTGAAAAAGGACAG 1200
DB 1220 AAAAAGGCAATTTTGGAGCCCTTGAGACTATACAGAGACAGTCTGAAAAAGGACAG 1279
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DB 1280 CTACAGAGACTGTGACGTAAACAAAGGGGAGCCGATTAATAGCCGTTTGTACAGATGCG 1339
QY 1261 TGTGCTGCTGTTGTGATCTCTCTGCTTTCCTTTTCCAGCCACCACTCACTCTC 1320
DB 1340 TGTGCTGCTGTTGTGATCTCTCTGCTTTCCTTTTCCAGCCACCACTCACTCTC 1399
QY 1321 CTGCTCGAATCTTCTTAACTTCAACCAAGCATATTCGTCAGAGCTCAAGTTTA 1380
DB 1400 CTGCTCGAATCTTCTTAACTTCAACCAAGCATATTCGTCAGAGCTCAAGTTTA 1459
QY 1381 TTTCAACCCAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTCTGTCTACGACCA 1440
DB 1460 TTTCAACCCAGAAAGCTCAATTTTGTCTTCAACATTTGTGAATTTCTGTCTACGACCA 1519
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DB 1520 ACAAGAGTTCTGCGAAGGAGATGTATACAGCTGCTGCTGCTGTTGTTGCTTCAATT 1579
QY 1501 CTTTACGCCAAACATATCATGATCCCAATGAAAGACAGGGGAAAGCCCTGCTCTTAAGATA 1560
DB 1580 CTTTACGCCAAACATATCATGATCCCAATGAAAGACAGGGGAAAGCCCTGCTCTTAAGATA 1639
QY 1561 TCCATCTCTCTCGAACAACAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
DB 1640 TCCATCTCTCTCGAACAACAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1699
QY 1621 ATTAATGTTGGTTCAGAAACCGGACATAGCCCGTTTATTGGTTCCTACAACT---AG 1676
DB 1700 ATTAATGTTGGTTCAGAAACCGGACATAGCCCGTTTATTGGTTCCTACAACTAGAGAG 1759
QY 1677 AAACCTCAGAAACAACAACCAAGTGAATTTTGGAGCAATGTGTTGTTTGGCTGC 1736
DB 1760 AAACCTCAGAAACAACAACCAAGTGAATTTTGGAGCAATGTGTTGTTTGGCTGC 1819
QY 1737 AGGCAATAGGATAGGATTAATCATTCAGAAAAAGCTCAGACATTTCTTAAGCATGGG 1796
DB 1820 AGGCAATAGGATAGGATTAATCATTCAGAAAAAGCTCAGACATTTCTTAAGCATGGG 1879
QY 1797 ATCTTAATCATTAAGGTTTCCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1856
DB 1880 ATCTTAATCATTAAGGTTTCCTTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1939
QY 1857 CCAAGCAATATATATACAAACAACATCCAGCTTCAAGGACAGAGAGTGGCGAATCTTC 1916
DB 1940 CCAAGCAATATATATACAAACAACATCCAGCTTCAAGGACAGAGAGTGGCGAATCTTC 1999
QY 1917 CTCACAGAGAACGGCCATATTTATGTGTGAGATGCAAAAGATATGCGCAAGATGTA 1976
DB 2000 CTCACAGAGAACGGCCATATTTATGTGTGAGATGCAAAAGATATGCGCAAGATGTA 2059
QY 1977 CATGATCCCTTGTGCAATATATAGCAAAAGAGTGTGAGTTGAAAACTAGAAGCAATG 2036
DB 2060 CATGATCCCTTGTGCAATATATATAGCAAAAGAGTGTGAGTTGAAAACTAGAAGCAATG 2119

QY 2037 AAAACCTTGGCCACTTTAAAGAGAAAAACCTTACCTTACAGATATTTGTCATATA 2093
DB 2120 AAAACCTTGGCCACTTTAAAGAGAAAAACCTTACCTTACAGATATTTGTCATATA 2176
RESULT 9
ADM43216
ID ADM43216 standard; cDNA; 2091 BP.
XX
AC ADM43216;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human methionine synthase reductase CDS del 1726-1728 variant.
XX
KW Human; ss; Methionine synthase reductase polypeptide; HemTRR; cancer;
KW cardiovascular disease; neural tube defect; hyperhomocysteinemia;
XX chromosome 5p15.2-p15.3; SNP; single nucleotide polymorphism.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2091
FT /*tag= a
FT /product= "hemTRRdelR559"
FT /partial
FT /note= "No stop codon shown"
FT replace(66,A)
FT variation
FT /*tag= b
FT /standard name= "single_nucleotide polymorphism"
FT replace(110,A)
FT /*tag= c
FT /standard name= "single_nucleotide polymorphism"
FT replace(1726,TTGT)
FT /*tag= d
XX
PN US2003082676-A1.
XX
PD 01-MAY-2003.
XX
PE 10-AUG-1999; 99US-00371347.
XX
PR 16-JAN-1998; 98US-0071622P.
XX 15-JAN-1999; 99US-00232028.
XX
PA (GRAV/) GRAVEL R. A.
XX (ROZE/) ROZEN R.
XX (LECL/) LECLERC D.
XX (WILS/) WILSON A.
XX (ROSE/) ROSENBLATT D.
PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX
XX WPI; 2003-576610/54.
XX P-PsDB; ADM43217.
XX
PT New substantially pure nucleic acid encoding a mammalian methionine
PT synthase reductase polypeptide, useful for diagnosing, preventing or
PT treating conditions associated with altered methionine synthase activity,
XX e.g. cancer.
XX
PS Disclosure; SEQ ID NO 45; 26pp; English.
XX
XX The invention relates to a substantially pure nucleic acid that encodes a
XX mammalian methionine synthase reductase polypeptide, HemTRR, or that
XX hybridizes at high stringency to a nucleic acid appearing as ADM43208 or
XX ADM43209. Also included are a non-human animal where one or both genetic
XX alleles encoding the methionine synthase reductase polypeptide are
XX mutated, an antibody that specifically binds the above methionine
XX synthase reductase polypeptide, a method of detecting the presence of the
XX above polypeptide, a method for detecting sequence variants for
XX methionine synthase reductase in a mammal, methods of treating or
XX preventing cancer (or cardiovascular disease or neural tube defects) in a

CC subject, methods of screening for a compound that modulates methionine
CC synthase reductase biological activity and a method for detecting an
CC increased risk of developing a neural tube defect in a mammalian embryo
CC or foetus. The nucleic acid is useful in diagnosing, preventing or
CC treating conditions associated with altered methionine synthase activity,
CC such as cancer, cardiovascular disease or neural tube defects, or in
CC screening for a compound that modulates methionine synthase reductase
CC biological activity. Naturally occurring variants of the polypeptide are
CC also associated with hyperhomocysteinemia. The gene for hMTFR is
CC located on chromosome 5p15.2-p15.3. The present sequence is the coding
CC sequence of a variant human hMTFR cDNA.
XX

Sequence 2091 BP; 591 A; 489 C; 480 G; 531 T; 0 U; 0 Other;

Query Match 80.1%; Score 1677; DB 11; Length 2091;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGAGGTTTCTGTTACTATATGCTACACAGAGGAGAGGCAAGGCCATCGCAGAA 60
DB 1 ATGAGAGGTTTCTGTTACTATATGCTACACAGAGGAGAGGCAAGGCCATCGCAGAA 60
QY 61 GAAATGTGAGCAAGCTGTGTACATGATGATTTCTGCAGATCTTCATCTGATTAAGTAA 120
DB 61 GAAATGTGAGCAAGCTGTGTACATGATGATTTCTGCAGATCTTCATCTGATTAAGTAA 120
QY 121 TCCGATTAAGTATGACCTTAACCAAGCAAGCTCTCTGTGTGTGTGTTTCTACACG 180
DB 121 TCCGATTAAGTATGACCTTAACCAAGCAAGCTCTCTGTGTGTGTGTTTCTACACG 180
QY 121 TCCGATTAAGTATGACCTTAACCAAGCAAGCTCTCTGTGTGTGTGTTTCTACACG 180
DB 121 TCCGATTAAGTATGACCTTAACCAAGCAAGCTCTCTGTGTGTGTGTTTCTACACG 180
QY 181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACGAACCAACA 240
DB 181 GGCACCGGAGACCCACCCGACACAGCCCGCAAGTTTGTAAAGAAATACGAACCAACA 240
QY 241 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGGGTTACTGGGCTCGGTGATTCAGAA 300
DB 241 CTGCGGTTGATTTCTTGTCTCACTGCGGTATGGGTTACTGGGCTCGGTGATTCAGAA 300
QY 301 TACACCTACTTTTGCATGCGGAGGAGAAATATGATTAACGACTTCAGAGCTTGAGCC 360
DB 301 TACACCTACTTTTGCATGCGGAGGAGAAATATGATTAACGACTTCAGAGCTTGAGCC 360
QY 361 CGGCAATTTCTATGACATGACATGACATGACATGACATGACATGACATGACATGAC 420
DB 361 CGGCAATTTCTATGACATGACATGACATGACATGACATGACATGACATGACATGAC 420
QY 421 CCGTGAATGCTGGAATCTGCGCAGCCCTCAGAAAGCAATTTAGTCAAGCAGAGCAAA 480
DB 421 CCGTGAATGCTGGAATCTGCGCAGCCCTCAGAAAGCAATTTAGTCAAGCAGAGCAAA 480
QY 481 GAGAGATTAAGTGGCGCACTCCCGGTGGCACTCATCTTGAAGAGCAGACCTTGTG 540
DB 481 GAGAGATTAAGTGGCGCACTCCCGGTGGCACTCATCTTGAAGAGCAGACCTTGTG 540
QY 541 AAGTCAGAGCTGCTACATGATGATCTCAAGTGAAGTCTTGAAGTCTTGAAGTCTTGA 600
DB 541 AAGTCAGAGCTGCTACATGATGATCTCAAGTGAAGTCTTGAAGTCTTGAAGTCTTGA 600
QY 601 AGAAGGATCTGAGGTTTGAAGCAAAATGACGTGAACAGCAACCAATCCAATGTTGTA 660
DB 601 AGAAGGATCTGAGGTTTGAAGCAAAATGACGTGAACAGCAACCAATCCAATGTTGTA 660
QY 661 ATTGAAGACTTTGAGTCTTACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 661 ATTGAAGACTTTGAGTCTTACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 AATATTCCTGTTTACCCCAAGATATTTACAGGTATATTCATGCAAGGAGTCTCTGG 780
DB 721 AATATTCCTGTTTACCCCAAGATATTTACAGGTATATTCATGCAAGGAGTCTCTGG 780
QY 781 GAGGAAAGCCAAAGTATCTGTGACTTCAAGCAGATCAGTTTCAAGTCCAAATTTCAAG 840
DB 781 GAGGAAAGCCAAAGTATCTGTGACTTCAAGCAGATCAGTTTCAAGTCCAAATTTCAAG 840

QY 841 GCAATTCAACTTACTACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 GCAATTCAACTTACTACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 TCAAAATACAGCTTTTCTATGAGGCTGAGAGTGCCTTGAAGGTATGCTGCTTACAGT 960
DB 901 TCAAAATACAGCTTTTCTATGAGGCTGAGAGTGCCTTGAAGGTATGCTGCTTACAGT 960
QY 961 GATTCGAGGTACAAAGCTTACCTCAAAAGCTGAGCTTGAAGATTAAGAGAGCAGCTGC 1020
DB 961 GATTCGAGGTACAAAGCTTACCTCAAAAGCTGAGCTTGAAGATTAAGAGAGCAGCTGC 1020
QY 1021 GTTCCTTTGAAAATTAAGGACACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1080
DB 1021 GTTCCTTTGAAAATTAAGGACACAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1080
QY 1081 CCGCGGGAGATGTTCTCTCAGATTCATTTTACCTGAGTCTTGAATCCGAGCAATTCCT 1140
DB 1081 CCGCGGGAGATGTTCTCTCAGATTCATTTTACCTGAGTCTTGAATCCGAGCAATTCCT 1140
QY 1141 AAAAAGCAATTTTGGAGCCCTTGTGACATATACAGTACAGTCTGAAAAGCCAGAG 1200
DB 1141 AAAAAGCAATTTTGGAGCCCTTGTGACATATACAGTACAGTCTGAAAAGCCAGAG 1200
QY 1201 CTACAGAGCTGTGACATTAACAGGGGCAAGCCGATTAATACCCGCTTTGATGAGATGCC 1260
DB 1201 CTACAGAGCTGTGACATTAACAGGGGCAAGCCGATTAATACCCGCTTTGATGAGATGCC 1260
QY 1261 TGTGCTGCTGTGTGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 TGTGCTGCTGTGTGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
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DB 1321 CTGCTCGAATCTTCTCTAACTTCAACCCAGACATATTCGTGCAAGCTCAAGTTTA 1380
QY 1381 TTTTCAACCCAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACGCA 1440
DB 1381 TTTTCAACCCAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACGCA 1440
QY 1441 ACAGAGGTTCTGCGGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
DB 1441 ACAGAGGTTCTGCGGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
QY 1501 CTTCAAGCCAAACATATCATGATCCATGAAGACAGGGGAAAGCCCTGGCTCTTAAGATA 1560
DB 1501 CTTCAAGCCAAACATATCATGATCCATGAAGACAGGGGAAAGCCCTGGCTCTTAAGATA 1560
QY 1561 TCCATCTCTCTGGAACAAATTTTTCACCTTACAGATGACCCCTCAATCCCATC 1620
DB 1561 TCCATCTCTCTGGAACAAATTTTTCACCTTACAGATGACCCCTCAATCCCATC 1620
QY 1621 ATTAATGTTGGTCCAGAAAGCCGATGACCCGTTTATGGGTTCTTCAACAATAGA 1677
DB 1621 ATTAATGTTGGTCCAGAAAGCCGATGACCCGTTTATGGGTTCTTCAACAATAGA 1677

RESULT 10
AD087538
ID AD087538 standard; cDNA; 3270 BP.
XX
XX AD087538;
AC
XX 07-OCT-2004 (first entry)
DT
XX
XX Human tumour-associated antigenic target (TAT) cDNA sequence #4416.
DE human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX
XX Homo sapiens.
XX

QY	1201	TTACAGAGCGTGTGACGTAACAAAGGGGACGCGATTATACCGCTTTGTACAGAGATGCC	1260
Dp	1312	CTACAGAGCTGTGCAGTAAACAGGGGACGCGATTATACCGCTTTGTACAGAGATGCC	1371
QY	1261	TGTGCGCTGCTGTGTGGATCTCCCTCCGCTTTCCCTTTGCCAGCCACCACTGAGTCTC	1320
Dp	1372	TGTGCGCTGCTGTGTGGATCTCCCTCCGCTTTCCCTTTGCCAGCCACCACTGAGTCTC	1431
QY	1321	CTGCTCGAACAACATTCCTTAAACCTTCAACCGACACATATGTGTGCAAGCTCAAGTTTA	1380
Dp	1432	CTGCTCGAACAACATTCCTTAAACCTTCAACCGACACATATGTGTGCAAGCTCAAGTTTA	1491
QY	1381	TTTCAACCCAGGAAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACTGCCACA	1440
Dp	1492	TTTCAACCCAGGAAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACTGCCACA	1551
QY	1441	ACAGAGGTTCTGCGGAGGGAGATGTACAGGCTGCGCTGCTGTGTGTTGCTTCAAGTT	1500
Dp	1552	ACAGAGGTTCTGCGGAGGGAGATGTACAGGCTGCGCTGCTGTGTGTTGCTTCAAGTT	1611
QY	1501	CTTCAGCCAAACATTCATGATGCCATCCATGAAGACAGCGGGAAGCCCTGCTGCTTAAGATA	1560
Dp	1612	CTTCAGCCAAACATTCATGATGCCATCCATGAAGACAGCGGGAAGCCCTGCTGCTTAAGATA	1671
QY	1561	TCGATCTCTCCTCGAACACAACAAATTCYTTCCACTTACCAATGACCCCTCAATCCCAATC	1620
Dp	1672	TCGATCTCTCCTCGAACACAACAAATTCYTTCCACTTACCAATGACCCCTCAATCCCAATC	1731
QY	1621	ATATATGAGGGATCCAGGAACCGGCAATACCCCGTTATTTGGGTTCTTAACAAT---AG	1676
Dp	1732	ATATATGAGGGATCCAGGAACCGGCAATACCCCGTTATTTGGGTTCTTAACAATGAGAG	1791
QY	1677	AAACTCCAAAGAACACACCCAGATGGAATTTTGTGAGCAATGTGGTGTCTTTTGTGCTGC	1736
Dp	1792	AAACTCCAAAGAACACACCCAGATGGAATTTTGTGAGCAATGTGGTGTCTTTTGTGCTGC	1851
QY	1737	AGGCATAAGGATAGGGATTATCTATTCGAAAAGGCTCAACATTTCTTAAGCATGGG	1796
Dp	1852	AGGCATAAGGATAGGGATTATCTATTCGAAAAGGCTCAACATTTCTTAAGCATGGG	1911
QY	1797	ATCTTAACTCATCTAAAGGTTTCCCTTTCAGAGAGATCTCCGTGTGGGGAAGAGAAAGCC	1856
Dp	1912	ATCTTAACTCATCTAAAGGTTTCCCTTTCAGAGAGATCTCCGTGTGGGGAAGAGAAAGCC	1971
QY	1857	CCAGCAAAAGTATGTACAAAGACAATCCAGCTTCATGCGCCAGCAGGTGGCGAAGATCTTC	1916
Dp	1972	CCAGCAAAAGTATGTACAAAGACAATCCAGCTTCATGCGCGCAGCAGGTGGCGAAGATCTTC	2031
QY	1917	CTCCAGAGGAACCGGCATATTTATGTGTGTGGAGATGCAAGAAATATGCGCAAGGATGTA	1976
Dp	2032	CTCCAGAGGAACCGGCATATTTATGTGTGTGGAGATGCAAGAAATATGCGCAAGGATGTA	2091
QY	1977	CATGATGCGCTTGTGCAATATATAGCAAGAGGTTTGAGTTGAAAACCTAAGACATG	2036
Dp	2092	CATGATGCGCTTGTGCAATATATAGCAAGAGGTTTGAGTTGAAAACCTAAGACATG	2151
QY	2037	AAAACCCCTGGCCATTTTAAAGAGAAAAGCGTACTTCCAGGATATTTGGCTATTA	2093
Dp	2152	AAAACCCCTGGCCATTTTAAAGAGAAAAGCGTACTTCCAGGATATTTGGCTATTA	2208

RESULT 11	
AAAS8977	
ID	AAAS8977 standard; DNA, 3256 BP.
XX	
AC	
XX	AAAS8977;
DT	07-NOV-2000 (first entry)
XX	
DE	A human methionine synthase reductase DNA sequence with polymorphism
XX	
XX	Human; methionine synthase reductase; MTRR; cancer;
KW	cardiovascular disease; Down's Syndrome; neural tube defect;
FM	

prematu re coronary artery disease; ss.
Homo sapiens.
MO200042196-A2.
20-JUL-2000.
14-JAN-2000; 2000WO-IB000209.
15-JAN-1999; 99US-00232028.
10-AUG-1999; 99US-00371347.
(UTMC-) UNIV MCGILL.
Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
WPI; 2000-466131/40.
Mammalian methionine synthase reductase nucleic acid used for detecting
an increased risk of developing a neural tube defect, Down's Syndrome or
cardiovascular disease in a mammalian embryo or fetus.
Claim 8; Page; 85pp; English.
The present sequence represents a human methionine synthase reductase
(MTRR) DNA sequence, with a polymorphism comprising of a deletion of
nucleotides 1726-1728. Inhibitors of MTRR polypeptide and polynucleotide
are used for treating or preventing cancer, cardiovascular disease,
Down's Syndrome or neural tube defects in a subject. The cardiovascular
disease is prematu re coronary artery disease. The compounds are detected
by methods which screen for modulators of MTRR biological activity. MTRR
polypeptide or nucleic acid is examined for the presence of a
polymorphism in the parents or the embryo or foetus, and the information
used for detecting an increased risk of an embryo or foetus developing
cancer, cardiovascular disease, Down's Syndrome or neural tube defects.
note: the present sequence does not appear in the specification; it was
created using information provided
Sequence 3256 BP; 943 A; 705 C; 662 G; 946 T; 0 U; 0 Other;

Query Match	Best Local Similarity	76.2%	Score 1595;	DB 3,	Length 3256;
Query Match	Similarity	99.9%	Pred. No. 0;		
Matches 1645;	Conservative	0;	Mismatches	1;	Indels
					Gaps
					0
QY	1	ATGAGAGAGTTCTGTATCTATATATGTCACACAGCAGGGACAGGCAMAAGCCATCGCAGAA	60		
Db	80	ATGAGAGAGTTCTGTATCTATATATGTCACACAGCAGGGACAGGCAMAAGCCATCGCAGAA	139		
QY	61	GAATGTGTGAGCAAGCTGTGTGACATGAAATTTCTGAGAGATCTTCACTGATTTAGTAA	120		
Db	140	GAATGTGTGAGCAAGCTGTGTGACATGAAATTTCTGAGAGATCTTCACTGATTTAGTAA	199		
QY	121	TCCGATATAGTATGACTTTAAACCGAAACAGCTCCTCTGTGTGTGTGTGTTTCTTACACG	180		
Db	200	TCCGATATAGTATGACTTTAAACCGAAACAGCTCCTCTGTGTGTGTGTGTTTCTTACACG	259		
QY	181	GGCACCCGAGACCCACCCGACACAGCCCGCAAGTTGTTAAAGAAATACAGAACCAACA	240		
Db	260	GGCACCCGAGACCCACCCGACACAGCCCGCAAGTTGTTAAAGAAATACAGAACCAACA	319		
QY	241	CTGCGCGGTGATTTCTTTGGTCACTCGCGGATGCGGTACAGGGCTCGGGTGAATTCAGAA	300		
Db	320	CTGCGCGGTGATTTCTTTGGTCACTCGCGGATGCGGTACAGGGCTCGGGTGAATTCAGAA	379		
QY	301	TACACTTACTTTTGCATATGGGGGAGATTAATTGATTAACGACTTCAAGAGCTTGAAGCC	360		
Db	380	TACACTTACTTTTGCATATGGGGGAGATTAATTGATTAACGACTTCAAGAGCTTGAAGCC	439		
QY	361	CGGCATTTCTATGACACTGAGCATGACAGATGACTGTGTAGGTTTGAACCTGTGGTTGAG	420		
Db	440	CGGCATTTCTATGACACTGAGCATGACAGATGACTGTGTAGGTTTGAACCTGTGGTTGAG	499		


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QY 421 CCGTGGATTTGAGACTCTGGCCAGAGCCCTCAGAAAGCATTTTAAAGTCAAGCAGAGAGACA 480
DB 500 CCGTGGATTTGAGACTCTGGCCAGAGCCCTCAGAAAGCATTTTAAAGTCAAGCAGAGAGACA 559
QY 481 GAGGAGATTAAGTGGGCGCACTCCCGGTGGGATCACTCTGCATCTTTAGGAGCAGACCTTGG 540
DB 560 GAGGAGATTAAGTGGGCGCACTCCCGGTGGGATCACTCTGCATCTTTAGGAGCAGACCTTGG 619
QY 541 AAGTCAGAGCTGTACATCAATGAAATCTCAAGTCAGACTCTGAGATTCGATGATTCAGGA 600
DB 620 AAGTCAGAGCTGTACATCAATGAAATCTCAAGTCAGACTCTGAGATTCGATGATTCAGGA 679
QY 601 AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAACGAAACCAATCCAATGTTGTA 660
DB 680 AGAAAGATTTCTGAGGTTTGAAGCAAAATGCAAGTGAACGAAACCAATCCAATGTTGTA 739
QY 661 ATTGAAGACTTTGAGTCTCTCACTTACCCGTTGGGTACCCCACTCTCAAGCCTCTCTG 720
DB 740 ATTGAAGACTTTGAGTCTCTCACTTACCCGTTGGGTACCCCACTCTCAAGCCTCTCTG 799
QY 721 AATATTCCTGGTTTACCCCAAGATTTTACAGGTATCTGTGAGGAGTCTCTGGCCAG 780
DB 800 AATATTCCTGGTTTACCCCAAGATTTTACAGGTATCTGTGAGGAGTCTCTGGCCAG 859
QY 781 GAGAAAGCCAAATATCTGTGACTTCAAGAGATCCAGTTTTCAGTGGCAATTTCAAG 840
DB 860 GAGAAAGCCAAATATCTGTGACTTCAAGAGATCCAGTTTTCAGTGGCAATTTCAAG 919
QY 841 GAGATTCAACTTACAGAAATGATGCAATTAACCACTCTGTGTGATGATTTGACAT 900
DB 920 GAGATTCAACTTACAGAAATGATGCAATTAACCACTCTGTGTGATGATTTGACAT 979
QY 901 TCATAATACAGACTTTTCTATCAAGCTGTGAGATGCTTCAAGCTGATCTGCTTAAAGT 960
DB 980 TCATAATACAGACTTTTCTATCAAGCTGTGAGATGCTTCAAGCTGATCTGCTTAAAGT 1039
QY 961 GATTCTGAGGTACAAAGCCTTACCAAGAGCTGCACTTGAAGATTAAGAGAGAGAGAGAG 1020
DB 1040 GATTCTGAGGTACAAAGCCTTACCAAGAGCTGCACTTGAAGATTAAGAGAGAGAGAGAG 1099
QY 1021 GTCTCTTTGAAATTAAGGAGACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1100 GTCTCTTTGAAATTAAGGAGACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1159
QY 1081 CCGTGGGAGATTTCTCTCAAGTCAATTTTAACTGTGTGTTGAAATCCGAGCAATTTCT 1140
DB 1160 CCGTGGGAGATTTCTCTCAAGTCAATTTTAACTGTGTGTTGAAATCCGAGCAATTTCT 1219
QY 1141 AAAAAGGCAATTTTGGAGGCTTGTGAGCTATACAGTGAAGTGTGAAAAGGCGAGG 1200
DB 1220 AAAAAGGCAATTTTGGAGGCTTGTGAGCTATACAGTGAAGTGTGAAAAGGCGAGG 1279
QY 1201 CTACAGAGCTGTGAGTAAACAAAGGAGGAGCCGATTAATAGCCGCTTGTGACAGATGCC 1260
DB 1280 CTACAGAGCTGTGAGTAAACAAAGGAGGAGCCGATTAATAGCCGCTTGTGACAGATGCC 1339
QY 1261 TGTGCTGCTGTGTGATCTCTCTGCGCTTTTCCCTTCTTCCAGCAGCAGCACTGAGTCT 1320
DB 1340 TGTGCTGCTGTGTGATCTCTCTGCGCTTTTCCCTTCTTCCAGCAGCAGCACTGAGTCT 1399
QY 1321 CTGCTGGAACATTTCTTAACTTCAACCCAGACCAATATTCGTTGAGAGTCAAGTTTA 1380
DB 1400 CTGCTGGAACATTTCTTAACTTCAACCCAGACCAATATTCGTTGAGAGTCAAGTTTA 1459
QY 1381 TTTCAACCCAGAAAGCTCCATTTTGTCTCAACATTTGATGATTTCTGTCTACTGCGACA 1440
DB 1460 TTTCAACCCAGAAAGCTCCATTTTGTCTTCAACATTTGATGATTTCTGTCTACTGCGACA 1519
QY 1441 ACAGAGGTTTCTGGGAAAGGAGATATGACAGGCTGGCTGCTTGTGTGTTGCTTCAGTT 1500
DB 1520 ACAGAGGTTTCTGGGAAAGGAGATATGACAGGCTGGCTGCTTGTGTGTTGCTTCAGTT 1579
QY 1501 CTTGAGCAAAACATATGATGATCCCATGAAAGACAGGCGGAAAGCCCTGGCTCTTAAGATA 1560

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DB 1580 CTTGAGCCCAACATATGATCCATGAAAGCAGGAGGAAAGCCCTGCTCTTAAGATA 1639
QY 1561 TCCATCTCTCTCGAACAACAATTTCTTCCATTAACAGATGAGACCCCTCAATGCCATC 1620
DB 1640 TCCATCTCTCTCGAACAACAATTTCTTCCATTAACAGATGAGACCCCTCAATGCCATC 1699
QY 1621 ATAAATGTGGGTCCAGGAACCGGCAT 1646
DB 1700 ATAAATGTGGGTCCAGGAACCGGCAT 1725

RESULT 12
ID AA58976
ID AA58976 standard; DNA; 3255 BP.
XX
AC AA58976;
XX
DT 07-NOV-2000 (first entry)
XX
DE A human methionine synthase reductase DNA sequence with polymorphism.
XX
KW Human; methionine synthase reductase; MTRR; cancer;
KW cardiovascular disease; Down's Syndrome; neural tube defect;
KW premature coronary artery disease; ss.
XX
OS Homo sapiens.
XX
PN WO200042196-A2.
XX
PD 20-JUL-2000.
XX
PF 14-JAN-2000; 2000MO-IB000209.
XX
PR 15-JAN-1999; 99US-00232028.
PR 10-AUG-1999; 99US-00371347.
XX
PA (UWMC-) UNIV MCGILL.
XX
PI Gravel RA, Rozen R, Leclerc D, Wilson A, Rosenblatt D;
XX
DR MPI; 2000-466131/40.
XX
PT Mammalian methionine synthase reductase nucleic acid used for detecting
PT an increased risk of developing a neural tube defect, Down's Syndrome or
PT cardiovascular disease in a mammalian embryo or fetus.
XX
PS Claim 7; Page; 85pp; English.
XX
CC The present sequence represents a human methionine synthase reductase
CC (MTRR) DNA sequence, with a polymorphism comprising of a deletion of
CC nucleotides 1675-1678. Inhibitors of MTRR polypeptide and polynucleotide
CC are used for treating or preventing cancer, cardiovascular disease,
CC Down's Syndrome or neural tube defects in a subject. The cardiovascular
CC disease is premature coronary artery disease. The compounds are detected
CC by methods which screen for modulators of MTRR biological activity. MTRR
CC polypeptide or nucleic acid is examined for the presence of a
CC polymorphism in the parents or the embryo or foetus, and the information
CC used for detecting an increased risk of an embryo or foetus developing
CC cancer, cardiovascular disease, Down's Syndrome or neural tube defects.
CC note: the present sequence does not appear in the specification; it was
CC created using information provided
XX
SQ Sequence 3255 BP; 942 A; 704 C; 663 G; 946 T; 0 U; 0 Other;

Query Match 73.8%; Score 1544; DB 3; Length 3255;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1594; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGAGGTTTCTGTACTATATGCTTACACAGCAGGAGCAAGGCAAGGCTTCAGAGA 60
DB 80 ATGAGAGGTTTCTGTACTATATGCTTACACAGCAGGAGCAAGGCAAGGCTTCAGAGA 139

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CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
CC the specification or its complement and encoding any one of the amino
CC acid sequences given in the specification; an isolated polypeptide
CC comprising an amino acid sequence given in the specification; an antibody
CC that specifically binds to the polypeptide or its antigen-binding
CC fragment; an amplified polynucleotide containing an SNP given in the
CC specification and which is between about 16 and 1000 nucleotides in
CC length; a kit for detecting an SNP in a nucleic acid, comprising the
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
CC method for identifying an agent useful in treating or preventing
CC myocardial infarction. The novel detection method has cardiant activity.
CC The nucleic acids of the invention may be used in gene therapy. The
CC method is useful in identifying an individual who has an increased or
CC decreased risk for developing myocardial infarction and for preparing a
CC composition for treating or preventing myocardial infarction. This
CC polynucleotide sequence represents a human myocardial infarction-
CC associated gene containing one or more SNPs of the invention. Note: This
CC sequence was not shown in the specification. The sequence has come from
CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 3256 BP; 927 A; 691 C; 669 G; 940 T; 0 U; 29 Other;

Query Match 42.0%; Score 879; DB 13; Length 3256;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1579; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 67 TGTGAGCAGCTGTGATCATGATTTCTGCAGATCTTCAGTATTAATGATCCGAT 126
Db 160 TGTGAGCAGCTGTGATCATGATTTCTGCAGATCTTCAGTATTAATGATCCGAT 219
QY 127 AAGTATGACCTTAAACCGAAACAGCTCTCTTGTGTGTGTTGTTCTACACGCGAC 186
Db 220 AAGTATGACCTTAAACCGAAACAGCTCTCTTGTGTGTGTTGTTCTACACGCGAC 279
QY 187 GGAGACCCACCGCAGACGCGCGAAGTTGTTAAGAAATACGAAACCAACCTGCCG 246
Db 280 GGAGACCCACCGCAGACGCGCGAAGTTGTTAAGAAATACGAAACCAACCTGCCG 339
QY 247 GTTGATTTCTTGTCTCACTGCGGTATGGTTACTGCGGTCTGCGTATTCAGAAATAC 306
Db 340 GTTGATTTCTTGTCTCACTGCGGTATGGTTACTGCGGTCTGCGTATTCAGAAATAC 399
QY 307 TACTTTTGAATGGGGGAAAGATATTAATTAACGACTTCAAGACTTGAAGCCCGCAT 366
Db 400 TACTTTTGAATGGGGGAAAGATATTAATTAACGACTTCAAGACTTGAAGCCCGCAT 459
QY 367 TTCTATGACACTGACATGACATGATGATGTTAGAACTTGTGTGAGCCCTGG 426
Db 460 TTCTATGACACTGACATGACATGATGATGTTAGAACTTGTGTGAGCCCTGG 519
QY 427 ATTGCTGAATCTGCGCAGCCCTCAGAAAGCAATTTTGAAGTCAAGCAGAGGAG 486
Db 520 ATTGCTGAATCTGCGCAGCCCTCAGAAAGCAATTTTGAAGTCAAGCAGAGGAG 579
QY 487 ATTAAGTGGCGACTCCCGGTGGATCACTGATCTTGAAGACAGACTTGTGAAGTCA 546
Db 580 ATTAAGTGGCGACTCCCGGTGGATCACTGATCTTGAAGACAGACTTGTGAAGTCA 639
QY 547 GAGCTGCTACATTTGAATCTCAAGTGAAGTCTTGAAGTTCATGATTCAGAAAGAA 606
Db 640 GAGCTGCTACATTTGAATCTCAAGTGAAGTCTTGAAGTTCATGATTCAGAAAGAA 699
QY 607 GATCTGAGGTTTGAAGCAAAATGACATGAAAGCAACCAATGTTGTAATTGAA 666
Db 700 GATCTGAGGTTTGAAGCAAAATGACATGAAAGCAACCAATGTTGTAATTGAA 759
QY 667 GACTTTGAGTCTCTACTTACCCGTTCCGTAACCCCACTCTCAAGAGCTCTGAATATT 726
Db 760 GACTTTGAGTCTCTACTTACCCGTTCCGTAACCCCACTCTCAAGAGCTCTGAATATT 819
QY 727 CTGTGTTTACCCCAAGATATTTACAGGTACATCTGCAGAGGTCTTTGGCCAGAGGAA 786

Db 820 CCTGTGTACCCCCAGAAATATTTACAGTACATCTGCAGAGAGCTCTGGCCAGAGGAA 879
QY 787 AGCCAAGTATCTGTGACTTTCAGCAGATCCAGTTTTCAGAGTCCAAATTTCAAGGCA 846
Db 880 AGCCAAGTATCTGTGACTTTCAGCAGATCCAGTTTTCAGAGTCCAAATTTCAAGGCA 939
QY 847 CAATCTTACAGAAATGATGCAATTAACCACTGCTGCTGTAATGACATTTCAAT 906
Db 940 CAATCTTACAGAAATGATGCAATTAACCACTGCTGCTGTAATGACATTTCAAT 999
QY 907 ACAGACTTTTCCATGAGCTGAGATGCTTCAAGCTGATCTGCTTAAAGATGATTC 966
Db 1000 ACAGACTTTTCCATGAGCTGAGATGCTTCAAGCTGATCTGCTTAAAGATGATTC 1059
QY 967 GAGTACAAAGCTTCTCAAGACTGCACTTGAAGTAAAGAGAGCACTGCTCTT 1026
Db 1060 GAGTACAAAGCTTCTCAAGACTGCACTTGAAGTAAAGAGAGCACTGCTCTT 1119
QY 1027 TTGAAATTAAGGAGACACAAAGAAAGAGCTTACCTTACCCAGCATATACCTGG 1086
Db 1120 TTGAAATTAAGGAGACACAAAGAAAGAGCTTACCTTACCCAGCATATACCTGG 1179
QY 1087 GATGTTCTCTCAGTTCAATTTTACCTGCTGCTGTAATCCGAGCAATTCCTTAAAG 1146
Db 1180 GATGTTCTCTCAGTTCAATTTTACCTGCTGCTGTAATCCGAGCAATTCCTTAAAG 1239
QY 1147 GCATTTTTCGAGCCCTTGTGACATATACAGTACAGTGTGTAAGAGCGAGCTACAG 1206
Db 1240 GCATTTTTCGAGCCCTTGTGACATATACAGTACAGTGTGTAAGAGCGAGCTACAG 1299
QY 1207 GAGCTGTGAGTAAACAAAGGAGCGCATATATAGCCGTTTGTAGAGATGCTGTGCC 1266
Db 1300 GAGCTGTGAGTAAACAAAGGAGCGCATATATAGCGCTTGTAGAGATGCTGTGCC 1359
QY 1267 TGTGTTGATATCTCTCTGCTTCCCTTCTTTCGAGCAGCACTAGTCTCTGCTC 1326
Db 1360 TGTGTTGATATCTCTCTGCTTCCCTTCTTTCGAGCAGCACTAGTCTCTGCTC 1419
QY 1327 GAAATCTTCTTAACTTCAACCCAGACCATATTTGTGCAAGCTCAAGTTATTTTAC 1386
Db 1420 GAAATCTTCTTAACTTCAACCCAGACCATATTTGTGCAAGCTCAAGTTATTTTAC 1479
QY 1387 CCAGAAAGCTCCATTTTGTCTTCAACATTTGTGGAATTTCTGTCTACTGCAACAGAG 1446
Db 1480 CCAGAAAGCTCCATTTTGTCTTCAACATTTGTGGAATTTCTGTCTACTGCAACAGAG 1539
QY 1447 GTTCTGCGAAGGAGATGATGACAGGCTGCTGCTGTTGTGTTGCTTCACTTTCAG 1506
Db 1540 GTTCTGCGAAGGAGATGATGATGACAGGCTGCTGCTGTTGTGTTGCTTCACTTTCAG 1599
QY 1507 CCAGATATCATGATCCCATGAGAGCAGCGGAAAGCCCTGCTCTTAAGATATCATC 1566
Db 1600 CCAGATATCATGATCCCATGAGAGCAGCGGAAAGCCCTGCTCTTAAGATATCATC 1659
QY 1567 TCTCTCGAAGCAAAATTTCTTCACTTACAGATGACCCCTCAATCCCATCATTAATG 1626
Db 1660 TCTCTCGAAGCAAAATTTCTTCACTTACAGATGACCCCTCAATCCCATCATTAATG 1719
QY 1627 GTGCGTCCAGAAACCGGCAATAGCCCGTTTATT 1659
Db 1720 GTGCGTCCAGAAACCGGCAATAGCCCGTTTATT 1752

RESULT 15
ADQ39030 standard; DNA; 3274 BP.
XX ADQ39030;
XX AC ADQ39030;
XX XX
XX 18-NOV-2004 (first entry)
XX XX
XX Human SNP containing myocardial infarction-associated gene, SBO ID 693.


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Qy 1327 GAACATCTCTTAAGTTCACCCAGACCATATTCTGTGCAAGCTCAAGTTATTTCAC 1386
    |||||
Db 1438 GAACATCTCTCTTAAGTTCACCCAGACCATATTCTGTGCAAGCTCAAGTTATTTCAC 1497
    |||||
Qy 1387 CCAGGAAAGCTCGATTTGTCTTCAACATGTGGAAATTTCTGTCTACTGCGACACAGAG 1446
    |||||
Db 1498 CCAGGAAAGCTCGATTTGTCTTCAACATGTGGAAATTTCTGTCTACTGCGACACAGAG 1557
    |||||
Qy 1447 GTTCTGCGAAGGAGATGATGACAGCTGCGCTGTGTGTGTGCTTCAGTTCTTCAG 1506
    |||||
Db 1558 GTTCTGCGAAGGAGATGATGACAGCTGCGCTGTGTGTGTGCTTCAGTTCTTCAG 1617
    |||||
Qy 1507 CCAACATACATGATCCCATGAAAGACGCGGAAAGCCTGGCTCCTAAGATATCCATC 1566
    |||||
Db 1618 CCAACATACATGATCCCATGAAAGACGCGGAAAGCCTGGCTCCTAAGATATCCATC 1677
    |||||
Qy 1567 TCTCTGGAACAACAATTTCTTCCACTTACAGATGACCCCTCAATCCCATCATPATG 1626
    |||||
Db 1678 TCTCTGGAACAACAATTTCTTCCACTTACAGATGACCCCTCAATCCCATCATPATG 1737
    |||||
Qy 1627 GTGGGTCAGAGAACCGGCATAGCCCGTTTATT 1659
    |||||
Db 1738 GTGGGTCAGAGAACCGGCATAGCCCGTTTATT 1770
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OM nucleic - nucleic search, using sw model

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Gapop 60.0 , Gapext 60.0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1793	85.7	3259	3	US-09-318-448-23
2	1640	78.4	3242	4	US-09-949-016-4215
3	386	18.4	390	3	US-08-905-223-71
4	330	15.8	601	4	US-09-949-016-150019
5	330	15.8	35916	4	US-09-949-016-150019
6	279	13.3	601	4	US-09-949-016-150020
7	189	9.0	601	4	US-09-949-016-150037
8	158	7.5	2475	4	US-09-566-921-88
9	155	7.4	601	4	US-09-949-016-150030
10	145	6.9	601	4	US-09-949-016-150031
11	137	6.5	601	4	US-09-949-016-150046
12	137	6.5	601	4	US-09-949-016-150047
13	125	6.0	601	4	US-09-949-016-150029
14	121	5.8	601	4	US-09-949-016-150041
15	121	5.8	601	4	US-09-949-016-150042
16	119	5.7	601	4	US-09-949-016-150008
17	119	5.7	601	4	US-09-949-016-150055
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19	94	4.5	601	4	US-09-949-016-150032
20	78	3.7	244	4	US-09-471-276-495
21	78	3.7	601	4	US-09-949-016-150007
22	76	3.6	601	4	US-09-949-016-150018
23	30	1.4	1681	4	US-09-023-655-453
24	20	1.0	273	4	US-09-513-999C-14761
25	20	1.0	440	3	US-09-397-787-305
26	20	1.0	444	4	US-09-621-976-14139
27	20	1.0	445	3	US-09-397-787-274

c 28	20	1.0	174259	4	US-09-949-016-11968	Sequence 11968, A
c 29	20	1.0	174262	4	US-09-949-016-14259	Sequence 14259, A
c 30	19	0.9	169	1	US-08-166-346A-8	Sequence 8, Appl1
c 31	19	0.9	459	4	US-09-621-976-8324	Sequence 8324, Ap
c 32	19	0.9	3969	3	US-09-518-386B-4	Sequence 4, Appl1
c 33	19	0.9	4396	3	US-09-821-736-1	Sequence 1, Appl1
c 34	19	0.9	14721	4	US-09-949-016-13507	Sequence 13507, A
c 35	19	0.9	25199	4	US-09-949-016-13361	Sequence 13361, A
c 36	19	0.9	129658	4	US-09-949-016-17195	Sequence 17195, A
c 37	19	0.9	186734	4	US-09-949-016-14870	Sequence 14870, A
c 38	19	0.9	193689	4	US-09-949-016-12350	Sequence 12350, A
c 39	19	0.9	193689	4	US-09-949-016-13088	Sequence 13088, A
c 40	19	0.9	200663	4	US-09-949-016-12569	Sequence 12569, A
c 41	19	0.9	203093	4	US-09-949-016-14445	Sequence 14445, A
c 42	18	0.9	78	2	US-08-749-852-56	Sequence 56, Appl
c 43	18	0.9	78	2	US-08-749-852-58	Sequence 58, Appl
c 44	18	0.9	511	4	US-09-902-540-1374	Sequence 1374, Ap
c 45	18	0.9	531	4	US-09-252-991A-2223	Sequence 2223, Ap

ALIGNMENTS

RESULT 1						
US-09-318-448-23						
Sequence 23, Application US/09318448						
Patent No. 6210950						
GENERAL INFORMATION:						
APPLICANT: Johnson, William G.						
APPLICANT: Steenroos, Edward S.						
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING						
FILE REFERENCE: 601-1-057						
CURRENT APPLICATION NUMBER: US/09/318,448						
CURRENT FILING DATE: 1999-05-25						
NUMBER OF SEQ ID NOS: 46						
SOFTWARE: PatentIn Ver. 2.0						
SEQ ID NO 23						
LENGTH: 3259						
TYPE: DNA						
ORGANISM: Homo sapiens						
US-09-318-448-23						
Query Match						
Best Local Similarity 99.8%; Pred. No. 0;						
Matches 2093; Conservative 0; Mismatches 0; Indels 4; Gaps 1;						
Qy	1	ATGAGGAGGTTCTGTTACTATATGCTACACAGCAGGACGACCAAGGCCATCGCAGAA	60			
Db	80	ATGAGGAGGTTCTGTTACTATATGCTACACAGCAGGACGACCAAGGCCATCGCAGAA	139			
Qy	61	GAATGTGTGACCAAGCTGTGTGATGATTTTCTGCAATCTTCACTGTATTAGTAA	120			
Db	140	GAATGTGTGACCAAGCTGTGTGATGATTTTCTGCAATCTTCACTGTATTAGTAA	199			
Qy	121	TCGATTAATGATGACCTTAAACCGAAACAGCTCTCTGTTGTGTGTTTCTACACG	180			
Db	200	TCGATTAATGATGACCTTAAACCGAAACAGCTCTCTGTTGTGTGTTTCTACACG	259			
Qy	181	GGCAGCGAGACCCACCGACAGAGCCGACAGTTGTTAAGAAATACGAACCAACA	240			
Db	260	GGCAGCGAGACCCACCGACAGAGCCGACAGTTGTTAAGAAATACGAACCAACA	319			
Qy	241	CTGCCGTTGATTTCTTGTCTCACTGCGGTATGGTTACTGAGTCTCGGTATTGAA	300			
Db	320	CTGCCGTTGATTTCTTGTCTCACTGCGGTATGGTTACTGAGTCTCGGTATTGAA	379			
Qy	301	TACACTTATTTGCAATGGGGGAAGATATGATTAACGATTCGAAGCTTGAGGC	360			
Db	380	TACACTTATTTGCAATGGGGGAAGATATGATTAACGATTCGAAGCTTGAGGC	439			
Qy	361	CGGATTTTATGACACTGACATGAGATGACTGTGTGATTTAGAACTTGTTGAG	420			

Db 440 CGGCAATTTCTATGACACTGACATGACAGATGACTGTGTAGGTTTAAACCTTGTGGTTGAG 499
Qy 421 CCGTGATGTCGTGACTCTGCGCCAGCCCTGAGAAAGCAATTTAGTTCAGACAGAGCA 480
Db 500 CCGTGATGTCGTGACTCTGCGCCAGCCCTGAGAAAGCAATTTAGTTCAGACAGAGCA 559
Qy 481 GAGGAGATTAAGTGGCGCACTCCGGTGGCATCACCTGCAATCTTTAGAGACAGACCTTGTG 540
Db 560 GAGGAGATTAAGTGGCGCACTCCGGTGGCATCACCTGCAATCTTTAGAGACAGACCTTGTG 619
Qy 541 AAGTCAGAGCTGTCAGACATTTGAATCTCAAGTGGAGCTTGGAGATTCGATGATTCAGAG 600
Db 620 AAGTCAGAGCTGTCAGACATTTGAATCTCAAGTGGAGCTTGGAGATTCGATGATTCAGAG 679
Qy 601 AGAAGAGATTCGAGATTTTGAAGCAAAATGACAGTGAACAGCAACCAATCCAAATGTTGA 660
Db 680 AGAAGAGATTCGAGATTTTGAAGCAAAATGACAGTGAACAGCAACCAATCCAAATGTTGA 739
Qy 661 ATTGAAGATCTTGAATGCTCTCACTTACCCGTTCCGATACCCCACTTCAACAAGCTCTCTG 720
Db 740 ATTGAAGATCTTGAATGCTCTCACTTACCCGTTCCGATACCCCACTTCAACAAGCTCTCTG 799
Qy 721 AATATTCCTGGTTTACCCCGAGAAATTTTACAGGTACATCTGACAGAGAGTCTCTTGGCAG 780
Db 800 AATATTCCTGGTTTACCCCGAGAAATTTTACAGGTACATCTGACAGAGAGTCTCTTGGCAG 859
Qy 781 GAGGAAAGCCAGATATCTGTGACTTCAGACAGATCCAGTCTTTCAGAGTCCAAATTTCAAG 840
Db 860 GAGGAAAGCCAGATATCTGTGACTTCAGACAGATCCAGTCTTTCAGAGTCCAAATTTCAAG 919
Qy 841 GCAGTTCAACTTACTAGAAATGATGCAATAAAACCACTGCTGTGTAATTTGACATTT 900
Db 920 GCAGTTCAACTTACTAGAAATGATGCAATAAAACCACTGCTGTGTAATTTGACATTT 979
Qy 901 TCAATTCAGAGCTTTTCTATAGCCCTGAGAGTCCCTGAGGATCTGAGTCCCTTAACAGT 960
Db 980 TCAATTCAGAGCTTTTCTATAGCCCTGAGAGTCCCTGAGGATCTGAGTCCCTTAACAGT 1039
Qy 961 GATTCTGAGGTACAAAGCCTACTCCAAAGACTGCAAGTGAAGTAAGAGAGCACTGC 1020
Db 1040 GATTCTGAGGTACAAAGCCTACTCCAAAGACTGCAAGTGAAGTAAGAGAGCACTGC 1099
Qy 1021 GTCTTTTGAATTAAGGACAGACAAAGAGAGAGCTTACCTCCAGCATATA 1080
Db 1100 GTCTTTTGAATTAAGGACAGACAAAGAGAGAGCTTACCTCCAGCATATA 1159
Qy 1081 CCGCGGAGATGTTCTCCAGTTCATTTTACCGTGGTCTGTAAGAACCGAGCAATTCCT 1140
Db 1160 CCGCGGAGATGTTCTCCAGTTCATTTTACCGTGGTCTGTAAGAACCGAGCAATTCCT 1219
Qy 1141 AAAAAGCATTTTTCGAGCCCTTGTGACTATACAGTGAACAGTCTGAAAAAGCGCAGG 1200
Db 1220 AAAAAGCATTTTTCGAGCCCTTGTGACTATACAGTGAACAGTCTGAAAAAGCGCAGG 1279
Qy 1201 CTACAGAGAGCTGTGACAGTAAACAAGGGGACGCGATTAAGCGCTTGTACAGATGCC 1260
Db 1280 CTACAGAGAGCTGTGACAGTAAACAAGGGGACGCGATTAAGCGCTTGTACAGATGCC 1339
Qy 1261 TGGGCGCTGTTGATCTCTCTCCGCTTCCCTTCCCTTCCGACAGCAACCACTCAAGTCTC 1320
Db 1340 TGGGCGCTGTTGATCTCTCTCCGCTTCCCTTCCCTTCCGACAGCAACCACTCAAGTCTC 1399
Qy 1321 CTGCTCGAAGATCTTCTTAACCTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTA 1380
Db 1400 CTGCTCGAAGATCTTCTTAACCTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTA 1459
Qy 1381 TTTTACCCAGAGAAAGCTTCATTTTGTCTTCAACATTTGATGAAATTTCTGTCTACTGCCACA 1440
Db 1460 TTTTACCCAGAGAAAGCTTCATTTTGTCTTCAACATTTGATGAAATTTCTGTCTACTGCCACA 1519
Qy 1441 ACAGAGGTTCTGCGGAGAGAGATATTAACAGGCTGCGCTGCTGTTGGTTCCTCAAGTT 1500
Db 1520 ACAGAGGTTCTGCGGAGAGAGATATTAACAGGCTGCGCTGCTGTTGGTTCCTCAAGTT 1579

Qy 1501 CTTACGCCAAACATACATGATCCCATGAGACAGCGGAGAAAGCCCTGCTCTTAAGATA 1560
Db 1580 CTTACGCCAAACATACATGATCCCATGAGACAGCGGAGAAAGCCCTGCTCTTAAGATA 1639
Qy 1561 TCCATCTCTCTCTGAAACAAATTTTTCCTTACCTTACAGATGACCCCTCAATCCCATTC 1620
Db 1640 TCCATCTCTCTCTGAAACAAATTTTTCCTTACCTTACAGATGACCCCTCAATCCCATTC 1699
Qy 1621 ATATAGTGGGTTCAGAGAACCGGACATAGCCCGTTTATTTGGGTTCTCTACAAAT----AG 1676
Db 1700 ATATAGTGGGTTCAGAGAACCGGACATAGCCCGTTTATTTGGGTTCTCTACAAATAGAGAG 1759
Qy 1677 AAATCCMAAGAACCAACCCAGATGAGAAATTTTGAAGCAATGTGTTTGTGCTGC 1736
Db 1760 AAATCCMAAGAACCAACCCAGATGAGAAATTTTGAAGCAATGTGTTTGTGCTGC 1819
Qy 1737 AGGCAATAGATAGGATTTATCTATTCAAGAAAGACTCAACATTTCTTAAAGCATGGG 1796
Db 1820 AGGCAATAGATAGGATTTATCTATTCAAGAAAGACTCAACATTTCTTAAAGCATGGG 1879
Qy 1797 ATCTTAATCATCTAAAGGTTTCTCTCAAGAGATGCTCTGTGTTGGAGAGAGAAAGCC 1856
Db 1880 ATCTTAATCATCTAAAGGTTTCTCTCAAGAGATGCTCTGTGTTGGAGAGAGAAAGCC 1939
Qy 1857 CCAGCAAGATATGTCAGAGCAACATCCAGCTTCATGCGCAGCAGGTGGCGAGAAATCTTC 1916
Db 1940 CCAGCAAGATATGTCAGAGCAACATCCAGCTTCATGCGCAGCAGGTGGCGAGAAATCTTC 1999
Qy 1917 CTCACAGAGAGGCGCATTTTATGTGTGTGAGAGATGCAAAAGATTTGGCCAAAGATGTA 1976
Db 2000 CTCACAGAGAGGCGCATTTTATGTGTGTGAGAGATGCAAAAGATTTGGCCAAAGATGTA 2059
Qy 1977 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGGTTGAGTTGAAAACTAAGAGCAATG 2036
Db 2060 CATGATGCCCTTGTGCAATTAATTAAGCAAGAGGTTGAGTTGAAAACTAAGAGCAATG 2119
Qy 2037 AAAACCTGCGCATTTAAGAGAGAGAAACGCTACCTTCAAGATATTTGGTCATTA 2093
Db 2120 AAAACCTGCGCATTTAAGAGAGAGAAACGCTACCTTCAAGATATTTGGTCATTA 2176

RESULT 2
US-09-949-016-4215
; Sequence 4215, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 4215
; LENGTH: 3242
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4215

Query Match 78.4%; Score 1640; DB 4; Length 3242;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2090; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
Qy 1 ATGAGAGGTTTCTGTTACTATATGCTTACACAGAGGAGCAAGGCAATGCGAGAA 60
|||||

80 ATGAGAGGTTTCTGTACTATATGCTACACAGCAGGAGCAGCAAGCCATCCGAGAA 139
QY
61 GAAATGTGACCAAGCTGTGTATCATGTATTTCTGAGATCTTCACTGTATGTAGA 120
DB
140 GAAATATGTGACCAAGCTGTGTATCATGTATTTCTGAGATCTTCACTGTATGTAGA 199
QY
121 TCCGATTAAGTATGACCTTAATAAACCGGAAACAGCTCTCTGTGTGTGTGTCTACACG 180
DB
200 TCCGATTAAGTATGACCTTAATAAACCGGAAACAGCTCTCTGTGTGTGTGTCTACACG 259
QY
181 GGCACCGAGAGCCCAACCCGACAAGCCCGCAAGTTTGAAGAAATACAGAACCAACA 240
DB
260 GGCACCGAGAGCCCAACCCGACAAGCCCGCAAGTTTGAAGAAATACAGAACCAACA 319
QY
241 CTGCGCGGTGATTTCTTTGCTCACTGCGGTATGGGTTACTGGGTCTCGGTATTCAGAA 300
DB
330 CTGCGCGGTGATTTCTTTGCTCACTGCGGTATGGGTTACTGGGTCTCGGTATTCAGAA 379
QY
301 TACACCTACTTTTGAAGTGGGGGAAAGATTAATGATTAACGACTTCAAGAGCTTGAGCC 360
DB
380 TACACCTACTTTTGAAGTGGGGGAAAGATTAATGATTAACGACTTCAAGAGCTTGAGCC 439
QY
361 CCGCATTTCTATGACACTGACATGACATGATGATGTATGATTTAGAACTTGTGTAG 420
DB
440 CCGCATTTCTATGACACTGACATGACATGATGATGTATGATTTAGAACTTGTGTAG 499
QY
421 CCGTGATTTGCTGACACTGCGCAAGCCCTCAGAAAGCAATTTTATGTTCAAGCAGAGCA 480
DB
500 CCGTGATTTGCTGACACTGCGCAAGCCCTCAGAAAGCAATTTTATGTTCAAGCAGAGCA 559
QY
481 GAGGAGTAAAGTGGGCACTCCCGGTGGGATCACTGCACTCTGAGAGCAGACCTGTG 540
DB
560 GAGGAGTAAAGTGGGCACTCCCGGTGGGATCACTGCACTCTGAGAGCAGACCTGTG 619
QY
541 AAGTCAGAGCTGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB
620 AAGTCAGAGCTGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 679
QY
601 AGAAGAGATTTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATTCATGTTGTA 660
DB
680 AGAAGAGATTTGAGGTTTGAAGCAAAATGCAAGTGAACAGCAACCAATTCATGTTGTA 739
QY
661 ATTGAAGACTTTGAGGCTCACTTACCGGTGGGATCCCGCACTCTCAAGGCTGTG 720
DB
740 ATTGAAGACTTTGAGGCTCACTTACCGGTGGGATCCCGCACTCTCAAGGCTGTG 799
QY
721 AATATTCCTGTTTACCCCAAGATATTTACAGGTATCTGCAAGAGTCTTGTGCGCAG 780
DB
800 AATATTCCTGTTTACCCCAAGATATTTACAGGTATCTGCAAGAGTCTTGTGCGCAG 859
QY
781 GAGGAAAGCCAAATCTGTGACTTCAAGATCCAGTTTTCAGTGTCCAAATTTCAAG 840
DB
860 GAGGAAAGCCAAATCTGTGACTTCAAGATCCAGTTTTCAGTGTCCAAATTTCAAG 919
QY
841 GCGATTCATTTCTACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB
920 GCGATTCATTTCTACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 979
QY
901 TCAATATACAGATTTTCTATCAGCTGAGATGCTTCAAGCTGTGATCTGCTTACAGT 960
DB
980 TCAATATACAGATTTTCTATCAGCTGAGATGCTTCAAGCTGTGATCTGCTTACAGT 1039
QY
961 GATTCGAGGTACAAAGCTTCAAGAGCTGAGCTTGAAGATTAAGAGAGCAGCTGC 1020
DB
1040 GATTCGAGGTACAAAGCTTCAAGAGCTGAGCTTGAAGATTAAGAGAGCAGCTGC 1099
QY
1021 GTGCTTTGAAAATTAAGAGAGACAAAGAAAGAGAGCTTCAAGCTTCAAGCTTCA 1080
DB
1100 GTGCTTTGAAAATTAAGAGAGACAAAGAAAGAGAGCTTCAAGCTTCAAGCTTCA 1159
QY
1081 CTTGCGGAGATGTTCTCTCAGATTCATTTTATCTGTGTCTGAAATCCGAGCAATTCCT 1140
DB
1160 CTTGCGGAGATGTTCTCTCAGATTCATTTTATCTGTGTCTGAAATCCGAGCAATTCCT 1219

1141 AAAAGGATTTTTCGAGCCCTTGTGACTATACAGTGAACAGTGTGAAAAGCGCAG 1200
QY
1220 AAAAGGATTTTTCGAGCCCTTGTGACTATACAGTGAACAGTGTGAAAAGCGCAG 1279
DB
1201 CTACAGAGCTGTGCAATTAACAGAGGAGCCGATTAATAGCCCTTGTGTACAGATGCTC 1260
QY
1280 CTACAGAGCTGTGCAATTAACAGAGGAGCCGATTAATAGCCCTTGTGTACAGATGCTC 1339
DB
1261 TGTGCTGCTGTGTGAACT 1320
QY
1340 TGTGCTGCTGTGTGAACT 1399
DB
1321 CTGCTGAAACCTTCTTAACCTTCAACCCAGACCAATTAATGCTGTGCAAGCTCAAGTTTA 1380
QY
1400 CTGCTGAAACCTTCTTAACCTTCAACCCAGACCAATTAATGCTGTGCAAGCTCAAGTTTA 1459
DB
1381 TTTCAACCAAGAAAGCTCAATTTGTCTTCAACATTTGTGAAATTTCTGTCTACTGACACA 1440
QY
1460 TTTCAACCAAGAAAGCTCAATTTGTCTTCAACATTTGTGAAATTTCTGTCTACTGACACA 1519
DB
1441 ACAAGGTTCTGCGGAGAGGATATGTACAGCTGTGCTGTGTGTGTGTGTGTGTGTGT 1500
QY
1520 ACAAGGTTCTGCGGAGAGGATATGTACAGCTGTGCTGTGTGTGTGTGTGTGTGTGT 1579
DB
1501 CTTGAGCCAAACATACATGCAATCCCATGAAAGCAGCGGAAAGCCCTGCTCTTAAGATA 1560
QY
1580 CTTGAGCCAAACATACATGCAATCCCATGAAAGCAGCGGAAAGCCCTGCTCTTAAGATA 1639
DB
1561 TCCATCTCTCTCTGAAACCAAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
QY
1640 TCCATCTCTCTCTGAAACCAAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1699
DB
1621 ATATATGTGTGTGTGCAAGAACCGGCAATAGCCCGTTTATTTGGTTCTTACAACAT 1676
QY
1700 ATATATGTGTGTGTGCAAGAACCGGCAATAGCCCGTTTATTTGGTTCTTACAACAT 1759
DB
1677 AAATCTCAAGAAACCAACCCAGATGAAATTTTGGAGCAATGTTTGTGTTTGGCTGC 1736
QY
1760 AAATCTCAAGAAACCAACCCAGATGAAATTTTGGAGCAATGTTTGTGTTTGGCTGC 1819
DB
1737 AGGCAATAGAGATGAGGATTTATCTATTCAGAAAGAGCTCAGACATTTCTTAAGCATG 1796
QY
1820 AGGCAATAGAGATGAGGATTTATCTATTCAGAAAGAGCTCAGACATTTCTTAAGCATG 1879
DB
1797 ATCTTAATCTATTAAGGTTTCTTCTCAAGATGCTCTGTTGGGAGAGAGAGCC 1856
QY
1880 ATCTTAATCTATTAAGGTTTCTTCTCAAGATGCTCTGTTGGGAGAGAGAGCC 1939
DB
1857 CCAAGAAAGTATGTAACAAGCAACATCCAGCTTCAATGCGCAGCAGGTGCGAAGATCTTC 1916
QY
1940 CCAAGAAAGTATGTAACAAGCAACATCCAGCTTCAATGCGCAGCAGGTGCGAAGATCTTC 1999
DB
1917 CTTCAGAGAAAGGCGCAATTTATGTGTGTGAGATGCAAGAAATATGCGCAAGATGTA 1976
QY
2000 CTTCAGAGAAAGGCGCAATTTATGTGTGTGAGATGCAAGAAATATGCGCAAGATGTA 2059
DB
1977 CATGATGCTCTTGTGCAATTAATAGCAAGAGGTTGAGTTGAAAACCTAGAGCAATG 2036
QY
2060 CATGATGCTCTTGTGCAATTAATAGCAAGAGGTTGAGTTGAAAACCTAGAGCAATG 2119
DB
2037 AAAACCTGCGCACTTTAAAGAAAGAAACCTTCAAGATTTTGTGATTA 2093
QY
2120 AAAACCTGCGCACTTTAAAGAAAGAAACCTTCAAGATTTTGTGATTA 2176
DB

RESULT 3
US-08-905-223-71
Sequence 71, Application US/08905223
Patent No. 6222029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duclercq, Aymeric

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 15957
LENGTH: 35916
TYPE: DNA
ORGANISM: Human
US-09-949-016-15957

Query Match 15.8%; Score 330; DB 4; Length 35916;
Best Local Similarity 99.7%; Pred. No. 2.3e-159;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGAGCCGTGATTTGCTGGAATCTGGCCAGCCCTCAGAAAGCATT 460
DB 10781 GTTTAGAACTTGTGAGCCGTGATTTGCTGGAATCTGGCCAGCCCTCAGAAAGCATT 10840
QY 461 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCCACTCCCGGTGGCATCACTGCAT 520
DB 10841 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCCACTCCCGGTGGCATCACTGCAT 10900
QY 521 CCTTGAGACAGACCTTGTGAAGTCAAGCTGCTACATTTGAATCTCAAGTCGAGCTTC 580
DB 10901 CCTTGAGACAGACCTTGTGAAGTCAAGCTGCTACATTTGAATCTCAAGTCGAGCTTC 10960
QY 581 TGAGATTCGATGATTCAGAGAAAGAGATTTGAGGTTTGAAGCAAAATGACAGTAAACA 640
DB 10961 TGAGATTCGATGATTCAGAGAAAGAGATTTGAGGTTTGAAGCAAAATGACAGTAAACA 11020
QY 641 GCAACCAATCCAAATGTTGATTTGAAGACTTTGAGTCTCACTTACCCTGCGTACCCC 700
DB 11021 GCAACCAATCCAAATGTTGATTTGAAGACTTTGAGTCTCACTTACCCTGCGTACCCC 11080
QY 701 CACTCTCAAGCCTCTCTGATATTTCTGTTTACCCCAAGATTTTACAGGTACATC 760
DB 11081 CACTCTCAAGCCTCTCTGATATTTCTGTTTACCCCAAGATTTTACAGGTACATC 11140
QY 761 TGCAGAGTCTCTGGCCAGG 781
DB 11141 TGCAGAGTCTCTGGCCAGG 11161

RESULT 6

US-09-949-016-150020
Sequence 150020, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 150020
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-150020

Query Match

13.3%; Score 279; DB 4; Length 601;

Best Local Similarity 99.5%; Pred. No. 3.5e-133;
Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 401 GTTTAGAACTTGTGAGCCGTGATTTGCTGGAATCTGGCCAGCCCTCAGAAAGCATT 460
DB 165 GTTTAGAACTTGTGAGCCGTGATTTGCTGGAATCTGGCCAGCCCTCAGAAAGCATT 224
QY 461 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCCACTCCCGGTGGCATCACTGCAT 520
DB 225 TTAGGTCAAGCAGAGCAAGAGAGATTAAGTGGCCACTCCCGGTGGCATCACTGCAT 284
QY 521 CCTTGAGACAGACCTTGTGAAGTCAAGCTGCTACATTTGAATCTCAAGTCGAGCTTC 580
DB 285 CCTTGAGACAGACCTTGTGAAGTCAAGCTGCTACATTTGAATCTCAAGTCGAGCTTC 344
QY 581 TGAGATTCGATGATTCAGAGAAAGAGATTTGAGGTTTGAAGCAAAATGACAGTAAACA 640
DB 345 TGAGATTCGATGATTCAGAGAAAGAGATTTGAGGTTTGAAGCAAAATGACAGTAAACA 404
QY 641 GCAACCAATCCAAATGTTGATTTGAAGACTTTGAGTCTCACTTACCCTGCGTACCCC 700
DB 405 GCAACCAATCCAAATGTTGATTTGAAGACTTTGAGTCTCACTTACCCTGCGTACCCC 464
QY 701 CACTCTCAAGCCTCTCTGATATTTCTGTTTACCCCAAGATTTTACAGGTACATC 760
DB 465 CACTCTCAAGCCTCTCTGATATTTCTGTTTACCCCAAGATTTTACAGGTACATC 524
QY 761 TGCAGAGTCTCTGGCCAGG 781
DB 525 TGCAGAGTCTCTGGCCAGG 545

RESULT 7

US-09-949-016-150037
Sequence 150037, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 150037
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-150037

Query Match 9.0%; Score 189; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 8.6e-87;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1369 AGCTCAAGTTATTTTACCCAGGAAGCTCCATTTGCTTCAACATTTGGAATTTCTG 1428
DB 18 AGCTCAAGTTATTTTACCCAGGAAGCTCCATTTGCTTCAACATTTGGAATTTCTG 77
QY 1429 TCTACTGCCACAAGAGGTTCTGGGAAAGGAGATATGACAGGCTGCTGCTTGTG 1488
DB 78 TCTACTGCCACAAGAGGTTCTGGGAAAGGAGATATGACAGGCTGCTGCTTGTG 137
QY 1489 GTTGCTTCAAGTTCTTCAAGCAATCATGATCTCCATGAAAGACGCGGAAAGCCCTG 1548
DB 138 GTTGCTTCAAGTTCTTCAAGCAATCATGATCTCCATGAAAGACGCGGAAAGCCCTG 197

QY 1549 GCTCCTTAG 1557
Db 198 GCTCCTTAG 206

RESULT 8

US-09-566-921-88
; Sequence 89, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 88
; LENGTH: 2475
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 255828.26
; LOCATION: 1001, 1011
; OTHER INFORMATION: a, t, c, g, or other
US-09-566-921-88

Query Match 7.5%; Score 158; DB 4; Length 2475;
Best Local Similarity 100.0%; Pred. No. 8.9e-71;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 525 GAGACAGACCTTGTGAGTCAAGCTGTACACATTAATCAAGTCAGCTTCTGAG 584
Db 16 GAGACAGACCTTGTGAGTCAAGCTGTACACATTAATCAAGTCAGCTTCTGAG 75
QY 585 ATTGGATGATTCAGGAAGAAAGATTCAGGTTTGAAGCAAAATGCAATGAAACGAA 644
Db 76 ATTGGATGATTCAGGAAGAAAGATTCAGGTTTGAAGCAAAATGCAATGAAACGAA 135
QY 645 CCAATCCAAATGTTGTAATGAAGCTTTGAGTCTGAC 682
Db 136 CCAATCCAAATGTTGTAATGAAGCTTTGAGTCTGAC 173

RESULT 9

US-09-949-016-150030
; Sequence 150030, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150030
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150030

Query Match 7.4%; Score 155; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 2.9e-69;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 904 AATACAGACTTTTCCATCAGCTGAGATGCTTCAAGCTGATCTGCCCTAAGTAT 963
Db 320 AATACAGACTTTTCCATCAGCTGAGATGCTTCAAGCTGATCTGCCCTAAGTAT 379
QY 964 TCTGAGTCAAAAGCTTCTCCAAAGACTGCACTTGAAGATTAAGAAGACACTGCGTC 1023
Db 380 TCTGAGTCAAAAGCTTCTCCAAAGACTGCACTTGAAGATTAAGAAGACACTGCGTC 439
QY 1024 CTTTGAATAATAAGGACAGACAAAGAAAGG 1058
Db 440 CTTTGAATAATAAGGACAGACAAAGAAAGG 474

RESULT 10

US-09-949-016-150031
; Sequence 150031, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150031
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150031

Query Match 6.9%; Score 145; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 4.1e-64;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 904 AATACAGACTTTTCCATCAGCTGAGATGCTTCAAGCTGATCTGCCCTAAGTAT 963
Db 156 AATACAGACTTTTCCATCAGCTGAGATGCTTCAAGCTGATCTGCCCTAAGTAT 215
QY 964 TCTGAGTCAAAAGCTTCTCCAAAGACTGCACTTGAAGATTAAGAAGACACTGCGTC 1023
Db 216 TCTGAGTCAAAAGCTTCTCCAAAGACTGCACTTGAAGATTAAGAAGACACTGCGTC 275
QY 1024 CTTTGAATAATAAGGACAGACAA 1048
Db 276 CTTTGAATAATAAGGACAGACAA 300

RESULT 11

US-09-949-016-150046
; Sequence 150046, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 150046
;; LENGTH: 601
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-150046

Query Match 6.5%; Score 137; DB 4; Length 601;
Best Local Similarity 99.5%; Pred. No. 5.5e-60;
Matches 187; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1761 TTCAGAAAAGACTCTGATGATTTCTTAAGCATGGATTTTAATCTTAAGTTTC 1820
Db 413 TTCAGAAAAGACTCTGATGATTTCTTAAGCATGGATTTTAATCTTAAGTTTC 472
Qy 1821 TTCTCAAGATGCTCTGTTGGGAGAGAGAAAGCCCGAAGATGTAACAAGCAAC 1880
Db 473 TTCTCAAGATGCTCTGTTGGGAGAGAGAAAGCCCGAAGATGTAACAAGCAAC 532
Qy 1881 ATCCAGCTTCATGGCCAGAGGTGGGAGAAATCTCTCCAGAGAAAGCGCATATTAT 1940
Db 533 ATCCAGCTTCATGGCCAGAGGTGGGAGAAATCTCTCCAGAGAAAGCGCATATTAT 592
Qy 1941 GTGTGTGG 1948
Db 593 GTGTGTGG 600

RESULT 12

US-09-949-016-150047
; Sequence 150047, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150047
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150047

Query Match 6.5%; Score 137; DB 4; Length 601;
Best Local Similarity 99.5%; Pred. No. 5.5e-60;
Matches 187; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1761 TTCAGAAAAGACTCTGATGATTTCTTAAGCATGGATTTTAATCTTAAGTTTC 1820
Db 191 TTCAGAAAAGACTCTGATGATTTCTTAAGCATGGATTTTAATCTTAAGTTTC 250
Qy 1821 TTCTCAAGATGCTCTGTTGGGAGAGAGAAAGCCCGAAGATGTAACAAGCAAC 1880
Db 251 TTCTCAAGATGCTCTGTTGGGAGAGAGAAAGCCCGAAGATGTAACAAGCAAC 310
Qy 1881 ATCCAGCTTCATGGCCAGAGGTGGGAGAAATCTCTCCAGAGAAAGCGCATATTAT 1940
Db 311 ATCCAGCTTCATGGCCAGAGGTGGGAGAAATCTCTCCAGAGAAAGCGCATATTAT 370

Qy 1941 GTGTGTGG 1948
Db 371 GTGTGTGG 378

RESULT 13

US-09-949-016-150029
; Sequence 150029, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150029
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150029

Query Match 6.0%; Score 125; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 8.4e-54;
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 779 AGAGGAAAGCCAGATATCTGATCTGATCAGAGATCCAGTTTCAAGTCCCAATTCA 838
Db 379 AGAGGAAAGCCAGATATCTGATCTGATCAGAGATCCAGTTTCAAGTCCCAATTCA 438
Qy 839 AGGAGTTCACTTCTAGCAATGATGCTTAATAAACCACTGTGTGAATTTGACA 898
Db 439 AGGAGTTCACTTCTAGCAATGATGCTTAATAAACCACTGTGTGAATTTGACA 498
Qy 899 TTTCA 903
Db 499 TTTCA 503

RESULT 14

US-09-949-016-150041
; Sequence 150041, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150041
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150041

Query Match 5.8%; Score 121; DB 4; Length 601;

Best Local Similarity 100.0%; Pred. No. 9.7e-52;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1556 AGATATCCATCTCTCTCGAACAACAATCTTTCACATGACGATGACCCCTCAATCC 1615
|
Db 124 AGATATCCATCTCTCTCGAACAACAATCTTTCACATGACGATGACCCCTCAATCC 183

QY 1616 CCATCATTAATGGTGGGTCCAGAAACCGGCATAGCCCGTTTATTGGGTCTTCAACATA 1675
|
Db 184 CCATCATTAATGGTGGGTCCAGAAACCGGCATAGCCCGTTTATTGGGTCTTCAACATA 243

QY 1676 G 1676
|
Db 244 G 244

RESULT 15

US-09-949-016-150042
; Sequence 150042, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150042
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150042

Query Match 5.8%; Score 121; DB 4; Length 601;

Best Local Similarity 100.0%; Pred. No. 9.7e-52;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1556 AGATATCCATCTCTCTCGAACAACAATCTTTCACATGACGATGACCCCTCAATCC 1615
|
Db 95 AGATATCCATCTCTCTCGAACAACAATCTTTCACATGACGATGACCCCTCAATCC 154

QY 1616 CCATCATTAATGGTGGGTCCAGAAACCGGCATAGCCCGTTTATTGGGTCTTCAACATA 1675
|
Db 155 CCATCATTAATGGTGGGTCCAGAAACCGGCATAGCCCGTTTATTGGGTCTTCAACATA 214

QY 1676 G 1676
|
Db 215 G 215

Search completed: August 27, 2005, 16:18:22
Job time : 237.308 secs

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OM nucleic - nucleic search, using sw model

Run on: August 27, 2005, 00:17:56 ; Search time 898.684 Seconds
(without alignments)
15238.608 Million cell updates/sec

Title: US-09-371-347A-47

Perfect score: 2093
Sequence: 1 atgagagaggttctgttact.....ttcagatatgtgcataa 2093

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 7331713 seqs, 3271544945 residues

Word size : 0

Total number of hits satisfying chosen parameters: 14663426

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Published Applications NA.*
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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	2093	100.0	2093	10	US-09-371-347-47
2	1793	85.7	2097	10	US-09-371-347-1
3	1793	85.7	3259	10	US-09-371-347-24
4	1742	83.2	2097	10	US-09-371-347-41
5	1742	83.2	2097	10	US-09-371-347-43
6	1677	80.1	2094	10	US-09-371-347-45
7	879	42.0	3256	21	US-10-741-600-692

	8	879	42.0	3274	21	US-10-741-600-693	Sequence 693, App
	9	330	15.8	591	16	US-10-029-386-6369	Sequence 6369, App
	10	328	15.7	379	16	US-10-029-386-60100	Sequence 20100, A
	11	279	13.3	591	16	US-10-029-386-1735	Sequence 1735, App
	12	277	13.2	379	16	US-10-029-386-15435	Sequence 15435, A
	13	266	12.7	43985	21	US-10-741-600-17757	Sequence 17757, A
	14	188	9.0	525	16	US-10-029-386-6533	Sequence 6533, App
	15	175	8.4	175	16	US-10-029-386-14338	Sequence 14338, A
	16	158	7.5	2475	10	US-09-909-5678-38	Sequence 38, App1
	17	158	7.5	2475	22	US-10-765-760-88	Sequence 88, App1
	18	158	7.5	21852	21	US-10-741-600-17986	Sequence 17986, A
	19	150	7.2	201	21	US-10-741-600-15583	Sequence 15583, A
	20	150	7.2	201	21	US-10-741-600-15584	Sequence 15584, A
	21	150	7.2	201	21	US-10-741-600-15589	Sequence 15589, A
	22	150	7.2	201	21	US-10-741-600-15590	Sequence 15590, A
	23	150	7.2	201	21	US-10-741-600-15592	Sequence 15592, A
	24	150	7.2	201	21	US-10-741-600-15594	Sequence 15594, A
	25	150	7.2	201	21	US-10-741-600-15598	Sequence 15598, A
	26	150	7.2	201	21	US-10-741-600-15599	Sequence 15599, A
	27	150	7.2	201	21	US-10-741-600-15600	Sequence 15600, A
	28	150	7.2	201	21	US-10-741-600-15605	Sequence 15605, A
	29	150	7.2	201	21	US-10-741-600-15609	Sequence 15609, A
	30	150	7.2	201	21	US-10-741-600-15610	Sequence 15610, A
	31	150	7.2	201	21	US-10-741-600-15612	Sequence 15612, A
	32	150	7.2	201	21	US-10-741-600-15613	Sequence 15613, A
	33	150	7.2	201	21	US-10-741-600-15614	Sequence 15614, A
	34	150	7.2	201	21	US-10-741-600-15620	Sequence 15620, A
	35	150	7.2	201	21	US-10-741-600-15621	Sequence 15621, A
	36	150	7.2	201	21	US-10-741-600-15623	Sequence 15623, A
	37	150	7.2	201	21	US-10-741-600-15625	Sequence 15625, A
	38	150	7.2	201	21	US-10-741-600-15629	Sequence 15629, A
	39	150	7.2	201	21	US-10-741-600-15630	Sequence 15630, A
	40	150	7.2	201	21	US-10-741-600-15631	Sequence 15631, A
	41	150	7.2	201	21	US-10-741-600-15637	Sequence 15637, A
	42	150	7.2	201	21	US-10-741-600-15640	Sequence 15640, A
	43	150	7.2	201	21	US-10-741-600-15641	Sequence 15641, A
	44	150	7.2	201	21	US-10-741-600-15643	Sequence 15643, A
	45	150	7.2	201	21	US-10-741-600-53894	Sequence 53894, A

ALIGNMENTS

RESULT 1
US-09-371-347-47
; Sequence 47, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE.
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 2093
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-371-347-47

Query Match 100.0% Score 2093; DB 10; Length 2093;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||

[illegible]

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Db	1141	AAAAAGCATTTTGTGCAAGCCCTTGTCACATATACAGTACAGTGTGTGA AAAAGCGCAGG	1200
OY	1201	CTACAGAGCTGTGTGCATTAACAAGGGGAGCCGATATATAGCCGTTTGTATACAGATGCC	1260
Db	1201	CTACAGAGCTGTGTGCATTAACAAGGGGAGCCGATATATAGCCGTTTGTATACAGATGCC	1260
OY	1261	TGTGCTGCTTGTGTGGATCTCTCTCTGCTTCCCTTCTTGCCAGCCACCATCAGTCTC	1320
Db	1261	TGTGCTGCTTGTGTGGATCTCTCTCTGCTTCCCTTCTTGCCAGCCACCATCAGTCTC	1320
OY	1321	CTGCTCGAACATCTTCCCTAAACTTCAACCAGACCATATTCGTGTGAGAGTCAGTTA	1380
Db	1321	CTGCTCGAACATCTTCCCTAAACTTCAACCAGACCATATTCGTGTGAGAGTCAGTTA	1380
OY	1381	TTTTCAACCAGAAGAGCTCCATTTTGTCTTCAACATTTGTGAAATTTCTGTCTACAGCAC	1440
Db	1381	TTTTCAACCAGAAGAGCTCCATTTTGTCTTCAACATTTGTGAAATTTCTGTCTACAGCAC	1440
OY	1441	ACAGAGGTTCTGCGGAAGGAGTAGTAGAGGCTGSGCTGSGCTGTTGTTGGCTTCAGTT	1500
Db	1441	ACAGAGGTTCTGCGGAAGGAGTAGTAGAGGCTGSGCTGSGCTGTTGTTGGCTTCAGTT	1500
OY	1501	CTTACAGCCMAACATATCATGTCAATCCCATGMAAGACAGCGGGGAAAAGCCCTGCTCTAAGATA	1560
Db	1501	CTTACAGCCMAACATATCATGTCAATCCCATGMAAGACAGCGGGGAAAAGCCCTGCTCTAAGATA	1560
OY	1561	TCCATCTCTCCTCGSAAACAAATTTCTTCCACTTACAGATGACCCCTCATGCCATC	1620
Db	1561	TCCATCTCTCCTCGSAAACAAATTTCTTCCACTTACAGATGACCCCTCATGCCATC	1620
OY	1621	ATPATGTGTGGTCCAGAAACCGGCATAGCCCCGTTTATGGGTTCTTACAAACATAGAAAC	1680
Db	1621	ATPATGTGTGGTCCAGAAACCGGCATAGCCCCGTTTATGGGTTCTTACAAACATAGAAAC	1680
OY	1681	TCCAGAAACAAACACCCAGATGGAAATTTGGAGCAATGTGTGTTTGGCTGCAGGC	1740
Db	1681	TCCAGAAACAAACACCCAGATGGAAATTTGGAGCAATGTGTGTTTGGCTGCAGGC	1740
OY	1741	ATAAGSATAGGGATTTATCTATTTCAGAAAAGAGCTCAGACATTTCTTAAGCATGGATCT	1800
Db	1741	ATAAGSATAGGGATTTATCTATTTCAGAAAAGAGCTCAGACATTTCTTAAGCATGGATCT	1800
OY	1801	TAACTCATCTAAGAGTTTCTTCTCAAGAGATGCTCTGTGGGAGAGAGAACCCCCAG	1860
Db	1801	TAACTCATCTAAGAGTTTCTTCTCAAGAGATGCTCTGTGGGAGAGAGAACCCCCAG	1860
OY	1861	CMAAGTATGTATCAGACAAACATCCAAGCTTACATGGCCAGAGTGGCGAGATCTCTCTCC	1920
Db	1861	CMAAGTATGTATCAGACAAACATCCAAGCTTACATGGCCAGAGTGGCGAGATCTCTCTCC	1920
OY	1921	AGGAGAACGGCCATATTTATGTGTGTGGAGATGCAAAAGATATATGSCCAAAGATGTACATG	1980
Db	1921	AGGAGAACGGCCATATTTATGTGTGTGGAGATGCAAAAGATATATGSCCAAAGATGTACATG	1980
OY	1981	ATGCCCTTGTGCAATATATATAGCAAAAGGTTGAGTTGAABAACTAGAGCAATGAAAA	2040
Db	1981	ATGCCCTTGTGCAATATATATAGCAAAAGGTTGAGTTGAABAACTAGAGCAATGAAAA	2040
OY	2041	CCCTGTGGCCATTTTAAAGAGAAAAAGCTACCTTACAGATATTTGGTCACTA	2093
Db	2041	CCCTGTGGCCATTTTAAAGAGAAAAAGCTACCTTACAGATATTTGGTCACTA	2093

RESULT 2
US-09-371-347-1
; Sequence 1, Application US/09371347
; Publication No. US2003008267A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Grave et al.,
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE

TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
FILE OF INVENTION: DEFECTS CARDIOVASCULAR DISEASE, AND CANCER
FILE REFERENCE: 50004/003003
CURRENT APPLICATION NUMBER: US/09/371,347
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: 60/071,622
PRIOR FILING DATE: 1998-01-16
PRIOR APPLICATION NUMBER: 09/232,028
PRIOR FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2097
TYPE: DNA
ORGANISM: Homo sapiens
US-09-371-347-1

Query Match 85.7%; Score 1793; DB 10; Length 2097;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2093; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 ATGAGAGGTTCTGTTACTATATGCTACACAGAGGAGAGGCAAGCCATCGAGAA 60
DB 1 ATGAGAGGTTCTGTTACTATATGCTACACAGAGGAGAGGCAAGCCATCGAGAA 60
QY 61 GAAATGTCAGCAAGCTGTGTCATGATTTCTGAGATCTTCACTGATTTAGTAA 120
DB 61 GAAATGTCAGCAAGCTGTGTCATGATTTCTGAGATCTTCACTGATTTAGTAA 120
QY 121 TCCGATTAAGTATGACTTAATAAACCAGAAAGCTCTCTGTTGTTGTTCTACACAG 180
DB 121 TCCGATTAAGTATGACTTAATAAACCAGAAAGCTCTCTGTTGTTGTTCTACACAG 180
QY 181 GGCACCGAGAGCCACCCGACACAGCCGCAAGTTGTTAAGAAATACAGAAACCAAA 240
DB 181 GGCACCGAGAGCCACCCGACACAGCCGCAAGTTGTTAAGAAATACAGAAACCAAA 240
QY 241 CTGCGGTTGATTTCTTCTGCTACCTGCGGATAGGTTACTGCTGCTGCTGCTGCTG 300
DB 241 CTGCGGTTGATTTCTTCTGCTACCTGCGGATAGGTTACTGCTGCTGCTGCTGCTG 300
QY 301 TACACCTACTTTTGAAGTGGGGAGATTAATTGATTAAGCACTTCAAGAGCTTGAGCC 360
DB 301 TACACCTACTTTTGAAGTGGGGAGATTAATTGATTAAGCACTTCAAGAGCTTGAGCC 360
QY 361 CGGCACTTTCTATGACACTGAGACATGCAATGACTGTGATGTTAGAACCTTGTTGAG 420
DB 361 CGGCACTTTCTATGACACTGAGACATGCAATGACTGTGATGTTAGAACCTTGTTGAG 420
QY 421 CCGTGAATGTCGAGACTGTGCGGACGCTTCAAGAAACATTTTAAAGTCAAGAGAGCA 480
DB 421 CCGTGAATGTCGAGACTGTGCGGACGCTTCAAGAAACATTTTAAAGTCAAGAGAGCA 480
QY 481 GAGAGATTAAGTGGCGCACTCCGCGTGGATCACTGCACTCTTGAGAGACAGCTTGG 540
DB 481 GAGAGATTAAGTGGCGCACTCCGCGTGGATCACTGCACTCTTGAGAGACAGCTTGG 540
QY 541 AAGTCAGAGCTGTCACATTTGATCTCAAGTGAAGCTTCTGAGATTCAGATTCAGAA 600
DB 541 AAGTCAGAGCTGTCACATTTGATCTCAAGTGAAGCTTCTGAGATTCAGATTCAGAA 600
QY 601 AGAAAGATTTGAGGTTTGAAGCAAAATGAGTAAAGCAACCAATTCGAATGTTGTA 660
DB 601 AGAAAGATTTGAGGTTTGAAGCAAAATGAGTAAAGCAACCAATTCGAATGTTGTA 660
QY 661 ATGAGAGCTTTGAGTCTCACTTACCCGTTGCGTACCCCACTCTCAAGAGCTCTG 720
DB 661 ATGAGAGCTTTGAGTCTCACTTACCCGTTGCGTACCCCACTCTCTCAAGAGCTCTG 720
QY 721 AATATTCCTGTTTACCCCAAGATATTTAAGATACATTCAGAGAGTCTCTTGGCCAG 780
DB 721 AATATTCCTGTTTACCCCAAGATATTTAAGATACATTCAGAGAGTCTCTTGGCCAG 780

QY 781 GAGAAAGCAAGTATCTGATGCTTACAGAGATTCAGATTTTCAAGTGCATTTCAAG 840
DB 781 GAGAAAGCAAGTATCTGATGCTTACAGAGATTCAGATTTTCAAGTGCATTTCAAG 840
QY 841 GCAATTCATCTTACAGATGATGCTTAAACCACTCTGCTGTGATGATTTGAGACT 900
DB 841 GCAATTCATCTTACAGATGATGCTTAAACCACTCTGCTGTGATGATTTGAGACT 900
QY 901 TCAATTCAGATTTTCTTATGAGCTGAGATGCTTCAAGGATGATCTGCTTAACT 960
DB 901 TCAATTCAGATTTTCTTATGAGCTGAGATGCTTCAAGGATGATCTGCTTAACT 960
QY 961 GATTCGAGTACCAAGCTTACCAAGACTGAGCTTGAAGATTAAGAGAGAGAGAGAG 1020
DB 961 GATTCGAGTACCAAGCTTACCAAGACTGAGCTTGAAGATTAAGAGAGAGAGAGAG 1020
QY 1021 GTCTTTTGAATAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 GTCTTTTGAATAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 CCGTGGGAGATGCTCTCAAGTCTTCTGATGCTTCTGATGCTTCTGATGCTTCTG 1140
DB 1081 CCGTGGGAGATGCTCTCAAGTCTTCTGATGCTTCTGATGCTTCTGATGCTTCTG 1140
QY 1141 AAAAAGCATTTTTCGAGCCCTGTCAGTATTAACAGTGAAGTGTGAAAAAGCGCAG 1200
DB 1141 AAAAAGCATTTTTCGAGCCCTGTCAGTATTAACAGTGAAGTGTGAAAAAGCGCAG 1200
QY 1201 CTACAGAGCTGTGAGTAAACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB 1201 CTACAGAGCTGTGAGTAAACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1261 TGTGCTGCTGTTGATGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
DB 1261 TGTGCTGCTGTTGATGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
QY 1321 CTGCTGAAATCTTCTTAACTTCAACCCAGACATTTCTGTCAGTCAAGTTTAA 1380
DB 1321 CTGCTGAAATCTTCTTAACTTCAACCCAGACATTTCTGTCAGTCAAGTTTAA 1380
QY 1381 TTTCAACCAAGAAAGCTCAATTTTCTTCAATTTGATGAAATTTCTGTCAGTCA 1440
DB 1381 TTTCAACCAAGAAAGCTCAATTTTCTTCAATTTGATGAAATTTCTGTCAGTCA 1440
QY 1441 ACAAGGTTCTGCGAGAGAGATGATGAGAGCTGCTGCTGCTGCTGCTGCTGCTG 1500
DB 1441 ACAAGGTTCTGCGAGAGAGATGATGAGAGCTGCTGCTGCTGCTGCTGCTGCTG 1500
QY 1501 CTTGAGCCAAATCATGATCCCATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
DB 1501 CTTGAGCCAAATCATGATCCCATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY 1561 TCCATCTCTCTGAGCAACAAATTTTCACTTACAGATGAGCCCTCAATCCCATC 1620
DB 1561 TCCATCTCTCTGAGCAACAAATTTTCACTTACAGATGAGCCCTCAATCCCATC 1620
QY 1621 ATTAATGTTGTTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
DB 1621 ATTAATGTTGTTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
QY 1677 AAATTCAG 1736
DB 1681 AAATTCAG 1740
QY 1737 AGGATTAAGATTAAGGATTAATTTTCAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 1796
DB 1741 AGGATTAAGATTAAGGATTAATTTTCAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1797 ATCTTAATCACTTAAGGATTTCTTCTCAAGAGATGCTCTGTTGGAGAGAGAGAG 1856
DB 1801 ATCTTAATCACTTAAGGATTTCTTCTCAAGAGATGCTCTGTTGGAGAGAGAGAGAG 1860
QY 1857 CAGCAAGATTAATTAAG 1916

Db 1861 CCGAGCAAGATGATGACAAAGCAATCTCAGCTTCATGCGCAGAGGGGGAAGATCTTC 1920
Qy 1917 CTCAGAGAGAAAGGACATATTTATGTGTGAGATCAAGAAATATGCGCAAGATGTA 1976
Db 1921 CTCAGAGAGAAAGGACATATTTATGTGTGAGATCAAGAAATATGCGCAAGATGTA 1980
Qy 1977 CATGATGCTCTGTGCAATATATAGCAAGAGGTTGAGTTGAAAACTAGAAGCAATG 2036
Db 1981 CATGATGCTCTGTGCAATATATATAGCAAGAGGTTGAGTTGAAAACTAGAAGCAATG 2040
Qy 2037 AAAACCTGGCCCTTTAAAAAGAAAGAAAGCTTACCTTCAGATATATTTGTCATTA 2093
Db 2041 AAAACCTGGCCCTTTAAAAAGAAAGAAAGCTTACCTTCAGATATATTTGTCATTA 2097

RESULT 3
US-09-371-347-24
; Sequence 24, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371.347
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071.622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232.028
; PRIOR FILING DATE: 1999-01-15
; SOFTWARE: PaedSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 3259
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-24

Query Match 85.7%; Score 1793; DB 10; Length 3259;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2093; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 ATGAGAGGTTTCTGTACTATATGCTACACAGCAGGAGCAAGCAAGGCGCATGCGAGAA 60
Db 80 ATGAGAGGTTTCTGTACTATATGCTACACAGCAGGAGCAAGCAAGGCGCATGCGAGAA 139
Qy 61 GAATGTGTGAGCAAGCTGTGTGATCATGATTTTCTGCAATCTTCACTGTATTAAGTAA 120
Db 140 GAATGTGTGAGCAAGCTGTGTGATCATGATTTTCTGCAATCTTCACTGTATTAAGTAA 199
Qy 121 TCGGATAGTATGACTTAAAAACCGAAACAGCTCCTGTGTGTGTGTTGTTCTACCAAG 180
Db 200 TCGGATAGTATGACTTAAAAACCGAAACAGCTCCTGTGTGTGTGTTCTACCAAG 259
Qy 181 GGACCGGAGACCCACCGACACAGCCGCGCAAGTTTGTAAAGAAATACAGAACCAACA 240
Db 260 GGACCGGAGACCCACCGACACAGCCGCGCAAGTTTGTAAAGAAATACAGAACCAACA 319
Qy 241 CTGCGCGGTGATTTCTTTGTCTACCTGCGGTATAGGTTTACGGGTCTCGGTGATTGAA 300
Db 320 CTGCGCGGTGATTTCTTTGTCTACCTGCGGTATAGGTTTACGGGTCTCGGTGATTGAA 379
Qy 301 TACACCTACTTTTGCATAGGGGGAGATATTGATAAGACTTCAAGAGCTTGAGCC 360
Db 380 TACACCTACTTTTGCATAGGGGGAGATATTGATAAGACTTCAAGAGCTTGAGCC 439
Qy 361 CGGATTTCTATGACACTGACATGACATGACATGCTGTAGGTTTGAAGCTTGTGTGAG 420
Db 440 CGGATTTCTATGACACTGACATGACATGACATGCTGTAGGTTTGAAGCTTGTGTGAG 499
Qy 421 CCGTGATTTGCTGAGCTCTGCGCAGCCCTCAGAAAGCAATTTTAGGTCAAGCAGAGCAA 480

Db 500 CCGTGATTTGCTGAGCTCTGCGCAGCCCTCAGAAAGCAATTTTAGGTCAAGCAGAGCAA 559
Qy 481 GAGAGATTAAGTGGGCGCATCTCCGGTGGATCATCGTCACTCTTGAGGACAGACTTGTG 540
Db 560 GAGAGATTAAGTGGGCGCATCTCCGGTGGATCATCGTCACTCTTGAGGACAGACTTGTG 619
Qy 541 AAGTCAGACTGCTACATATTGAATCTCAAGTGCAGCTTCTGAGATTGATGATTCAGGA 600
Db 620 AAGTCAGACTGCTACATATTGAATCTCAAGTGCAGCTTCTGAGATTGATGATTCAGGA 679
Qy 601 AGAAGAGATTCTGAGGTTTGAAGCAAAATGCAAGTAAGCAAGCAACCAATCCAAATGTTGA 660
Db 680 AGAAGAGATTCTGAGGTTTGAAGCAAAATGCAAGTAAGCAAGCAACCAATCCAAATGTTGA 739
Qy 661 ATTGAAGCTTTGAGTCTCATCTTACCCGTTGGGTACCCCACTCTCAAGAGCTTCTG 720
Db 740 ATTGAAGCTTTGAGTCTCATCTTACCCGTTGGGTACCCCACTCTCAAGAGCTTCTG 799
Qy 721 AATATTCCTGTGTTTACCCCGAGAAATTTTACAGGTACATCTGAGAGTCTCTGGCCAG 780
Db 800 AATATTCCTGTGTTTACCCCGAGAAATTTTACAGGTACATCTGAGAGTCTCTGGCCAG 859
Qy 781 GAGGAAGCCAGTATCTGTGACTTGAAGAGATCCAGTTTCAAGTGCATTTGCAAG 840
Db 860 GAGGAAGCCAGTATCTGTGACTTGAAGAGATCCAGTTTCAAGTGCATTTGCAAG 919
Qy 841 GCAGTTCAACTTACTACGATGATGCCATTAAGCAACCACTCTGCTGTAGAAATGACATT 900
Db 920 GCAGTTCAACTTACTACGATGATGCCATTAAGCAACCACTCTGCTGTAGAAATGACATT 979
Qy 901 TCAATATCAGACTTTTCTATCAGCTCGAGATGCTTCAAGCTGATCTGCCATTAAGT 960
Db 980 TCAATATCAGACTTTTCTATCAGCTCGAGATGCTTCAAGCTGATCTGCCATTAAGT 1039
Qy 961 GATTCGAGGTACAAAGCCCTACCCAAAGCTGAGCTTGAAGATTAAGAGAGCACTGC 1020
Db 1040 GATTCGAGGTACAAAGCCCTACCCAAAGCTGAGCTTGAAGATTAAGAGAGCACTGC 1099
Qy 1021 GTCCCTTTGAAAAATAAGGACAGACAAAGAAAGAAAGAGCTTACCTTACCCAGCATATA 1080
Db 1100 GTCCCTTTGAAAAATAAGGACAGACAAAGAAAGAAAGAGCTTACCTTACCCAGCATATA 1159
Qy 1081 CTTGCGGAGATTTCTCTCAAGTTCAATTTTACTGCTGTCTTGAATTCGAGCAATTCCT 1140
Db 1160 CTTGCGGAGATTTCTCTCAAGTTCAATTTTACTGCTGTCTTGAATTCGAGCAATTCCT 1219
Qy 1141 AAAAAGCAATTTTGGAGAGCCCTGTGGAATAACAGAGACAGTGTGAAAAAGCCAGG 1200
Db 1220 AAAAAGCAATTTTGGAGAGCCCTGTGGAATAACAGAGACAGTGTGAAAAAGCCAGG 1279
Qy 1201 CTACAGAGCTGTGACAGTAAACAAAGGGGAGCCGATTAATAGCCGTTTGTACAGATGCC 1260
Db 1280 CTACAGAGCTGTGACAGTAAACAAAGGGGAGCCGATTAATAGCCGTTTGTACAGATGCC 1339
Qy 1261 TGTGCTGTGTTGGATCTCTCTGCTGCTTCCCTTCTTCCAGCCACCACTCAAGTCTC 1320
Db 1340 TGTGCTGTGTTGGATCTCTCTGCTGCTTCCCTTCTTCCAGCCACCACTCAAGTCTC 1399
Qy 1321 CTGCTGGAACATTTCTTAACTTCAACCAAGCCATTTTCGTGTCAGAGCTCAAGTTTA 1380
Db 1400 CTGCTGGAACATTTCTTAACTTCAACCAAGCCATTTTCGTGTCAGAGCTCAAGTTTA 1459
Qy 1381 TTTCAACCCAGAAAGCTCATTTTGTCTTCAACATTTGGAATTTCTGTCTATGCGACA 1440
Db 1460 TTTCAACCCAGAAAGCTCATTTTGTCTTCAACATTTGGAATTTCTGTCTATGCGACA 1519
Qy 1441 ACAAGATTTCTGGAAGGAGATGATACAGCTGAGCTGAGCTTGTGTGTTGCTTCAATT 1500
Db 1520 ACAAGATTTCTGGAAGGAGATGATACAGCTGAGCTGAGCTTGTGTGTTGCTTCAATT 1579
Qy 1501 CTTGACCCAAACATAATGATCTCCATGAAAGACAGGGGAAAGCCCTGGCTCTTAAGATA 1560

Db 1580 CTTGAGCCAAACATACATCCATCCATGAAAGACAGCGGMAAGCCCTGCTCTTAAGATA 1639
Qy 1561 TCCATCTCTCTGGAACAATCTTCCATTAACGATGACCCCTCAATCCCATC 1620
Db 1640 TCCATCTCTCTGGAACAATCTTCCATTAACGATGACCCCTCAATCCCATC 1699
Qy 1621 ATATGTTGGTTCAGGAACCGGCAATGCGCTTATTTGGTCTCAACAT---AG 1676
Db 1700 ATATGTTGGTTCAGGAACCGGCAATGCGCTTATTTGGTCTCAACATGAGAG 1759
Qy 1677 AAATCTCAAGAACACACCAATGGAATTTTGGACATGTGTTTGGTCTC 1736
Db 1760 AAATCTCAAGAACACACCAATGGAATTTTGGACATGTGTTTGGTCTC 1819
Qy 1737 AGGCAATAGGATGAGGATTAATCAATCAGAAAAGCTCAGCATTTCTTAAGATGAG 1796
Db 1820 AGGCAATAGGATGAGGATTAATCAATCAGAAAAGCTCAGCATTTCTTAAGATGAG 1879
Qy 1797 ATCTTAATCATTAAGGTTCTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1856
Db 1880 ATCTTAATCATTAAGGTTCTCTCAAGAGATGCTCTGTTGGGAGAGAGAGCC 1939
Qy 1857 CCAGCAAGATATGACAGACATCATGCTTCATGCGCAGCAGGTCGAGATCTTC 1916
Db 1940 CCAGCAAGATATGACAGACATCATGCTTCATGCGCAGCAGGTCGAGATCTTC 1999
Qy 1917 CTCGAGAGAAAGGCAATTTATGTTGATGAGATGCAAAATTTGGCCAAAGATGTA 1976
Db 2000 CTCGAGAGAAAGGCAATTTATGTTGATGAGATGCAAAATTTGGCCAAAGATGTA 2059
Qy 1977 CATGATGCTCTGCAATTAATTAAGCAAGAGTTGAGTTGAAAACTAGAGCATG 2036
Db 2060 CATGATGCTCTGCAATTAATTAAGCAAGAGTTGAGTTGAAAACTAGAGCATG 2119
Qy 2037 AAAACCTGCGCACTTTAAAGAGAAAAAGCTTACGATATTTGTCTATA 2093
Db 2120 AAAACCTGCGCACTTTAAAGAGAAAAAGCTTACGATATTTGTCTATA 2176

RESULT 4
US-09-371-347-41
; Sequence 41, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE.
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-41

Query Match 83.2%; Score 1742; DB 10; Length 2097;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2092; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

Qy 1 AAGAGAGGTTCTGTTACTATATGCTAGACAGGAGGAGGCAAGGCAATCGAGAA 60
Db 1 AAGAGAGGTTCTGTTACTATATGCTAGACAGGAGGAGGCAAGGCAATCGAGAA 60
Qy 61 GAAATGTGACAGACTGTGATCAATGATTTTCTGAGATCTTCACTGATTAAGTGA 120
Db 61 GAAATGTGACAGACTGTGATCAATGATTTTCTGAGATCTTCACTGATTAAGTGA 120

Db 61 GAAATGTGACAGACTGTGATCAATGATTTTCTGAGATCTTCACTGATTAAGTGA 120
Qy 121 TCCGATTAAGTATGACCTAATAAAGCCGAAACAGCTCTGTTGTTGTTGTTCTACAG 180
Db 121 TCCGATTAAGTATGACCTAATAAAGCCGAAACAGCTCTGTTGTTGTTGTTCTACAG 180
Qy 181 GGCACCGGAGACCCACCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
Db 181 GGCACCGGAGACCCACCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACA 240
Qy 241 CTGCGGATGATTTCTTTGCTCACTGCGGATGAGTTATCTGAGTCTCGGTATTCAGA 300
Db 241 CTGCGGATGATTTCTTTGCTCACTGCGGATGAGTTATCTGAGTCTCGGTATTCAGA 300
Qy 301 TACACCTACTTTTGCAATGGGGGAAAGATTAATGATTAACAGACTTCAAGAGCTGAGCC 360
Db 301 TACACCTACTTTTGCAATGGGGGAAAGATTAATGATTAACAGACTTCAAGAGCTGAGCC 360
Qy 361 CGGCAATTTCTATGACACTGACATGCAATGACATGCTGTGATGATTTAGAACCTTGTTAG 420
Db 361 CGGCAATTTCTATGACACTGACATGCAATGACATGCTGTGATGATTTAGAACCTTGTTAG 420
Qy 421 CCGTGAATGCTGACCTGCGCAGGCTCAGAAACATTTTAAAGTCAAGCAGAGACA 480
Db 421 CCGTGAATGCTGACCTGCGCAGGCTCAGAAACATTTTAAAGTCAAGCAGAGACA 480
Qy 481 GAGGAGATTAAGTGGGCACTCCCGGTGATACCTGATCTCTTGAAGCACAACCTTG 540
Db 481 GAGGAGATTAAGTGGGCACTCCCGGTGATACCTGATCTCTTGAAGCACAACCTTG 540
Qy 541 AAGTCAAGCTCTCACTCAATGATCTCAATGATCTCAATGATCTCAATGATCTCAATG 600
Db 541 AAGTCAAGCTCTCACTCAATGATCTCAATGATCTCAATGATCTCAATGATCTCAATG 600
Qy 601 AGAAAGATTTGAGGTTTGAAGCAAAATGCAATGCAAGCAAGCAATTCATGTTGA 660
Db 601 AGAAAGATTTGAGGTTTGAAGCAAAATGCAATGCAAGCAAGCAATTCATGTTGA 660
Qy 661 ATTGAAGCTTGAAGCTTCACTTACCGGTTGGTATCCCGCACTCTCAAGGCTCTCG 720
Db 661 ATTGAAGCTTGAAGCTTCACTTACCGGTTGGTATCCCGCACTCTCAAGGCTCTCG 720
Qy 721 AATATTCCTGTTTACCCCGCAAGATTTTACAGTATCTGAGAGTCTCTGCGCAG 780
Db 721 AATATTCCTGTTTACCCCGCAAGATTTTACAGTATCTGAGAGTCTCTGCGCAG 780
Qy 781 GAGGAAAGCAATGATGATGATCTTCAAGAGATTCAGATTCAGATTCAGATTCAGAT 840
Db 781 GAGGAAAGCAATGATGATGATCTTCAAGAGATTCAGATTCAGATTCAGATTCAGAT 840
Qy 841 GCGATTCATTAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 900
Db 841 GCGATTCATTAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 900
Qy 901 TCAAAATACAGACTTTTCTTATGAGCTGAGATGCTTCAAGGATCTGAGGATCTG 960
Db 901 TCAAAATACAGACTTTTCTTATGAGCTGAGATGCTTCAAGGATCTGAGGATCTG 960
Qy 961 GATTCGAGTACCAAGCTCTCAAGAGCTGAGCTTGAAGATTAAGAGAGAGAGAGAG 1020
Db 961 GATTCGAGTACCAAGCTCTCAAGAGCTGAGCTTGAAGATTAAGAGAGAGAGAGAG 1020
Qy 1021 GTTCCTTTGAAATTAAGGAGACACAAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1021 GTTCCTTTGAAATTAAGGAGACACAAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 1080
Qy 1081 CCGCGGAGATGTTCTCTCAAGTTCAATTTTACCTGATCTTGAATCCGAGCAATTCCT 1140
Db 1081 CCGCGGAGATGTTCTCTCAAGTTCAATTTTACCTGATCTTGAATCCGAGCAATTCCT 1140
Qy 1141 AAAAGGCAATTTTTCAGAGCTTGTGAGCTATACAGTACAGTGTGAGAGAGAGAG 1200
Db 1141 AAAAGGCAATTTTTCAGAGCTTGTGAGCTATACAGTACAGTGTGAGAGAGAGAG 1200

1201 CTACAGAGCTGTGCACTAAACAAAGGGGAGCCGATTAATAGCCGTTTGTACAGATGCG 1260
1201 CTACAGAGCTGTGCACTAAACAAAGGGGAGCCGATTAATAGCCGTTTGTACAGATGCG 1260
1261 TGTGCTGCTGTGTGGATCTCTCTCTGCTTTCCCTTTCTTGCAAGCACAAGTCTC 1320
1261 TGTGCTGCTGTGTGGATCTCTCTCTGCTTTCCCTTTCTTGCAAGCACAAGTCTC 1320
1261 TGTGCTGCTGTGTGGATCTCTCTCTGCTTTCCCTTTCTTGCAAGCACAAGTCTC 1320
1321 CTGCTGGAACATCTTCTTAACTTCAACCCAGACATATTCGATGCAAGCTCAAGTTTA 1380
1321 CTGCTGGAACATCTTCTTAACTTCAACCCAGACATATTCGATGCAAGCTCAAGTTTA 1380
1381 TTTCACCCAGAAAGCTCCATTTTGTCTTCAAGATTTGATGCAAGTCTTCTACAGCA 1440
1381 TTTCACCCAGAAAGCTCCATTTTGTCTTCAAGATTTGATGCAAGTCTTCTACAGCA 1440
1441 ACAGAGGTTCTGCGAAAGGAGATGATACAGGCTGCTGCTTTGTTGTTGCTTCACT 1500
1441 ACAGAGGTTCTGCGAAAGGAGATGATACAGGCTGCTGCTTTGTTGTTGCTTCACT 1500
1501 CTTCAGCAGAAACATACATGATCCCATGAGAGAGGAGGAGAGCCCTGCTCTCAAGATA 1560
1501 CTTCAGCAGAAACATACATGATCCCATGAGAGAGGAGGAGAGCCCTGCTCTCAAGATA 1560
1561 TCCATCTCTCTGGAACAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
1561 TCCATCTCTCTGGAACAAACAAATTTCTTCACTTACAGATGACCCCTCAATCCCATC 1620
1621 ATATAGTGGGTCCAGGAACCGGATGACCCCGTTTATGAGTTTCTTCAACAT---AG 1676
1621 ATATAGTGGGTCCAGGAACCGGATGACCCCGTTTATGAGTTTCTTCAACAT---AG 1676
1677 AAATCTCAAGAAACAACCCAGATGAAATTTTGGAGCAATGATGTTGTTTGGCTGC 1736
1677 AAATCTCAAGAAACAACCCAGATGAAATTTTGGAGCAATGATGTTGTTTGGCTGC 1736
1681 AAATCTCAAGAAACAACCCAGATGAAATTTTGGAGCAATGATGTTGTTTGGCTGC 1740
1681 AAATCTCAAGAAACAACCCAGATGAAATTTTGGAGCAATGATGTTGTTTGGCTGC 1740
1737 AGGATTAAGATAGGATTAATCTTCAAGAAAGAGCTCAGACATTTCTTAAAGATGG 1796
1737 AGGATTAAGATAGGATTAATCTTCAAGAAAGAGCTCAGACATTTCTTAAAGATGG 1796
1741 AGGATTAAGATAGGATTAATCTTCAAGAAAGAGCTCAGACATTTCTTAAAGATGG 1800
1741 AGGATTAAGATAGGATTAATCTTCAAGAAAGAGCTCAGACATTTCTTAAAGATGG 1800
1797 ATCTTAATCTTAAAGGTTTCTTCTCAAGAGATGCTCTGTTGGAGAGAGAGAGCC 1856
1797 ATCTTAATCTTAAAGGTTTCTTCTCAAGAGATGCTCTGTTGGAGAGAGAGAGAGCC 1856
1801 ATCTTAATCTTAAAGGTTTCTTCTCAAGAGATGCTCTGTTGGAGAGAGAGAGCC 1860
1801 ATCTTAATCTTAAAGGTTTCTTCTCAAGAGATGCTCTGTTGGAGAGAGAGAGCC 1860
1857 CAGAGAAAGATGATCAAGACATCATGATGATGATGATGATGATGATGATGATGATGAT 1916
1857 CAGAGAAAGATGATCAAGACATCATGATGATGATGATGATGATGATGATGATGATGAT 1916
1861 CAGAGAAAGATGATCAAGACATCATGATGATGATGATGATGATGATGATGATGATGAT 1920
1861 CAGAGAAAGATGATCAAGACATCATGATGATGATGATGATGATGATGATGATGATGAT 1920
1917 CTTCAGAGAAAGGATTAATTTATGTTGTGAGATGATGATGATGATGATGATGATGAT 1976
1917 CTTCAGAGAAAGGATTAATTTATGTTGTGAGATGATGATGATGATGATGATGATGATGAT 1976
1921 CTTCAGAGAAAGGATTAATTTATGTTGTGAGATGATGATGATGATGATGATGATGATGAT 1980
1921 CTTCAGAGAAAGGATTAATTTATGTTGTGAGATGATGATGATGATGATGATGATGATGAT 1980
1977 CATGATGCTCTTGTGCAAAATTAATGAGAGAGTTGAGTTGAAAACTGAGAGCATG 2036
1977 CATGATGCTCTTGTGCAAAATTAATGAGAGAGTTGAGTTGAAAACTGAGAGCATG 2036
1981 CATGATGCTCTTGTGCAAAATTAATGAGAGAGTTGAGTTGAAAACTGAGAGCATG 2040
1981 CATGATGCTCTTGTGCAAAATTAATGAGAGAGTTGAGTTGAAAACTGAGAGCATG 2040
2037 AAAAGCTGAGCACTTAAAGAAAGAAAGAAAGCTTCAAGATGATTTGATGATTA 2093
2037 AAAAGCTGAGCACTTAAAGAAAGAAAGAAAGCTTCAAGATGATTTGATGATTA 2093
2041 AAAAGCTGAGCACTTAAAGAAAGAAAGAAAGCTTCAAGATGATTTGATGATTA 2097
2041 AAAAGCTGAGCACTTAAAGAAAGAAAGAAAGCTTCAAGATGATTTGATGATTA 2097

RESULT 5
US-09-371-347-43
; Sequence 43. Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE;
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371.347

; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 2097
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-43

Query Match 83.2%; Score 1742; DB 10; Length 2097;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2092; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

1 ATGAGAGGTTTCTGTTACTATATGCTTACACAGAGGAGACAGGCAAGCCATCCGAGAA 60
1 ATGAGAGGTTTCTGTTACTATATGCTTACACAGAGGAGACAGGCAAGCCATCCGAGAA 60
61 GAAATGTGAGAGAGCTGAGTACATGATTTTCTGAGATCTTCACTGATTAATGATA 120
61 GAAATGTGAGAGAGCTGAGTACATGATTTTCTGAGATCTTCACTGATTAATGATA 120
121 TCCGATTAAGTACCTTAAACCCGAAACAGCTCTTGTGTTGTTGTTTCTACACG 180
121 TCCGATTAAGTACCTTAAACCCGAAACAGCTCTTGTGTTGTTGTTTCTACACG 180
181 GGCACCGGAGACCCACCCGACACAGCCCGGCAAGTTGTTAAGAAATACAGAACCA 240
181 GGCACCGGAGACCCACCCGACACAGCCCGGCAAGTTGTTAAGAAATACAGAACCA 240
181 GGCACCGGAGACCCACCCGACACAGCCCGGCAAGTTGTTAAGAAATACAGAACCA 240
241 CTGCGGTTGATTTCTTCTGCTCACTGCGGATGAGTTACTGGGCTCGGTTGATGAA 300
241 CTGCGGTTGATTTCTTCTGCTCACTGCGGATGAGTTACTGGGCTCGGTTGATGAA 300
301 TACACCTACTTTTGAATGAGGAGGAGATTAATGATTAACGACTTCAAGAGCTTGA 360
301 TACACCTACTTTTGAATGAGGAGGAGATTAATGATTAACGACTTCAAGAGCTTGA 360
301 TACACCTACTTTTGAATGAGGAGGAGATTAATGATTAACGACTTCAAGAGCTTGA 360
361 CGGATTTCTATGACCTGACATGAGATGATGATGATGATGATGATGATGATGATGAT 420
361 CGGATTTCTATGACCTGACATGAGATGATGATGATGATGATGATGATGATGATGAT 420
421 CGGTGATGCTGAGCTCTGCGCAGCCCTCAGAAACATTTTGAAGTCAAGAGAGCAA 480
421 CGGTGATGCTGAGCTCTGCGCAGCCCTCAGAAACATTTTGAAGTCAAGAGAGCAA 480
481 GAGAGATTAAGTGGGCACTCCCGATGATCACTGATCTTGAAGACAGACTTGTG 540
481 GAGAGATTAAGTGGGCACTCCCGATGATCACTGATCTTGAAGACAGACTTGTG 540
481 GAGAGATTAAGTGGGCACTCCCGATGATCACTGATCTTGAAGACAGACTTGTG 540
541 AAGTCAAGCTGTACACATTTGAATCTCAAGTGAAGTCTTGAAGTCAAGTCAAGTCA 600
541 AAGTCAAGCTGTGTACACATTTGAATCTCAAGTGAAGTCTTGAAGTCAAGTCAAGTCA 600
541 AAGTCAAGCTGTGTACACATTTGAATCTCAAGTGAAGTCTTGAAGTCAAGTCAAGTCA 600
601 AGAAGGATTTCTGAGGTTTGAAGCAAAATGAGTGAACAGCAACCAATCCATGTTGTA 660
601 AGAAGGATTTCTGAGGTTTGAAGCAAAATGAGTGAACAGCAACCAATCCATGTTGTA 660
601 AGAAGGATTTCTGAGGTTTGAAGCAAAATGAGTGAACAGCAACCAATCCATGTTGTA 660
661 ATTGAAGCTTTGAGTCTTCACTTACCCGTTGGTACCCCACTCTCAAGGCTCTCTG 720
661 ATTGAAGCTTTGAGTCTTCACTTACCCGTTGGTACCCCACTCTCAAGGCTCTCTG 720
721 AATATTCCTGTTTACCCCAAGATTTTAATGAGTCACTTGAAGAGTCTCTTGGCAG 780
721 AATATTCCTGTTTACCCCAAGATTTTAATGAGTCACTTGAAGAGTCTCTTGGCAG 780
721 AATATTCCTGTTTACCCCAAGATTTTAATGAGTCACTTGAAGAGTCTCTTGGCAG 780
781 GAGGAAGCAAGATATCTGATCTTCAAGAGATCCAGTCTTCAAGTCAAGTCAAGTCA 840
781 GAGGAAGCAAGATATCTGATCTTCAAGAGATCCAGTCTTCAAGTCAAGTCAAGTCA 840
781 GAGGAAGCAAGATATCTGATCTTCAAGAGATCCAGTCTTCAAGTCAAGTCAAGTCA 840

Oy	841	GCAGTTCAACTTACATCAAGAAATGAGCCATAAAAAACA	CTCGCTGAGTAAATTTGAACTT	900
Dp	841	GCAGTTCAACTTACATCAAGAAATGAGCCATAAAAAACA	CTCGCTGAGTAAATTTGAACTT	900
Oy	901	TCAATAACAGACTTTCCTATCAGCTTGAGATGCTTCAG	CGCTGATCTGCCCTTAACAGT	960
Dp	901	TCAATAACAGACTTTCCTATCAGCTTGAGATGCTTCAG	CGCTGATCTGCCCTTAACAGT	960
Oy	961	GATTCTGAGGTACAAAGCTTACTCCAAAGACTGCACTT	GAAAGATAAAGAGCACTGC	1020
Dp	961	GATTCTGAGGTACAAAGCTTACTCCAAAGACTGCACTT	GAAAGATAAAGAGCACTGC	1020
Oy	1021	GTCCCTTTGAAAAATPAAAGCAGACAAAGAAAGAAAG	AGGTACTTAAACCCACATATA	1080
Dp	1021	GTCCCTTTGAAAAATPAAAGCAGACAAAGAAAGAAAG	AGGTACTTAAACCCACATATA	1080
Oy	1081	CCTGCGGGATGTTCTCTCAGTTCATTTTACCTGATCT	CTTGAAATCCAGCAATTCCT	1140
Dp	1081	CCTGCGGGATGTTCTCTCAGTTCATTTTACCTGATCT	CTTGAAATCCAGCAATTCCT	1140
Oy	1141	AAAAAGGCATTTTTGCGAGCCCTTGATGACTATAC	CAGTGTGAAGACGCAAGG	1200
Dp	1141	AAAAAGGCATTTTTGCGAGCCCTTGATGACTATAC	CAGTGTGAAGACGCAAGG	1200
Oy	1201	CTACAGAGCTGTGTGATPAAACAGGGCAGCCGATT	TAGCCGCTTTGTATGAGATGCC	1260
Dp	1201	CTACAGAGCTGTGTGATPAAACAGGGCAGCCGATT	TAGCCGCTTTGTATGAGATGCC	1260
Oy	1261	TGTGCTGCTGTTGATCTGCTGCTGCTTCCCTTTC	TCGACGACCACTAGTCTC	1320
Dp	1261	TGTGCTGCTGTTGATCTGCTGCTGCTTCCCTTTC	TCGACGACCACTAGTCTC	1320
Oy	1321	CTGCTCGAACACTCTTCTTAACTTCAACCCAGAC	CAATATTCGTGTGCAAGCTCAAGTTTA	1380
Dp	1321	CTGCTCGAACACTCTTCTTAACTTCAACCCAGAC	CAATATTCGTGTGCAAGCTCAAGTTTA	1380
Oy	1381	TTTTCACCCAGAAAAGCTTCATTTTGTCTTCAAC	ATTGTGTGAATTTCTGTCTATCTGCCACA	1440
Dp	1381	TTTTCACCCAGAAAAGCTTCATTTTGTCTTCAAC	ATTGTGTGAATTTCTGTCTATCTGCCACA	1440
Oy	1441	ACAGAGGTCTGCGGAGAGGAGTATGTACAGGCTG	CGGCTTGTTGCTTCACTGTT	1500
Dp	1441	ACAGAGGTCTGCGGAGAGGAGTATGTACAGGCTG	CGGCTTGTTGCTTCACTGTT	1500
Oy	1501	CTTCAAGCCAAACATACATGATCCCATGAAACAG	ACGGGGAAGCCCTGACTTAAGATA	1560
Dp	1501	CTTCAAGCCAAACATACATGATCCCATGAAACAG	ACGGGGAAGCCCTGACTTAAGATA	1560
Oy	1561	TCATCTCTCTCGAACCAAAATTCCTTCACTTAC	CAAGATGACCCCTCAATCCCATTC	1620
Dp	1561	TCATCTCTCTCGAACCAAAATTCCTTCACTTAC	CAAGATGACCCCTCAATCCCATTC	1620
Oy	1621	ATATATGTGTGGTCCAGGAACCGGCAATGACCC	CGTTATTTGGGTTCTTACATAGAGAG	1680
Dp	1621	ATATATGTGTGGTCCAGGAACCGGCAATGACCC	CGTTATTTGGGTTCTTACATAGAGAG	1680
Oy	1677	AAACTCCAAAGAACACCCAGATGGAATTTTGGAG	CAATGTGTTTGGCTGC	1736
Dp	1677	AAACTCCAAAGAACACCCAGATGGAATTTTGGAG	CAATGTGTTTGGCTGC	1736
Oy	1681	AAACTCCAAAGAACACCCAGATGGAATTTTGGAG	CAATGTGTTTGGCTGC	1736
Dp	1681	AAACTCCAAAGAACACCCAGATGGAATTTTGGAG	CAATGTGTTTGGCTGC	1736
Oy	1737	AGGCAATAGATAGGATTAATCTATTCGAAAAGAG	CTCAGACATTTCTTAAGCATGGG	1796
Dp	1737	AGGCAATAGATAGGATTAATCTATTCGAAAAGAG	CTCAGACATTTCTTAAGCATGGG	1796
Oy	1797	ATCTTAACTCATCTTAAAGGTTTCCTTCAAGAG	ATGTCTCTGTGTGGGAGAGAAAGCC	1860
Dp	1797	ATCTTAACTCATCTTAAAGGTTTCCTTCAAGAG	ATGTCTCTGTGTGGGAGAGAAAGCC	1860
Oy	1857	CCAGCAAGTATGTACAGAACACATCCAGCTTCA	TGCGACAGAGTGGCAGAACTCTC	1916
Dp	1857	CCAGCAAGTATGTACAGAACACATCCAGCTTCA	TGCGACAGAGTGGCAGAACTCTC	1916
Oy	1917	CTCAGAGGAACGGCATATTTATGTGTGAGAGT	CAAAAGAAATATGGCCAAAGATGTA	1976

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Db      1921 CTCGAGAGAACGCCCATATTTTAATGTGTGTGAGATGCAGAAATATGTGCCAAGATGTA 1980
QY      1977 CATGATGCCCTTGTGTGCAAAATATATAGCAAGAGGTTGAGTGTGAAAACTAGAAAGCAATG 2036
Db      1981 CATGATGCCCTTGTGTGCAAAATATATAGCAAGAGGTTGAGTGTGAAAACTAGAAAGCAATG 2040
QY      2037 AAAACCTGTGGCACTTTTAAAAAGAAAGAAAAAGCGTAACTTCAGAGATATTGTGCTATTA 2093
Db      2041 AAAACCTGTGGCACTTTTAAAAAGAAAGAAAAAGCGTAACTTCAGAGATATTGTGCTATTA 2097

RESULT 6
US-09-371-347-45
; Sequence 45, Application US/09371347
; Publication No. US20030082676A1
; GENERAL INFORMATION:
; APPLICANT: Roy A. Gravel et al.
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
; TITLE OF INVENTION: CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBES
; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/003003
; CURRENT APPLICATION NUMBER: US/09/371,347
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/071,622
; PRIOR FILING DATE: 1998-01-16
; PRIOR APPLICATION NUMBER: 09/232,028
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-371-347-45

Query Match      80.1%; Score 1677; DB 10; Length 2094;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGAGGAGGTTCTGTTACTTATGCTTACACAGAGAGGAGACAGCAAGGCCATGGCAGAA 60
Db      1 ATGAGGAGGTTCTGTTACTTATGCTTACACAGAGAGGAGACAGCAAGGCCATGGCAGAA 60
QY      61 GAAATGTGTGAGCAAGCTGTGTGATCATGAGATTTCTGCAGATCTTCACTGATTAGTGAA 120
Db      61 GAAATGTGTGAGCAAGCTGTGTGATCATGAGATTTCTGCAGATCTTCACTGATTAGTGAA 120
QY      121 TCCGATTAAGTATGACCTTAAAAACCGAAACAGCTCCTTGTGTGTGTGTTCTTACACAG 180
Db      121 TCCGATTAAGTATGACCTTAAAAACCGAAACAGCTCCTTGTGTGTGTGTTCTTACACAG 180
QY      181 GGCACCGGAGACCCACCCGACACACAGCCCGCAAGTTTGTTAAGAAATACAGAACCAACA 240
Db      181 GGCACCGGAGACCCACCCGACACACAGCCCGCAAGTTTGTTAAGAAATACAGAACCAACA 240
QY      241 CTGCGCGGTGATTTCTTTTGTGCTCACCTGCGGTATGGGTTACTCGGGTCTCGGTGATTCA 300
Db      241 CTGCGCGGTGATTTCTTTTGTGCTCACCTGCGGTATGGGTTACTCGGGTCTCGGTGATTCA 300
QY      301 TACACCTTACTTTTGCAATGGGGGGAGATTAATTGATTAACGACTTCAAGACTTGGAGCC 360
Db      301 TACACCTTACTTTTGCAATGGGGGGAGATTAATTGATTAACGACTTCAAGACTTGGAGCC 360
QY      361 CGGCAATTTCTATGACATCTGACATAGCAGATGACCTGTGTGATTTTGAACCTTGTGTGAG 420
Db      361 CGGCAATTTCTATGACATCTGACATAGCAGATGACCTGTGTGATTTTGAACCTTGTGTGAG 420
QY      421 CCGTGATATTGTGCACTCTGGCCAGCCCTCGAAGAGCAATTTTAGTCAAGCAGAGACA 480
Db      421 CCGTGATATTGTGCACTCTGGCCAGCCCTCGAAGAGCAATTTTAGTCAAGCAGAGACA 480
QY      481 GAGGAGATTAATGGCGCACTCCCGGTGGCATCACTTGATCTTTGAGAGACAGACTTGTG 540

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481 GAGGAAATTAAGTGGCGACTCCGGTGGCATCACTGGCATCTTGGAGACAGACTTGTG 540
541 AAGTCAGAGCTGTACACATTTGAATCTCAAGTCAGAGCTTCTGAGATTCGATTCAGGA 600
541 AAGTCAGAGCTGTACACATTTGAATCTCAAGTCAGAGCTTCTGAGATTCGATTCAGGA 600
601 AGAAGGATTCGAGCTTTGAAAGCAAAATGAGTGAACAGCAACCAATCCATGTTGTA 660
601 AGAAGGATTCGAGCTTTGAAAGCAAAATGAGTGAACAGCAACCAATCCATGTTGTA 660
661 ATTAAGACTTTAGTCTCACTTACCCGTTGGGTACCCCACTCTCAAGGCTCTG 720
661 ATTAAGACTTTAGTCTCACTTACCCGTTGGGTACCCCACTCTCAAGGCTCTG 720
721 AATATTCGTGTTTACCCCGAATATTTTACAGGTATCTGAGAGAGTCTTGGCCAG 780
721 AATATTCGTGTTTACCCCGAATATTTTACAGGTATCTGAGAGAGTCTTGGCCAG 780
781 GAGGAAAGCCAGATATCTGTGACTTCAAGCATTCAGTCTTCAAGTCCATTTCAAG 840
781 GAGGAAAGCCAGATATCTGTGACTTCAAGCATTCAGTCTTCAAGTCCATTTCAAG 840
841 GCAGTCAACTTACTGAGATGATGCAATTAACCACTGCTGGTGAATTTGACAT 900
841 GCAGTCAACTTACTGAGATGATGCAATTAACCACTGCTGGTGAATTTGACAT 900
901 TCAATATCAGACTTTTCTTCACTCAAGCTGAGATGCTTCAAGCTTCAAGCTTCAAGT 960
901 TCAATATCAGACTTTTCTTCACTCAAGCTGAGATGCTTCAAGCTTCAAGCTTCAAGT 960
961 GATTCGAGGTACAAAGCTTCTCAAGCATCTGAGATGCTTCAAGGTAAAGAGAGCATGC 1020
961 GATTCGAGGTACAAAGCTTCTCAAGCATCTGAGATGCTTCAAGGTAAAGAGAGCATGC 1020
1021 GTCTTTTGAATTAAGGAGACACAAAGAGAGAGGAGTACTTACCCCGACATTA 1080
1021 GTCTTTTGAATTAAGGAGACACAAAGAGAGAGGAGTACTTACCCCGACATTA 1080
1081 CCGTGGGATGTTCTCTCAAGTCAATTTTACCTGCTTGAATCCGAGCAATTTCT 1140
1081 CCGTGGGATGTTCTCTCAAGTCAATTTTACCTGCTTGAATCCGAGCAATTTCT 1140
1141 AAAAAGGCAATTTTGGAGAGCCCTTGTGACATTAACAGTGAAGTCTGAAAAGCCGAG 1200
1141 AAAAAGGCAATTTTGGAGAGCCCTTGTGACATTAACAGTGAAGTCTGAAAAGCCGAG 1200
1201 CTACAGAGGCTGTGAGTGAACAAAGGAGGAGCCGATTAATAGCCGCTTGAAGAGATGCC 1260
1201 CTACAGAGGCTGTGAGTGAACAAAGGAGGAGCCGATTAATAGCCGCTTGAAGAGATGCC 1260
1261 TGTGCTGCTGTGTGATCT 1320
1261 TGTGCTGCTGTGTGATCT 1320
1321 CTGCTGGAACATCTTCTTAACTTCAACCAAGACCAATATTCGTGTGAGAGCTCAAGTTA 1380
1321 CTGCTGGAACATCTTCTTAACTTCAACCAAGACCAATATTCGTGTGAGAGCTCAAGTTA 1380
1381 TTTCACCCAGAGAAAGCTTCTTGAATCTGATGATGATGATGATGATGATGATGATGAT 1440
1381 TTTCACCCAGAGAAAGCTTCTTGAATCTGATGATGATGATGATGATGATGATGATGAT 1440
1441 ACAGAGGTTCTGCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
1441 ACAGAGGTTCTGCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
1501 CTTCAGGCTTCTGCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
1501 CTTCAGGCTTCTGCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
1561 TTCAATCT 1620
1561 TTCAATCT 1620

1561 TTCAATCT 1620
1621 AATATGTTGGGTTCAGAGAACCGGACATAGCCCGTATTATGGGTTCTTACACATAGA 1677
1621 AATATGTTGGGTTCAGAGAACCGGACATAGCCCGTATTATGGGTTCTTACACATAGA 1677
RESULT 7
US-10-741-600-692
; Sequence 692, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: PatsSeq for Windows Version 4.0
; SEQ ID NO 692
; LENGTH: 3256
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-692
Query Match 42.0%; Score 879; DB 21; Length 3256;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1579; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
67 TGTGAGCAGCTGTGTATCATGATTTTCTGAGATCTTCACTGATTAAGTGAATCCGAT 126
160 TGTGAGCAGCTGTGTATCATGATTTTCTGAGATCTTCACTGATTAAGTGAATCCGAT 219
127 AAGTATGACTTAAACCGAAACAGCTCTCTGTTGTGTGTTCTACACAGGCGACC 186
220 AAGTATGACTTAAACCGAAACAGCTCTCTGTTGTGTGTTCTACACAGGCGACC 279
187 GAGAGCCACCGGACACAGCCCGCAAGTTGTTAAGAAATACAAACCAACATGCGG 246
280 GAGAGCCACCGGACACAGCCCGCAAGTTGTTAAGAAATACAAACCAACATGCGG 339
247 GTTATTTCTTTGCTACCTGCGGTATGAGTTATCTGGGTCTGGGTATTCAGAAATCAC 306
340 GTTATTTCTTTGCTACCTGCGGTATGAGTTATCTGGGTCTGGGTATTCAGAAATCAC 399
307 TACTTTGCAATGGGAGGAAATATGATTAACGACTTCAAGAGCTTGAAGCCGCGCAT 366
400 TACTTTGCAATGGGAGGAAATATGATTAACGACTTCAAGAGCTTGAAGCCGCGCAT 459
367 TTCTATGACATGACATGACATGACATGATGATGATGATGATGATGATGATGATGATGAT 426
460 TTCTATGACATGACATGACATGACATGATGATGATGATGATGATGATGATGATGATGAT 519
427 ATGCTGACATCTGCGAGAGCCCTCAGAAAGCAATTTTATAGTCAAGAGAGCAAGGAG 486
520 ATGCTGACATCTGCGAGAGCCCTCAGAAAGCAATTTTATAGTCAAGAGAGCAAGGAG 579
487 ATAGTGGGCACTCCCGGTGATCACTGACCTCTTGAAGAGCAAGCTTGAAGTCA 546
580 ATAGTGGGCACTCCCGGTGATCACTGACCTCTTGAAGAGCAAGCTTGAAGTCA 639
547 GAGCTCTACATTAATCTCAAGTCAAGCTTCTGAGATTCGATGATTCAGAGAGAG 606
640 GAGCTCTACATTAATCTCAAGTCAAGCTTCTGAGATTCGATGATTCAGAGAGAG 659
607 GATTCGAGGTTTGAAGCAAAATGAGTGAACAGCAACCAATCCATGTTGTAATGAA 666
700 GATTCGAGGTTTGAAGCAAAATGAGTGAACAGCAACCAATCCATGTTGTAATGAA 759
667 GACTTGAAGCTCACTTACCCGTTGGGTACCCCACTCTCAAGGCTCTGAAATAT 726
760 GACTTGAAGCTCACTTACCCGTTGGGTACCCCACTCTCAAGGCTCTGAAATAT 819

QY 727 CCTGTTTACCCCGAATATTATTCAGATACATCTGACAGAGTCTCTTGCCGACAGAGAA 786
 DB 820 CCGGTTTACCCCGAATATTATTCAGATACATCTGACAGAGTCTCTTGCCGACAGAGAA 879
 QY 787 AGCCAAATCTGTGATCTTCAAGATCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTT 846
 DB 880 AGCCAAATCTGTGATCTTCAAGATCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTT 939
 QY 847 CAATCTACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 906
 DB 940 CAATCTACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 999
 QY 907 ACAGACTTTTCTATCAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 966
 DB 1000 ACAGACTTTTCTATCAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1059
 QY 967 GAGGTACAAAGCTTCTCAAAAGCTGCAAGTCTTGAAGATGATGATGATGATGATGATGATGAT 1026
 DB 1060 GAGGTACAAAGCTTCTCAAAAGCTGCAAGTCTTGAAGATGATGATGATGATGATGATGATGAT 1119
 QY 1027 TTGAATAATTAAGGACGACAAAGAAAGAGAGTACTTACCCGAGATATTAAGTCTGAG 1086
 DB 1120 TTGAATAATTAAGGACGACAAAGAAAGAGAGTACTTACCCGAGATATTAAGTCTGAG 1179
 QY 1087 GATGTTCTCTCAGATCTTCTTCTGATCTTGAATCTGATCTTGAATCTTGAATCTTGAATCTT 1146
 DB 1180 GATGTTCTCTCAGATCTTCTTCTGATCTTGAATCTTGAATCTTGAATCTTGAATCTTGAATCTT 1239
 QY 1147 GCAATTTTTCGAGACCTGTTGATCTTACAGTGAAGTCTGATGATGATGATGATGATGATGATGAT 1206
 DB 1240 GCAATTTTTCGAGACCTGTTGATCTTACAGTGAAGTCTGATGATGATGATGATGATGATGATGAT 1299
 QY 1207 GAGCTGTGAGTAAACAAGGACGACGATTAAGGCTTGTGAAGATGATGATGATGATGATGATGATGAT 1266
 DB 1300 GAGCTGTGAGTAAACAAGGACGACGATTAAGGCTTGTGAAGATGATGATGATGATGATGATGATGAT 1359
 QY 1267 TGCCTGTGAGTCTCTCTGCTGCTTCT 1326
 DB 1360 TGCCTGTGAGTCTCTCTGCTGCTTCT 1419
 QY 1327 GAACATCTTCTTAACTTCAACCCAGACCAATATGATGATGATGATGATGATGATGATGATGATGAT 1386
 DB 1420 GAACATCTTCTTAACTTCAACCCAGACCAATATGATGATGATGATGATGATGATGATGATGATGAT 1479
 QY 1387 CAGAGAAAGCTCTATTTTCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1446
 DB 1480 CAGAGAAAGCTCTATTTTCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1539
 QY 1447 GTTCTGCGAAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1506
 DB 1540 GTTCTGCGAAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1599
 QY 1507 CCAAAATATCATGATCTCCATGAGACAGCGGAAAGCCCTGCTCTTAAGATATCATC 1566
 DB 1600 CCAAAATATCATGATCTCCATGAGACAGCGGAAAGCCCTGCTCTTAAGATATCATC 1659
 QY 1567 TCTCTCTGAAACAATTTCTTCTCACTTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1626
 DB 1660 TCTCTCTGAAACAATTTCTTCTCACTTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1719
 QY 1627 GTGGGTCCAGAAACCGGATAGCCCGTTATT 1659
 DB 1720 GTGGGTCCAGAAACCGGATAGCCCGTTATT 1752

RESULT 8
 US-10-741-600-693

; Sequence 693, Application US/10741600
 ; Publication No. US20050026169A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001499
 ; CURRENT APPLICATION NUMBER: US/10/741,600
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 73997
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 693
 ; LENGTH: 3274
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-741-600-693

Query Match 42.0%; Score 879; DB 21; Length 3274;
 Best Local Similarity 99.1%; Pred. No. 0;
 Matches 1579; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 67 TGTGACAAAGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 126
 DB 178 TGTGACAAAGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 237
 QY 127 AAGTATGACCTAAACCGGAAACAGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 186
 DB 238 AAGTATGACCTAAACCGGAAACAGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 297
 QY 187 GGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACACTGCGG 246
 DB 298 GGAGACCCACCCGACACAGCCCGCAAGTTGTTAAGAAATACAGAACCAACACTGCGG 357
 QY 247 GTTGAATTTCTTCTCAGCTGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 306
 DB 358 GTTGAATTTCTTCTCAGCTGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 417
 QY 307 TACTTTTGAAGGGGGGGAATTAATGATTAACAGCTTCAAGAGCTTGAAGCCCGGACAT 366
 DB 418 TACTTTTGAAGGGGGGGAATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAAT 477
 QY 367 TTCTATGACACTGACATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426
 DB 478 TTCTATGACACTGACATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 537
 QY 427 ATTGTGACCTGTGACAGCCCTCAAGAAAGATTTAAGTCAAGACAGACAGAGAG 486
 DB 538 ATTGTGACCTGTGACAGCCCTCAAGAAAGATTTAAGTCAAGACAGACAGAGAG 597
 QY 487 ATTAAGTGGGACCTCCCGGTGATCACTGATCTCTTGAAGACAGACCTTGTGAAGTCA 546
 DB 598 ATTAAGTGGGACCTCCCGGTGATCACTGATCTCTTGAAGACAGACCTTGTGAAGTCA 657
 QY 547 GAGCTGTACATGAT 606
 DB 658 GAGCTGTACATGAT 717
 QY 607 GATTCGAGTTTGAAGCAAAATGAGTGAACAGCAACCAATCCAAATGTTGAATGAA 666
 DB 718 GATTCGAGTTTGAAGCAAAATGAGTGAACAGCAACCAATCCAAATGTTGAATGAA 777
 QY 667 GACTTGAAGTCTCACTTAACCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 726
 DB 778 GACTTGAAGTCTCACTTAACCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 837
 QY 727 CCGGTTTACCCCGAATATTATTCAGATACATCTGACAGAGTCTCTTGCCGACAGAGAA 786
 DB 838 CCGGTTTACCCCGAATATTATTCAGATACATCTGACAGAGTCTCTTGCCGACAGAGAA 897
 QY 787 AGCCAAATCTGTGATCTTCAAGATCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTT 846
 DB 898 AGCCAAATCTGTGATCTTCAAGATCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTT 957
 QY 847 CAATCTACTAGAT 906
 DB 958 CAATCTACTAGAT 1017
 QY 907 ACAGACTTTTCTATCAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 966

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Db 1018 ACAGACTTTTCTATACGCTGAGAGATGCTTACGGGTGATCTGCCCTTAACATGATTTCT 1077
Qy 967 GAGGTACAAAGCTTACTCCAAAGACTGCACTTGAAGATAAAGAGAGACACTGCTCTT 1026
Db 1078 GAGGTACAAAGCTTACTCCAAAGACTGCACTTGAAGATAAAGAGAGACACTGCTCTT 1137
Qy 1027 TTGAAAAATTAAGGACAGACAAAGAAAGAGACTTACTTACCCAGCATATACCTGGG 1086
Db 1138 TTGAAAAATTAAGGACAGACAAAGAAAGAGACTTACTTACCCAGCATATACCTGGG 1197
Qy 1087 GAGTGTCTCTCAGTTCATTTTAACTGGTGTCTGAATCGAGAAATCTCTTAAAG 1146
Db 1198 GAGTGTCTCTCAGTTCATTTTAACTGGTGTCTGAATCGAGAAATCTCTTAAAG 1257
Qy 1147 GCATTTTTCGAGACCTTGTGGACTATACAGTACAGTCTGAAAAAGCCAGCTTACG 1206
Db 1258 GCATTTTTCGAGACCTTGTGGACTATACAGTACAGTCTGAAAAAGCCAGCTTACG 1317
Qy 1207 GAGCTGTGCAGTAAACAAGGGGAGCCGATTAATAGCCGCTTTGTAGAGATGCTGTGCC 1266
Db 1318 GAGCTGTGCAGTAAACAAGGGGAGCCGATTAATAGCTTGTAGAGATGCTGTGCC 1377
Qy 1267 TGCTTGTGATCTCTCCCTCGCTTCCCTTCCCTTCCGAGCCACCACTCACTCTCCGCTC 1326
Db 1378 TGCTTGTGATCTCTCCCTCGCTTCCCTTCCCTTCCGAGCCACCACTCACTCTCCGCTC 1437
Qy 1327 GAACATCTTCTTAACTTCAACCCAGACATATTCGTGTCAGAGCTCAAGTTTATTTTAC 1386
Db 1438 GAACATCTTCTTAACTTCAACCCAGACATATTCGTGTCAGAGCTCAAGTTTATTTTAC 1497
Qy 1387 CCAAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTGTCTTACCTGCACAAAGAG 1446
Db 1498 CCAAGAAAGCTCCATTTTGTCTTCAACATTTGTGAATTTGTCTTACCTGCACAAAGAG 1557
Qy 1447 GTTCTGGGAGGAGATATGATACAGGCTGGCTGTGCTTGTGTTGTTCAATTTCTTACG 1506
Db 1558 GTTCTGGGAGGAGATATGATACAGGCTGGCTGTGCTTGTGTTGTTCAATTTCTTACG 1617
Qy 1507 CCAACATACATGATCCCATGAAAGACAGGCGGAAAGCCCTGGCTCTTAAGATATCCATC 1566
Db 1618 CCAACATACATGATCCCATGAAAGACAGGCGGAAAGCCCTGGCTCTTAAGATATCCATC 1677
Qy 1567 TCTCTCGAACAACAATTTCTTTCACATTAACAGATGACCCCTCAATCCCATCATATG 1626
Db 1678 TCTCTCGAACAACAATTTCTTTCACATTAACAGATGACCCCTCAATCCCATCATATG 1737
Qy 1627 GTGGGTCCAGGAACCGGATATGCCCCCTTATT 1659
Db 1738 GTGGGTCCAGGAACCGGATATGCCCCCTTATT 1770

RESULT 9
US-10-029-386-6369
; Sequence 6369, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: ABOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 6369
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008727.5
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; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.45
; OTHER INFORMATION: NT HIT: AF121205.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUE 3.30e+00
; OTHER INFORMATION: EST_HUMAN HIT: AU132586.1, EVALUE 0.00e+00
US-10-029-386-6369

Query Match 15.8%; Score 330; DB 16; Length 591;
Best Local Similarity 99.7%; Pred. No. 7,9e-170;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 401 GTTTAGAACTTGTGTTGAGCCGTGATTTGTCGACTCTGCGCAGCCCTCAGAAAGCAT 460
Db 38 GTTTAGAACTTGTGTTGAGCCGTGATTTGTCGACTCTGCGCAGCCCTCAGAAAGCAT 97
Qy 461 TTAGGTCAAGCAGAGGACAAAGAGATTAAGTGGCCCATCCCGGGGATCATCCTGCAT 520
Db 98 TTAGGTCAAGCAGAGGACAAAGAGATTAAGTGGCCCATCCCGGGGATCATCCTGCAT 157
Qy 521 CCTGAGGACAGACCTTGTGAAGTCAAGCTGCTACATTAATGATCAAGTGCAGCTTC 580
Db 158 CCTGAGGACAGACCTTGTGAAGTCAAGCTGCTACATTAATGATCAAGTGCAGCTTC 217
Qy 581 TGAGATTGATGATTCAGAGAAAGAAAGATTTGAGGTTTGAAGCAAAATGACAGTAA 640
Db 218 TGAGATTGATGATTCAGAGAAAGAAAGATTTGAGGTTTGAAGCAAAATGACAGTAA 277
Qy 641 GCAACCAATCCAATGTTGTAATTAAGACTTTGAGTCTCACTTACCCGTTGGTACCC 700
Db 278 GCAACCAATCCAATGTTGTAATTAAGACTTTGAGTCTCACTTACCCGTTGGTACCC 337
Qy 701 CACTTCAAGGCTTCTGATATTCCTGTTTACCCTCAAGAAATTTTACAGGTATATC 760
Db 338 CACTTCAAGGCTTCTGATATTCCTGTTTACCCTCAAGAAATTTTACAGGTATATC 397
Qy 761 TGCAGAGTCTCTTGGCCAGG 781
Db 398 TGCAGAGTCTCTTGGCCAGG 418

RESULT 10
US-10-029-386-20100
; Sequence 20100, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: ABOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20100
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008727.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.45
; OTHER INFORMATION: NT HIT: g114729757, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUE 1.80e+00
; OTHER INFORMATION: EST_HUMAN HIT: AU132586.1, EVALUE 0.00e+00
US-10-029-386-20100

Query Match 15.7%; Score 328; DB 16; Length 379;
Best Local Similarity 99.7%; Pred. No. 9,7e-169;
Matches 378; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 402 TTGGAACCTTGTGTTGAGCCGTGATTTGTCGACTCTGCGCAGCCCTCAGAAAGCAT 461
Db 1 TTGGAACCTTGTGTTGAGCCGTGATTTGTCGACTCTGCGCAGCCCTCAGAAAGCAT 60
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QY 462 TAGTCAAGCAGAGCAAGAGAGTAAGTGGCGCACTCCGGTGGCATCCTGCAATC 521
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|
DB 61 TAGTCAAGCAGAGCAAGAGAGTAAGTGGCGCACTCCGGTGGCATCCTGCAATC 120
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QY 522 CTTGAGACAGACTTTGTAGAGTCAAGAGTCTTACATTAATCTCAAGTGAAGTTCT 581
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|
|
DB 121 CTCGAGACAGACTTTGTAGAGTCAAGAGTCTTACATTAATCTCAAGTGAAGTTCT 180
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QY 562 GAGATTTGATGATTCAGAGAAAGAGATTCAGAGTTTGAAGCAAAATGCAATGAAACG 641
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DB 181 GAGATTTGATGATTCAGAGAAAGAGATTCAGAGTTTGAAGCAAAATGCAATGAAACG 240
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|
QY 642 CAACCAATCAATGTTGTAATTTGAAGACTTGAAGTCTTACATTAATCTCAAGTGAAGTTCT 701
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|
|
DB 241 CAACCAATCAATGTTGTAATTTGAAGACTTGAAGTCTTACATTAATCTCAAGTGAAGTTCT 300
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|
QY 702 ACTCTCAAGAGCTCTCTGAATATTTCTGAGTTTACCCCGAATATTTTACAGGTACATCT 761
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|
DB 301 ACTCTCAAGAGCTCTCTGAATATTTCTGAGTTTACCCCGAATATTTTACAGGTACATCT 360
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QY 762 GAGAGAGTCTCTTGGCCAG 780
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DB 361 GAGAGAGTCTCTTGGCCAG 379
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RESULT 11
US-10-029-386-1735
; Sequence 1735, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 1735
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021609.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
; OTHER INFORMATION: NT HIT: AF121205.1, EVALUR 0.00e+00
; OTHER INFORMATION: EST HUMAN HIT: AU132586.1, EVALUR 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUR 3.30e+00
US-10-029-386-1735
Query Match 13.3%; Score 279; DB 16; Length 591;
Best Local Similarity 99.5%; Pred. No. 8.4e-142;
Matches 379; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 581 TGAGATTCATGATTCAGAGAAAGAGATTCAGAGTTTGAAGCAAAATGCAATGAAACA 640
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DB 218 TGAGATTCATGATTCAGAGAAAGAGATTCAGAGTTTGAAGCAAAATGCAATGAAACA 277
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QY 641 GCAACCAATCAATGTTGTAATTTGAAGACTTGAAGTCTTACATTAATCTCAAGTGAAGTTCT 700
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DB 278 GCAACCAATCAATGTTGTAATTTGAAGACTTGAAGTCTTACATTAATCTCAAGTGAAGTTCT 337
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|
QY 701 CACTCTCAAGAGCTCTCTGAATATTTCTGAGTTTACCCCGAATATTTTACAGGTACATC 760
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DB 338 CACTCTCAAGAGCTCTCTGAATATTTCTGAGTTTACCCCGAATATTTTACAGGTACATC 397
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QY 761 TGCAGAGTCTCTTGGCCAG 781
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DB 398 TGCAGAGTCTCTTGGCCAG 418
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RESULT 12
US-10-029-386-15435
; Sequence 15435, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David R.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 15435
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021609.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
; OTHER INFORMATION: SWISSPROT HIT: Q9UPW0, EVALUR 1.80e+00
; OTHER INFORMATION: EST HUMAN HIT: AU132586.1, EVALUR 0.00e+00
; OTHER INFORMATION: NT HIT: G114729757, EVALUR 0.00e+00
US-10-029-386-15435
Query Match 13.2%; Score 277; DB 16; Length 379;
Best Local Similarity 99.5%; Pred. No. 1e-140;
Matches 377; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	702	ACCTCACAAGCCTCTCTGATATTCGGATTACCCCAATATTTCAGGTAATCT	761
Db	301	ACTCTCAACAAGCCTCTCTGATATTCGGATTACCCCAATATTTCAGGTAATCT	360
QY	762	GCAGAGATCTCTTTGGCCAG	780
Db	361	GCAGAGATCTCTTTGGCCAG	379

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RESULT 13
US-10-741-600-17757
; Sequence 17757, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 17757
; LENGTH: 43985
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-17757

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Query Match	12.7%	Score 266;	DB 21;	Length 43985;
Best Local Similarity	99.5%	Pred. No. 1.4e-134;		
Matches 366; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	401	GTTTAGAACTTGTGGTGAACCGTGATTCCTGAACCTTGACAGCCCTCAGAAAGCATT	460
Db	14836	GTTTAGAACTTGTGGTGAACCGTGATTCCTGAACCTTGACAGCCCTCAGAAAGCATT	14895
QY	461	TTAAGTCAMCAGAGCAAGCAAGAGAGATTAAGTGCCGCACTCCCGATGACATCCTGCAT	520
Db	14896	TTAAGTCAMCAGAGCAAGAGAGATTAAGTGCCGCACTCCCGATGACATCCTGCAT	14955
QY	521	CCTTGAGGACAGACCTTTGTGAAGTCAGAGCTGCTACACATTGAAATTCAGATCGAGCTTC	580
Db	14956	CCTTGAGGACAGACCTTTGTGAAGTCAGAGCTGCTACACATTGAAATTCAGATCGAGCTTC	15015
QY	581	TGAGATTGATGATTCAGAGAAAGGATTCAGAGTTTGAAGCAAAATGCAAGTGAACA	640
Db	15016	TGAGATTGATGATTCAGAGAAAGGATTCAGAGTTTGAAGCAAAATGCAAGTGAACA	15075
QY	641	GCAACCAATCCAAATGTTGTAATTTGAAGACTTGAAGTCTCACTTACCCGTCGGTACCCC	700
Db	15076	GCAACCAATCCAAATGTTGTAATTTGAAGACTTGAAGTCTCACTTACCCGTCGGTACCCC	15135
QY	701	CACCTTCACAAAGCCTCTCTGAATATTCCTGTGTTACCCCCAGAAATATTTACAGGTACATC	760
Db	15136	CACCTTCACAAAGCCTCTCTGAATATTCCTGTGTTACCCCCAGAAATATTTACAGGTACATC	15195
QY	761	TGCAGGAG 768	
Db	15196	TGCAGGAG 15203	

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RESULT 14
US-10-029-386-633/C
: Sequence 633, Application US/10029386
: Publication No. US20030194704A1
: GENERAL INFORMATION:
:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEOTIC ACID PROBES USEFUL FOR G
: TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
: FILE REFERENCE: AEOmica-x-2

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Query Match	9.0%	Score 188	DB 16	length 525
Best Local Similarity	100.0%	Pred. No. 8.7e-92		
Matches 188; Conservative	0	Mismatches	0	Indels 0; Gaps 0;

Oy	1761	TTGAGAAAAGGCTGCACACATTTCTCTTAAGGATGGATCTTAATCTAAAGTTTCC	1820
Db	234	TTGAGAAAAGGCTGCACACATTTCTCTTAAGCATGGATCTTAATCTAAAGTTTCC	175
Oy	1821	TTCTCAAGAGATGCTCCTGTGGGAGAGAGAGAGAGAGAGAGAGATGTATCAAGACAC	1880
Db	174	TTCTCAAGAGATGCTCCTGTGGGAGAGAGAGAGAGAGAGAGAGATGTATCAAGACAC	115
Oy	1881	ATCCAGCTTCATGGCCACAGATGGCGAGATCTCTCTCCAGAGAAAGCGGCATATTTAT	1940
Db	114	ATCCAGCTTCATGGCCACAGATGGCGAGATCTCTCTCCAGAGAAAGCGGCATATTTAT	55
Oy	1941	GTGTGTGG	1948
Db	54	GTGTGTGG	47

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RESULT 15
US-10-029-386-14338/C
; Sequence 14338, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CH
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: ABOICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 14338
; LENGTH: 175
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021609.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.48
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.58
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.52
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.57
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.79
; OTHER INFORMATION: SWISSPROT HIT: O61608, EVALUE 4.00e-04
; OTHER INFORMATION: EST HUMAN HIT: AA085543.1, EVALUE 7.00e-94
; OTHER INFORMATION: NT HIT: g113325067, EVALUE 5.00e-94
US-10-029-386-14338

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Query Match 8.48; Score 175; DB 16; Length 175;

Best Local Similarity 100.0%; Pred. No. 1.1e-84;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1766 AAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAATCATCTAAAGTTTCTTCTC 1825
 Db 175 AAAAGAGCTCAGACATTTCTTAAGCATGGATCTTAATCATCTAAAGTTTCTTCTC 116
 Qy 1826 AAGAGATGCTCCTGTTGGGAGAGAGAGCCAGCAAGTATGTACAGACAAATCCA 1885
 Db 115 AAGAGATGCTCCTGTTGGGAGAGAGAGCCAGCAAGTATGTACAGACAAATCCA 56
 Qy 1886 GCTTCATGGCCAGCAGATGGCCGAAATCTCTCCAGAGAAAGGCCATATTTAT 1940
 Db 55 GCTTCATGGCCAGCAGATGGCCGAAATCTCTCCAGAGAAAGGCCATATTTAT 1

Search completed: August 27, 2005, 17:33:35
 Job time : 901.684 secs

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